

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:48:24 ; Search time 15.7143 Seconds
(without alignments)
97.882 Million cell updates/sec

Title: US-09-674-716B-3
Perfect score: 81
Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	112	1 KWS16	Ig kappa chain V r
2	81	100.0	113	1 KWS51	Ig kappa chain V r
3	81	100.0	120	1 KWS67	Ig kappa chain pre
4	81	100.0	120	2 A29775	Ig kappa chain pre
5	81	100.0	120	2 B29775	Ig kappa chain pre
6	66	81.5	112	2 PL0273	Ig kappa chain V r
7	65	80.2	133	2 S40324	Ig kappa chain V r
8	64	79.0	83	2 S34095	Ig kappa chain V r
9	64	79.0	111	2 S20709	Ig kappa chain V r
10	64	79.0	120	2 S42267	Ig kappa chain V r
11	64	79.0	120	2 S42268	Ig kappa chain V r
12	64	79.0	133	1 K2HURP	Ig kappa chain pre
13	63	77.8	114	2 S49572	Ig kappa chain pre
14	61	75.3	101	2 PH1057	Ig light chain V r
15	61	75.3	113	1 K2HURF	Ig kappa chain V r
16	61	75.3	122	2 S40338	Ig kappa chain V r
17	60	74.1	112	2 PL0275	Ig kappa chain V r
18	60	74.1	133	2 S42611	Ig kappa chain V r
19	60	74.1	249	2 S41374	HUNVK protein Fv an
20	59	72.8	87	2 S34094	Ig kappa chain V r
21	59	72.8	91	2 S42186	Ig kappa chain V r
22	59	72.8	101	2 A33730	Ig kappa chain V r
23	59	72.8	103	2 PH1055	Ig light chain V r
24	59	72.8	103	2 PH1056	Ig light chain V r
25	59	72.8	112	2 A36259	Ig kappa chain V r
26	59	72.8	113	2 F30360	Ig kappa chain V r
27	59	72.8	132	2 C32513	Ig kappa chain pre
28	59	72.8	133	2 S23230	Ig kappa chain pre
29	59	72.8	140	2 S22658	Ig kappa chain pre

RESULT 1

KWS16

Ig kappa chain V region (M167) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996

C:Accession: A01908

R:Rudikoff, S.; Potter, M.

Biochemistry 17, 2703-2707, 1978

A:Title: kappa-Chain variable region from M167, a phosphorylcholine binding myeloma prot

A:Reference number: A01908; MUID:79000273; PMID:99160

A:Accession: A01908

A:Molecule type: protein

A:Residues: 1-112 <RUD>

C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-95/Domain: immunoglobulin homology <IMM>

F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 112;

Best Local Similarity 100.0%; Pred. No. 3.1e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16

Db 24 RSSKSLLYKDGKTYLN 39

RESULT 2

KWS51

Ig kappa chain V region (M511) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000

C:Accession: A01910

R:Appella, E.

Mol. Immunol. 17, 711-718, 1980

A:Title: Amino acid sequence of the light chain variable region of M511, a phosphorylch

A:Reference number: A01910; MUID:81052016; PMID:6776396

A:Accession: A01910

A:Molecule type: protein

A:Residues: 1-113 <APP>

C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-95/Domain: immunoglobulin homology <IMM>

F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 113;

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Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSKSLLYKDGKTYLN 39

RESULT 3
KWS67
Ig kappa chain precursor V region (VK167) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000
C:Accession: A01909
R:Jouvin-Marche, E.; Rudikoff, S.
Cell 25, 47-58, 1981
A:Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
A:Reference number: A01909; MUID:8200223; PMID:6791832
A:Accession: A01909
A:Molecule type: DNA
A:Residues: 1-120 <SEL>
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted

Query Match 100.0%; Score 81; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 44 RSSKSLLYKDGKTYLN 59

RESULT 4
A29775
Ig kappa chain precursor V region (mouse 24.2) - shrew mouse
C:Species: Mus pahari
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C:Accession: A29775
R:Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A:Title: Evolution of a V-kappa gene family.
A:Reference number: A91751; MUID:87006895; PMID:3093373
A:Accession: A29775
A:Molecule type: DNA
A:Residues: 1-120 <JOU>
A:Cross-references: GB:M1552; NID:gl97468; PIDN:AAA39036.1; PID:gl97469
A>Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region 24.2 #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 81; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 41 RSSKSLLYKDGKTYLN 59

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Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSKSLLYKDGKTYLN 39

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RESULT 3
KWS67
Ig kappa chain precursor V region (VK167) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000
C:Accession: A01909
R:Jouvin-Marche, E.; Rudikoff, S.
Cell 25, 47-58, 1981
A:Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
A:Reference number: A01909; MUID:8200223; PMID:6791832
A:Accession: A01909
A:Molecule type: DNA
A:Residues: 1-120 <SEL>
A>Note: the sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>
F:43-113/Disulfide bonds: #status predicted

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Query Match 100.0%; Score 81; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 44 RSSKSLLYKDGKTYLN 59

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RESULT 4
A29775
Ig kappa chain precursor V region (mouse 24.2) - shrew mouse
C:Species: Mus pahari
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C:Accession: A29775
R:Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A:Title: Evolution of a V-kappa gene family.
A:Reference number: A91751; MUID:87006895; PMID:3093373
A:Accession: A29775
A:Molecule type: DNA
A:Residues: 1-120 <JOU>
A:Cross-references: GB:M1552; NID:gl97468; PIDN:AAA39036.1; PID:gl97469
A>Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region 24.2 #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

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Query Match 100.0%; Score 81; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 41 RSSKSLLYKDGKTYLN 59

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RESULT 5
B29775
Ig kappa chain precursor V region (mouse 24.1) - shrew mouse
C:Species: Mus pahari
C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
C:Accession: B29775
R:Jouvin-Marche, E.; Rudikoff, S.
Immunogenetics 24, 191-201, 1986
A:Title: Evolution of a V-kappa gene family.
A:Reference number: A91751; MUID:87006895; PMID:3093373
A:Accession: B29775
A:Molecule type: DNA
A:Residues: 1-120 <JOU>
A:Cross-references: GB:M1553; NID:gl97470; PIDN:AAA39037.1; PID:gl97471
A>Note: this sequence was determined from the germline gene
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-120/Product: Ig kappa chain V region 24.1 #status predicted <MAT>
F:36-115/Domain: immunoglobulin homology <IMM>

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Query Match 100.0%; Score 81; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 44 RSSKSLLYKDGKTYLN 59

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RESULT 6
PL0273
Ig kappa chain V region (anti-DNA, D23VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0273
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A:Reference number: PL0231; MUID:90111618; PMID:2104919
A:Accession: PL0273
A:Molecule type: mRNA
A:Residues: 1-112 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:16-95/Domain: immunoglobulin homology <IMM>
F:24-39/Region: complementarity-determining 1
F:40-54/Region: framework 2
F:55-61/Region: complementarity-determining 2
F:62-93/Region: framework 3
F:94-102/Region: complementarity-determining 3
F:103-112/Region: framework 4

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Query Match 81.5%; Score 66; DB 2; Length 112;
Best Local Similarity 75.0%; Pred. No. 0.00097;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 24 KSSQSLLYRNGKTYLN 39

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RESULT 7
S40324
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40324
R:Klein, R.; Jaenichen, R.; Zachau, H.G.

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Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40324
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-133 <KLE>
A:Cross-references: EMBL:X72434
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-112/Domain: immunoglobulin homology <IMM>

Query Match 80.2%; Score 65; DB 2; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.0017; Mismatches 2; Indels 0; Gaps 0;
Matches 12; Conservative 2

QY 1 RSSKSLLYKDGKTYLN 16
|||:||||
Db 41 RSDQSLVYSDGNTYLN 56

RESULT 8
S34095
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S34095
R:Wagner, S.D.; Luzzatto, L.
Eur. J. Immunol. 23, 391-397, 1993
A:Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distributed
A:Reference number: S34076; MUID:93170387; PMID:8436174
A:Accession: S34095
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-83 <WAG>
A:Cross-references: EMBL:X67179
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-80/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 64; DB 2; Length 83;
Best Local Similarity 75.0%; Pred. No. 0.0015; Mismatches 2; Indels 0; Gaps 0;
Matches 12; Conservative 2

QY 1 RSSKSLLYKDGKTYLN 16
|||:||||
Db 9 RSSQSLVYSDGNTYLN 24

RESULT 9
S20709
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S20709
R:Brennan, D.M.; Hinds, M.G.; Welsh, J.H.; Tempest, P.R.; Harris, W.J.; Carr, F.J.; Osb
submitted to the EMBL Data Library, April 1992
A:Description: Binding specificity and variable region sequences of two monoclonal anti
A:Reference number: S20706
A:Accession: S20709
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-111 <BRE>
A:Cross-references: EMBL:Z11917; NID:G52655; PIDN:CAA77975.1; PID:G52656
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 64; DB 2; Length 111;
Best Local Similarity 75.0%; Pred. No. 0.0021; Mismatches 3; Indels 0; Gaps 0;
Matches 12; Conservative 3

QY 1 RSSKSLLYKDGKTYLN 16

Db 24 KSSQSLVYSDGKTYLN 39
|||:||||
RESULT 10
S42267
Ig kappa chain V region (A1) - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: S42267
R:Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zc
Eur. J. Immunol. 22, 1023-1029, 1992
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated A regi
A:Reference number: A49043; MUID:92201291; PMID:1551402
A:Accession: S42267
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <LAU>
A:Cross-references: EMBL:X63402
C:Genetics:
A:Introns: 17/3
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 64; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 0.0022; Mismatches 2; Indels 0; Gaps 0;
Matches 12; Conservative 2

QY 1 RSSKSLLYKDGKTYLN 16
|||:||||
Db 44 RSSQSLVYSDGNTYLN 59

RESULT 11
S42268
Ig kappa chain V region (A17) - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jan-2000
C:Accession: S42268
R:Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.; Zc
Eur. J. Immunol. 22, 1023-1029, 1992
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated A regi
A:Reference number: A49043; MUID:92201291; PMID:1551402
A:Accession: S42268
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <LAU>
A:Cross-references: EMBL:X63403
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 79.0%; Score 64; DB 2; Length 120;
Best Local Similarity 75.0%; Pred. No. 0.0022; Mismatches 2; Indels 0; Gaps 0;
Matches 12; Conservative 2

QY 1 RSSKSLLYKDGKTYLN 16
|||:||||
Db 44 RSSQSLVYSDGNTYLN 59

RESULT 12
K2HURP
Ig kappa chain precursor V-II region (RPM1) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 15-Aug-1997
C:Accession: A01890
R:Klobeck, H.G.; Meindl, A.; Combrato, G.; Solomon, A.; Zachau, H.G.
Nucleic Acids Res. 13, 6499-6513, 1985
A:Title: Human immunoglobulin kappa light chain genes of subgroups II and III.
A:Reference number: A93588; MUID:86041852; PMID:2997711
A:Accession: A01890

A:Molecule type: DNA

A:Residues: 1-133 <KLO>

A>Note: the sequence was determined from the differentiated gene

C:Genetics:

A:Gene: GDB:IGKV2

A:Cross-references: GDB:136265

A:Map position: 2p12-2p12

A:Introns: 1/11

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-133/Product: Ig kappa chain V-II region (RPMI) #status predicted <MAT>

F:21-43/Region: framework 1

F:36-115/Domain: immunoglobulin homology <IMM>

F:44-59/Region: complementarity-determining 1

F:60-74/Region: framework 2

F:75-81/Region: complementarity-determining 2

F:82-113/Region: framework 3

F:114-122/Region: complementarity-determining 3

F:123-133/Region: framework 4

F:43-113/Disulfide bonds: #status predicted

Query Match 79.0%; Score 64; DB 1; Length 133;

Best Local Similarity 75.0%; Pred. No. 0.0025;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16

DB 44 RSSQSLVTDGNTYLN 59

RESULT 13

S49572

Ig kappa chain precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Mar-1995 #sequence_revision 14-Jul-1995 #text_change 21-Jan-2000

C:Accession: S49572

R:Giachino, C.; Padovan, E.; Lanzavecchia, A.

submitted to the EMBL Data Library, November 1994

A:Description: K+1+ dual receptor B cells are present in the human peripheral repertoire

A:Reference number: S49571

A:Accession: S49572

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-114 <GIA>

A:Cross-references: EMBL:Z46626; NID:G575261; PIDN:CAAB6596.1; PID:G575262

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 77.8%; Score 63; DB 2; Length 114;

Best Local Similarity 75.0%; Pred. No. 0.0031;

Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16

DB 24 RSSQSLVTDGNTYLN 39

RESULT 14

PH1057

Ig light chain V region (clone 17a.145) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: PH1057

R:Tillman, D.M.; Jov, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IGM and Igg anti-DNA antibodies are the products of clonally selective B c

A:Reference number: PH0971; MUID:92381444; PMID:1512540

A:Accession: PH1057

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-101 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 75.3%; Score 61; DB 2; Length 101;

Best Local Similarity 80.0%; Pred. No. 0.0059;

Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 15

DB 24 RSSQSLVTDGNTYLN 38

RESULT 15

K2HUFR

Ig kappa chain V-II region (Fr) - human (tentative sequence)

C:Species: Homo sapiens (man)

C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000

C:Accession: A01886

R:Riesen, W.F.; Jaton, J.C.

Biochemistry 15, 3829-3833, 1976

A:Affile: Variable region sequence of the light chain from a Waldenstrom's Igm with spec

A:Reference number: A01886; MUID:76253627; PMID:821524

A:Accession: A01886

A:Molecule type: protein

A:Residues: 1-113 <RTB>

C:Comment: This chain was isolated from a Waldenstrom's macroglobulin that binds phospho

C:Genetics:

A:Gene: GDB:IGKV2

A:Cross-references: GDB:136265

A:Map position: 2p12-2p12

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer

F:16-95/Domain: immunoglobulin homology <IMM>

F:23-93/Disulfide bonds: #status predicted

Query Match 75.3%; Score 61; DB 1; Length 113;

Best Local Similarity 62.5%; Pred. No. 0.0067;

Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16

DB 24 RSSQSLVTRBGETYLN 39

Search completed: April 22, 2003, 12:54:45

Job time : 16.7143 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:46:53 ; Search time 8 Seconds
(without alignments)
82.953 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81

Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	81	100.0	112	1 KV2A_MOUSE	P01626 mus musculus
2	81	100.0	113	1 KV2C_MOUSE	P01628 mus musculus
3	81	100.0	120	1 KV2B_MOUSE	P01627 mus musculus
4	64	79.0	133	1 KV2F_HUMAN	P06310 homo sapien
5	61	75.3	113	1 KV2B_HUMAN	P01615 homo sapien
6	55	67.9	113	1 KV2F_MOUSE	P01630 mus musculus
7	54	66.7	113	1 KV2G_MOUSE	P01631 mus musculus
8	53	65.4	113	1 KV2D_HUMAN	P01617 homo sapien
9	52	64.2	113	1 KV2E_MOUSE	P03376 mus musculus
10	46.5	57.4	115	1 KV2A_HUMAN	P01614 homo sapien
11	45	55.6	117	1 KV2E_HUMAN	P06309 homo sapien
12	43	53.1	437	1 ERR1_YEAST	P42222 saccharomyc
13	42	51.9	343	1 Y535_METJA	Q57955 methanococc
14	41	50.6	112	1 KV2D_MOUSE	P01629 mus musculus
15	41	50.6	891	1 ACON_LEGPN	P37032 legionella
16	40	49.4	87	1 R31B_PALSO	Q8Y062 raietonia s
17	40	49.4	478	1 AMY_STRAY	P08486 streptomyce
18	40	49.4	481	1 GPGD_DROME	P41572 drosophila
19	40	49.4	713	1 ETF2_YABAM	Q9qb84 yaba monkey
20	39.5	48.8	134	1 KV4C_HUMAN	P06314 homo sapien
21	39	48.1	213	1 ZN80_CERAE	P51502 cercopithe
22	39	48.1	293	1 ZN80_MACMU	P51505 macaca mula
23	39	48.1	473	1 SNAC_BACSU	P05655 bacillus su
24	39	48.1	478	1 NIFE_METH	O27607 methanobact
25	39	48.1	561	1 YBJL_ECOLI	P75812 escherichia
26	39	48.1	561	1 YBJL_SALTI	Q8z851 salmonella
27	39	48.1	561	1 YBJL_SALTI	Q8z851 salmonella
28	39	48.1	562	1 YD26_YERPE	Q8zgh1 yersinia pe
29	39	48.1	580	1 GGT_ECOLI	P18956 escherichia
30	38	46.9	135	1 Y545_RICPR	Q9zd01 rickettsia
31	38	46.9	213	1 VTXE_BACSU	P06568 bacillus su
32	38	46.9	216	1 YDCM_METS1	P43368 methylophil
33	38	46.9	262	1 LPXA_SALTI	Q8z9a2 salmonella

34 38 46.9 262 1 LPXA_SALTI P32200 salmonella
35 38 46.9 262 1 LPXA_YERPE Q8zbs6 yersinia pe
36 38 46.9 273 1 ZN80_GORGO P51503 gorilla gor
37 38 46.9 273 1 ZN80_HUMAN P51504 homo sapien
38 38 46.9 284 1 F100_LEIMA P22045 leishmania
39 38 46.9 314 1 TOPI_VACCV P08585 vaccinia vi
40 38 46.9 314 1 TOPI_VARV P32989 variola vir
41 38 46.9 474 1 UCR2_EUGGR P43265 euglena gra
42 38 46.9 506 1 TRPE_YEAST P00899 saccharomyc
43 38 46.9 711 1 ETF2_MXVL Q9gk4 myxoma viru
44 38 46.9 711 1 ETF2_SFVKA Q9gk4 myxoma viru
45 38 46.9 714 1 GP85_TRYCR Q03877 trypanosoma

ALIGNMENTS

RESULT 1
KV2A_MOUSE STANDARD; PRT; 112 AA.
ID KV2A_MOUSE
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79000273; PubMed=99160;
RA Rudikoff S, Potter M.;
RT "kappa Chain variable region from M167, a phosphorylcholine binding
myeloma protein.";
RL Biochemistry 17:2703-2707(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY
CHAIN HAS ALSO BEEN DETERMINED.
PIR: A01908: KVMS16.
DR HSSP; P80362; IWTIL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;
Query Match 100.0%; Score 81; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. NO. 2.7e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSSKSLLYKDGKTYLN 16
DB 24 RSSKSLLYKDGKTYLN 39
RESULT 2
KV2C_MOUSE STANDARD; PRT; 113 AA.
ID KV2C_MOUSE
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE Ig kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RL phosphorylcholine-binding murine myeloma protein.";
RT Mol. Immunol. 17:711-718 (1980).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A01910; KVM551.
DR HSSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT CHAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EPR0DC4DA2B03450 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSKSLLYKDGKTYLN 39

RESULT 3
KV2B MOUSE STANDARD; PRT; 120 AA.
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VKAPPAL67 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82002223; PubMed=6791832;
RA Selsing E., Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region
RL genes.";
CC Cell 25:47-58 (1981).
CC -----
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CC -----
DR EMBL; J00562; AAA39032.1; -.
DR EMBL; K02415; AAA39051.1; -.
DR PIR; A01909; KVM567.
DR HSSP; P80362; IWL.

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 120
FT DOMAIN 21 43
FT DOMAIN 44 59
FT DOMAIN 60 74
FT DOMAIN 75 81
FT DOMAIN 82 113
FT DOMAIN 114 120
FT DISULFID 43 113
SQ SEQUENCE 120 AA; 13280 MW; 63BB571F0E4DE3E8 CRC64;

Query Match 100.0%; Score 81; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 3e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 44 RSSKSLLYKDGKTYLN 59

RESULT 4
KV2F HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Weindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RL III.";
CC Nucleic Acids Res. 13:6499-6513 (1985).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z00020; CAA77315.1; -.
DR PIR; A01890; KZHURP.
DR HSSP; P80362; IWL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133
FT DOMAIN 21 43
FT DOMAIN 44 59
FT DOMAIN 60 74
FT DOMAIN 75 81
FT DOMAIN 82 113
FT DOMAIN 114 122
FT DOMAIN 123 132
FT DISULFID 43 113
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

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Query Match      79.0%; Score 64; DB 1; Length 133;
Best Local Similarity 75.0%; Pred. No. 0.00032;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 44 RSSQSLVYSGNTYLN 59

RESULT 5
KV2B HUMAN
ID_KV2B HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=76253627; PubMed=821524;
RA Riessen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUPR.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
FW DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match      75.3%; Score 61; DB 1; Length 113;
Best Local Similarity 62.5%; Pred. No. 0.00089;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16
Db 24 RSSQSLVYREGTYLB 39

RESULT 6
KV2F MOUSE
ID_KV2F MOUSE STANDARD; PRT; 113 AA.
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX MEDLINE=83256427; PubMed=6409088;

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RA Chang J.-Y., Herbst H., Aebersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
light chains from a mouse hybridoma-derived anti-(streptococcal group
A polysaccharide) antibody containing an additional cysteine residue.
Application of the dimethylaminoazobenzene isothiocyanate technique
for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -1- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
CC PIR; A01913; KVM57S.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FW DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match      67.9%; Score 55; DB 1; Length 113;
Best Local Similarity 73.3%; Pred. No. 0.01;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYL 15
Db 24 RSSKSLLYHSGNTYL 38

RESULT 7
KV2G MOUSE
ID_KV2G MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
PROTEIN THAT BINDS DIGOXIN.
CC PIR; A01914; KVM526.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FW DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

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FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 66.7%; Score 54; DB 1; Length 113;
Best Local Similarity 62.5%; Pred. No. 0.015;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
   |||:|:|:|:|:|:|
Db 24 RSSQSLVHSGNGTYLN 39

RESULT 8
KV2D_HUMAN
ID KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCB1_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RT primary amyloidosis."
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis."
RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC PIR; A01888; K2HUTW.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23
   FRAMEWORK-1.
FT DOMAIN 24 39
   COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54
   FRAMEWORK-2.
FT DOMAIN 55 61
   COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93
   FRAMEWORK-3.
FT DOMAIN 94 102
   COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112
   FRAMEWORK-4.
FT DOMAIN 113 113
   BY SIMILARITY.
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 65.4%; Score 53; DB 1; Length 113;
Best Local Similarity 68.8%; Pred. No. 0.023;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
   |||:|:|:|:|:|:|
Db 24 RSSQSLVHSGNGTYLN 39

RESULT 9
KV2D_HUMAN
ID KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).

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KV2E_MOUSE
ID KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCB1_TaxID=10090;
RN [1]
RP SEQUENCE.
RX TISSUE=Hybridoma;
RX MEDLINE=85128968; PubMed=6441768;
RA Abersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide."
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1381(1984).
CC -1- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
CC PIR; A01912; KWSL17.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
   FRAMEWORK-1.
FT DOMAIN 24 39
   COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54
   FRAMEWORK-2.
FT DOMAIN 55 61
   COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93
   FRAMEWORK-3.
FT DOMAIN 94 102
   COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112
   FRAMEWORK-4.
FT DISULFID 23 93
   BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 64.2%; Score 52; DB 1; Length 113;
Best Local Similarity 73.3%; Pred. No. 0.034;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 15
   |||:|:|:|:|:|:|
Db 24 RSSKSLVHSGNGITYLN 38

RESULT 10
KV2A_HUMAN
ID KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).

```

```
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01885; K2HUCM.
DR HSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 57.4%; Score 46.5; DB 1; Length 115;
Best Local Similarity 70.6%; Pred. No. 0.32;
Matches 12; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 RSSKSLLYK-DGKTYLN 16
Db 25 RSSQSLLSDGSGNTYLN 41

RESULT 11
KV2E HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobek H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RL Nature 309:73-76(1984).

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CC -----
CC EMBL; Z00009; -; NOT_ANNOTATED_CDS.
CC PIR; A01889; K2HUGM.
CC HSP; P80362; 1WTL.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117
FT DOMAIN 5 27
FT DOMAIN 28 43
FT DOMAIN 44 58
FT DOMAIN 59 65
FT DOMAIN 66 97
FT DOMAIN 98 106
FT DOMAIN 107 116
FT DISULFID 27 97
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 55.6%; Score 45; DB 1; Length 117;
```

```
Best Local Similarity 56.2%; Pred. No. 0.59;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 28 RSSQSLLHNSGNYLD 43

RESULT 12
ERR1 YEAST STANDARD; PRT; 437 AA.
ID ERR1 YEAST
AC P42222;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Enolase related protein 1 (EC 4.2.1.11).
GN ERR1 OR YMR323W OR YM9924.15.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Churcher C.M., Louis E.J., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
RN* [2]
RP SEQUENCE OF 120-437 FROM N.A.
RC STRAIN=S288C / YPI;
RX MEDLINE=95304851; PubMed=7785338;
RA Pryde F.E., Huckle T.C., Louis E.J.;
RT "Sequence analysis of the right end of chromosome XV in Saccharomyces
RT cerevisiae: an insight into the structural and functional
RT significance of sub-telomeric repeat sequences.";
RL Yeast 11:371-382(1995).
CC -1- CATALYTIC ACTIVITY: 2-phospho-D-glycerate = phosphoenolpyruvate +
CC H(2)O.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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CC -----
CC EMBL; Z54141; CAA90841.1; -.
CC EMBL; U23472; AAC48992.1; -.
CC HSP; P00924; 4ENL.
CC SGP; S0005920; ERR1.
CC InterPro; IPR000941; Enolase.
CC Pfam; PF00113; enolase; 1.
CC PRINTS; PR00148; ENOLASE.
CC ProDom; PD000902; Enolase; 1.
CC TIGRFAMs; TIGR01060; eno; 1.
CC PROSITE; PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium.
FT ACT_SITE 160 160 BY SIMILARITY.
FT METAL 247 247 MAGNESIUM (BY SIMILARITY).
FT METAL 296 296 MAGNESIUM (BY SIMILARITY).
FT METAL 321 321 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 437 AA; 47312 MW; 143D6EF66FB03D13 CRC64;

Query Match 53.1%; Score 43; DB 1; Length 437;
Best Local Similarity 60.0%; Pred. No. 5.7;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SSKSLLYKDGKTYLN 16
Db 248 SAPSFYKDGKTYLN 262
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RESULT 13
Y535 METJA STANDARD; PRT; 343 AA.
ID Y535 METJA STANDARD; PRT; 343 AA.
AC Q57955;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0535.
GN MJ0535
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcales; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.P., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -!- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / APHA
FAMILY.
CC
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CC
CC EMBL; U67502; AAB98526.1; -.
DR TIGR; MJ0535; -.
DR InterPro; IPR000286; His deacetylase.
DR Pfam; PF00850; Hist deacetyl; 1.
DR PRINTS; PR01270; HDASUPER.
DR KQ Hypothetical protein; Hydrolase; Complete proteome.
SQ SEQUENCE 343 AA; 38174 MW; 8848EDB5757FDC233 CRC64;
Query Match 51.9%; Score 42; DB 1; Length 343;
Best Local Similarity 69.2%; Pred. No. 6.5;
Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 SKSLLYKDGKTYL 15
| | | | |
DB 73 SKSNFYVDGTYL 85
| | | | |

RESULT 14
KV2D MOUSE
ID KV2D MOUSE STANDARD; PRT; 112 AA.
AC P01629;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 13-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 2S1.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE.
RX MEDLINE=83055101; PubMed=7141411;
RA Hertz H., Chang J.Y., Abersold R., Braun D.G.;
RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for

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the group A streptococcal polysaccharide.";
RT Hoppe-Sevler's Z. Physiol. Chem. 363:1069-1076(1982).
CC -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC PIR; A01911; KVMSS1.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12221 MW; BD5EF5E6D789FBEC CRC64;
Query Match 50.6%; Score 41; DB 1; Length 112;
Best Local Similarity 66.7%; Pred. No. 2.8;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 RSSKSLLYKDGKTYL 15
| | | | |
DB 24 RSSKSLYQSKGTYL 38
| | | | |

RESULT 15
ACON LEGPN
ID ACON LEGPN STANDARD; PRT; 891 AA.
AC P37032;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aconitate hydratase (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase)
DE (Major iron-containing protein) (MICP) (IP210).
DE ACN.
OS Legionella pneumophila.
OC Bacteria; Proteobacteria; gamma subdivision; Legionellaceae group;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=446;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Philadelphia 1;
RC MEDLINE=93374864; PubMed=8366052;
RX Mengaud J.M., Horwitz M.A.;
RT "The major iron-containing protein of Legionella pneumophila is an
RT aconitase homologous with the human iron-responsive element-binding
RT protein.";
RL J. Bacteriol. 175:5666-5676(1993).
CC -!- CATALYTIC ACTIVITY: Citrate = cis-aconitate + H(2)O.
CC -!- PATHWAY: Tricarboxylic acid cycle.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- MISCELLANEOUS: ACONITASE HAS AN ACTIVE (4FE-4S) AND AN INACTIVE
CC (3FE-4S) FORMS. THE ACTIVE (4FE-4S) CLUSTER IS PART OF THE
CC CATALYTIC SITE THAT INTERCONVERTS CITRATE, CIS-ACONITASE, AND
CC ISOCITRATE.
CC -!- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC
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CC
CC
CC EMBL; L22081; AAA25295.1; -.
DR PIR; B48642; B48642.

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DR	HSP; P16276; 1B0J.				
DR	InterPro; IPR000573; Aconitase_C.				
DR	InterPro; IPR001030; Aconitase_N.				
DR	Pfam; PF00330; aconitase; 1.				
DR	Pfam; PF00694; Aconitase_C; 1.				
DR	PRINTS; PR00415; ACONITASE.				
DR	PRODOM; PD000511; Aconitase_N; 1.				
DR	PROSITE; PS00450; ACONITASE_1; 1.				
DR	PROSITE; PS01244; ACONITASE_2; 1.				
KW	Lyase; Tricarboxylic acid cycle;				
FT	LYASE; Tricarboxylic acid cycle;				
FT	METAL	435	435		
FT	METAL	501	501		
FT	METAL	501	501		
FT	METAL	504	504		
FT	METAL	504	504		
FT	METAL	504	504		
SQ	SEQUENCE	891 AA;	98209 MW;	F81FC99520859B48	CRC64;

Search completed: April 22, 2003, 12:51:45
Job time : 9 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:47:43 ; Search time 32 Seconds
(without alignments)
103.024 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81
Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21:*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriapi.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	75.3	239	4 Q8TCD0	Q8TCD0 homo sapien
2	57	70.4	114	4 Q9UL80	Q9UL80 homo sapien
3	50	61.7	758	10 Q9C9E8	Q9C9E8 arabidopsis
4	49	60.5	238	11 Q8VC16	Q8VC16 mus musculus
5	48	59.3	104	11 Q9JL82	Q9JL82 mus musculus
6	48	59.3	239	11 Q8VC55	Q8VC55 mus musculus
7	48	59.3	1561	17 Q26451	Q26451 methanobact
8	46	56.8	238	11 Q99M37	Q99M37 mus musculus
9	46	56.8	506	16 Q9L035	Q9L035 streptomyc
10	46	56.8	573	2 P97179	P97179 streptomyc
11	46	56.8	574	2 Q86876	Q86876 streptomyc
12	44	54.3	419	16 Q9CG26	Q9CG26 lactococcus
13	43	53.1	437	3 Q12007	Q12007 saccharomyc
14	43	53.1	481	3 Q9P8D3	Q9P8D3 sordaria ma
15	43	53.1	487	3 Q8X096	Q8X096 neurospora
16	43	53.1	489	3 Q9P8F3	Q9P8F3 gibberella

17	43	53.1	646	5	096602	096602 trypanosoma
18	43	53.1	822	16	Q56939	Q56939 versinia pe
19	42	51.9	239	16	Q9CMU7	Q9CMU7 pasteurella
20	42	51.9	245	16	Q67538	Q67538 aquifex aeo
21	42	51.9	434	5	Q23217	Q23217 caenorhabdi
22	42	51.9	755	17	Q97VH4	Q97VH4 sulfolobus
23	42	51.9	786	5	Q77209	Q77209 trypanosoma
24	41	50.6	418	16	Q9XDT5	Q9XDT5 clostridium
25	41	50.6	555	16	Q8RIQ5	Q8RIQ5 fusobacteri
26	41	50.6	635	2	Q45820	Q45820 clostridium
27	41	50.6	651	16	Q9WYL6	Q9WYL6 thermotoga
28	41	50.6	700	2	Q24781	Q24781 bacillus sp
29	40.5	50.0	241	12	Q9YMQ6	Q9YMQ6 coltivirus
30	40.5	50.0	249	12	Q9YMQ2	Q9YMQ2 coltivirus
31	40.5	50.0	249	12	Q9YMP2	Q9YMP2 coltivirus
32	40	49.4	87	16	Q8Y062	Q8Y062 ralstonia s
33	40	49.4	127	16	Q9KAX6	Q9KAX6 bacillus ha
34	40	49.4	233	17	Q59233	Q59233 pyrococcus
35	40	49.4	305	16	Q50934	Q50934 borrelia bu
36	40	49.4	364	3	P78905	P78905 schizosacch
37	40	49.4	459	2	Q59964	Q59964 streptomyc
38	40	49.4	464	16	Q9KEM8	Q9KEM8 bacillus ha
39	40	49.4	466	10	Q9MZX0	Q9MZX0 arabidopsis
40	40	49.4	489	3	Q94582	Q94582 schizosacch
41	40	49.4	521	16	Q9PQU6	Q9PQU6 ureaplasma
42	40	49.4	761	13	Q918H4	Q918H4 opsanus tau
43	40	49.4	1016	2	Q9LCV7	Q9LCV7 leuconostoc
44	40	49.4	1928	5	Q9U0H2	Q9U0H2 plasmodium
45	39.5	48.8	257	16	Q8U9V9	Q8U9V9 agrobacteri

ALIGNMENTS

RESULT 1

Q8TCD0 PRELIMINARY; PRT; 239 AA.

AC Q8TCD0; 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Hypothetical 26.2 kDa protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC022362; AAH22362.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match 75.3%; Score 61; DB 4; Length 239;
 Best Local Similarity 68.8%; Pred. NO. 0.029;
 Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16

Db 44 RSTQSLVSDGNTYLN 59

RESULT 2

Q9UL80 PRELIMINARY; PRT; 114 AA.

AC Q9UL80; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin light chain variable region (Fragment).

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; AAD56270.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 114
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;

Query Match 70.4%; Score 57; DB 4; Length 114;
Best Local Similarity 68.8%; Pred. No. 0.059;
Matches 11; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
   |||:|:|:|:|
Db 24 RSSQSPVSDGNTYLN 39

RESULT 3
Q9C9E8 PRELIMINARY; PRT; 758 AA.
ID Q9C9E8;
AC Q9C9E8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 84.8 kDa protein.
GN T10D10.3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLOMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzili A.,
RA Militescher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzer J.S., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uterback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820 (2000).
DR EMBL; AC016529; BAG52586.1; -.
DR InterPro; IPR002052; N6_Mtase.
DR InterPro; IPR002035; VWF_A.
DR SMART; SM00327; VWF; 1.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
```

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DR PROSITE; PS50234; VWFA; 1.
KW Hypothetical protein.
SQ SEQUENCE 758 AA; 84789 MW; 843F219D227036B CRC64;

Query Match 61.7%; Score 50; DB 10; Length 758;
Best Local Similarity 64.3%; Pred. No. 7.3;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SKSLLYKDGKTYLN 16
   |:|:|:|:|:|
Db 194 SQKLIYKDGKFLN 207

RESULT 4
Q8VCI6 PRELIMINARY; PRT; 238 AA.
ID Q8VCI6;
AC Q8VCI6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;

Query Match 60.5%; Score 49; DB 11; Length 238;
Best Local Similarity 56.2%; Pred. No. 2.9;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
   |||:|:|:|:|
Db 43 RSSQSLVHSNGNTYLN 58

RESULT 5
Q9JL82 PRELIMINARY; PRT; 104 AA.
ID Q9JL82;
AC Q9JL82;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Anti-myosin immunoglobulin light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
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RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206024; AAF69322.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON TER 1 104
FT SEQUENCE 104 AA; 11360 MW; 5DA8BBFDF5FOAALAE CRC64;
SQ
Query Match 59.3%; Score 48; DB 11; Length 104;
Best Local Similarity 56.2%; Pred. No. 1.7; Mismatches 2; Indels 0; Gaps 0;
Matches 9; Conservative 5;

QY 1 RSSKSLLYKDGKTYLN 16
Db 16 RSSQSLVHTNGNTYLH 31
|||||:::|::|::|

RESULT 6
Q8VC55 PRELIMINARY; PRT; 239 AA.
AC Q8VC55;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC021781; AAH21781.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;

Query Match 59.3%; Score 48; DB 11; Length 239;
Best Local Similarity 62.5%; Pred. No. 4.4; Mismatches 3; Indels 0; Gaps 0;
Matches 10; Conservative 3;

QY 1 RSSKSLLYKDGKTYLN 16
Db 44 KSTKSLNSDGTLYID 59
|||||:::|::|::|

RESULT 7
O26451 PRELIMINARY; PRT; 1561 AA.
AC O26451;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Magnesium chelatase subunit.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
RA Aldridge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltal: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AS000820; AB84857.1; -.
DR InterPro; IPR001589; Actbind actnin.
DR InterPro; IPR003672; COB/Mg_chltase.
DR Pfam; PF02514; COB/Mg_chel; 1.
DR PROSITE; PS00019; ACTININ_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1561 AA; 170574 MW; 764561FA31D719CE CRC64;

Query Match 59.3%; Score 48; DB 17; Length 1561;
Best Local Similarity 64.3%; Pred. No. 35; Mismatches 3; Indels 0; Gaps 0;
Matches 9; Conservative 2;

QY 3 SKSLLYKDGKTYLN 16
Db 224 SRELLYRDGKLYDN 237
|||||:::|::|::|

RESULT 8
Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Hypothetical 26.3 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020235; AAH02035.1; -.
DR HSSP; P01679; 2FEJ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003600; IG like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 56.8%; Score 46; DB 11; Length 238;
Best Local Similarity 53.3%; Pred. No. 9.4; Mismatches 5; Indels 2; Gaps 0;
Matches 8; Conservative 5;

QY 1 RSSKSLLYKDGKTYLN 15
Db 43 RSSQSLVHTNGNTYL 57
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RESULT 9
Q9L035

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ID Q9L035 PRELIMINARY; PRT; 506 AA.
AC Q9L035;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Secreted alpha-amylase.
GN AMLB OR SCO7020 OR SC1HL0.09.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Seeger K.J., Harris D.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RA Thomson N.R., Parkhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kieser H.M., Denapaita D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
RL the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Batsman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL352956; CAB88153.1; -.
DR HSSP; P29957; 1AQM.
DR InterPro; IPR000461; Alpha_amylase.
DR InterPro; IPR002044; CBD_4.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
SQ SEQUENCE 506 AA; 57868 MW; FCC92A3BED9D2DAE CRC64;

Query Match 56.8%; Score 46; DB 16; Length 506;
Best Local Similarity 57.1%; Pred. No. 22;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSKSKLLYKDGKTY 14
Db 306 RNGETLTKDGATY 319

RESULT 10
P97179 PRELIMINARY; PRT; 573 AA.
AC P97179;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Alpha-amylase.

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GN AMLB.
OS Streptomyces lividans.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin X.H., Gagnat J., Gerbaud C., Guerineau M., Virolette M.J.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z85949; CAB06622.1; -.
DR EMBL; Z86113; CAB06815.1; -.
DR HSSP; P29957; 1AQM.
DR InterPro; IPR000461; Alpha_amylase.
DR InterPro; IPR002044; CBD_4.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
SQ SEQUENCE 573 AA; 61214 MW; E474019661C9D6A2 CRC64;

Query Match 56.8%; Score 46; DB 2; Length 573;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSKSKLLYKDGKTY 14
Db 306 RNGETLTKDGATY 319

RESULT 11
Q86876 PRELIMINARY; PRT; 574 AA.
AC Q86876;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Alpha-amylase.
GN AML.
OS Streptomyces lividans.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1916;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TK21;
RA Isiegas C., Parro V., Mellado R.P.;
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13601; CAA73926.1; -.
DR HSSP; P29957; 1AQM.
DR InterPro; IPR000461; Alpha_amylase.
DR InterPro; IPR002044; CBD_4.
DR Pfam; PF00128; alpha-amylase; 1.
DR Pfam; PF02806; alpha-amylase_C; 1.
DR Pfam; PF00686; CBM_20; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
DR ProDom; PD001568; CBD_4; 1.
SQ SEQUENCE 574 AA; 61758 MW; A040AA1092C22270 CRC64;

Query Match 56.8%; Score 46; DB 2; Length 574;
Best Local Similarity 57.1%; Pred. No. 25;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSKSKLLYKDGKTY 14
Db 306 RNGETLTKDGATY 319

RESULT 12
Q9CG26 PRELIMINARY; PRT; 419 AA.
ID Q9CG26
AC Q9CG26;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)

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DR EMBL; Z73637; CAA98018.1; -
DR EMBL; Z75302; CAA99728.1; -
DR HSP; P00924; 4END.
DR SGD; S0005920; ERR1.
DR SGG; S0006202; ERR2.
DR InterPro; IPR000941; Enolase.
DR Pfam; PF01113; enolase; 1.
DR PRINTS; PR00148; ENOLASE.
DR ProDom; PD000902; Enolase; 1.
DR TIGRFAMs; TIGR01060; eno; 1.
DR PROSITE; PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
SQ SEQUENCE 437 AA; 47327 MW;
    FAF09C00B0E711C CRC64;

Query Match          53.1%; Score 43; DB 3; Length 437;
Best Local Similarity 60.0%; Pred. No. 59;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SSKSLLYKDGKTYLN 16
   |:|:|:|:|:|
Db 248 SAPSFVYKDGKDYLN 262

RESULT 14
Q9P8D3 PRELIMINARY; PRT; 481 AA.
ID AC Q9P8D3
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ATP citrate lyase, subunit 2 (EC 4.1.3.8).
ACL2.
OS Sordaria macrospora.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Sordaria.
NCBI_TaxID=5147;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=3346; TISSUE=MYCELIUM;
RA Nowrousian M., Kuck U., Loser K., Weltring K.M.;
RT "the fungal ac11 and ac12 genes encode two polypeptides with homology
RT to the N- and C-terminal parts of the animal ATP citrate lyase
RT polypeptide.";
RL Curr. Genet. 0:0-0(0).
DR EMBL; AJ243817; CAB76164.1; -.
KW Lyase.
SQ SEQUENCE 481 AA; 52240 MW; 44C93D3C4567EB28 CRC64;

Query Match          53.1%; Score 43; DB 3; Length 481;
Best Local Similarity 60.0%; Pred. No. 65;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SSKSLLYKDGKTYLN 16
   |:|:|:|:|:|
Db 2 SAKSILEADGKALN 16

RESULT 15
Q8X096 PRELIMINARY; PRT; 487 AA.
ID AC Q8X096
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable ATP citrate lyase subunit 2.
GN B14D6.320.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
[1]
RN SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,

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RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA German Neurospora Genome project;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL356173; CAB91741.2; -.
 KW Lyase.
 SQ SEQUENCE 487 AA; 52969 MW; 56BC196FCCE4CBA2 CRC64;
 Query Match 53.1%; Score 43; DB 3; Length 487;
 Best Local Similarity 60.0%; Pred. NO. 66;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 SSKSLLYKDGKTYLN 16
 DB 2 SAKSILEADGKAILN 16

Search completed: April 22, 2003, 12:53:45
 Job time : 35 secs

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:45:19 ; Search time 40.5714 Seconds
(without alignments)
52.550 Million cell updates/sec

Title: US-09-674-716B-3
Perfect score: 81
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 22: /SID82/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	81	100.0	16	21 AAY32254
2	81	100.0	100	22 AAE06969
3	81	100.0	116	21 AAY32262
4	81	100.0	145	21 AAY32261
5	77	95.1	16	19 AAW39818
6	77	95.1	113	19 AAW39882
7	77	95.1	113	19 AAW39804
8	76	93.8	131	12 AAR12232
9	76	93.8	132	12 AAR12354
10	75	92.6	16	19 AAW39815

11	75	92.6	16	19	AAW39824	Light chain CDR1 o
12	75	92.6	113	19	AAW39886	Light chain of the
13	75	92.6	113	19	AAW39801	Variable domain of
14	75	92.6	113	19	AAW39802	Variable domain of
15	75	92.6	113	19	AAW39803	Variable domain of
16	69	85.2	16	19	AAW39875	Light chain CDR1 o
17	69	85.2	16	19	AAW39839	Light chain CDR1 o
18	69	85.2	113	19	AAW39897	Variable domain of
19	69	85.2	114	19	AAW39805	Variable domain of
20	67	82.7	20	21	AAW70802	Murine anti-PAB-42
21	67	82.7	122	21	AAW70790	Murine anti-PAB-42
22	65	80.2	112	22	AAE06992	Human kappa light
23	64	79.0	93	21	AAW56670	Partial peptide fr
24	64	79.0	100	22	AAE06960	Mouse germline kap
25	64	79.0	100	22	AAE06961	Mouse germline kap
26	64	79.0	112	19	AAW53585	Light chain of a h
27	64	79.0	112	22	AAE06993	Human kappa light
28	64	79.0	112	22	AAE07003	Human kappa light
29	64	79.0	113	15	AAE07003	Light chain variab
30	64	79.0	113	21	AAU76445	Mouse monoclonal a
31	64	79.0	113	21	AAU76445	Mouse HBV pre-S1 a
32	64	79.0	113	21	AAE12170	Humanised HBV pre-
33	64	79.0	113	21	AAE12171	Humanised HBV pre-
34	64	79.0	132	20	AAV42306	Human anti-ganglio
35	64	79.0	133	21	AAV56735	Amino acid sequenc
36	64	79.0	139	21	AAV93724	The kappa chain of
37	64	79.0	247	23	AAU90900	Insulin/insulin-l
38	64	79.0	253	23	ABP45953	Human Blys binding
39	62.5	77.2	15	19	AAW39821	Light chain CDR1 o
40	61	75.3	16	23	AAU70328	Human kappa II lig
41	61	75.3	112	22	AAE07007	Human kappa light
42	60	74.1	16	20	AAV14404	Peptide CDR-L1 der
43	60	74.1	112	20	AAV24099	Figure 11 protein
44	60	74.1	112	20	AAE06999	Human kappa light
45	59	72.8	16	22	AAE86292	Murine derived ant

ALIGNMENTS

RESULT 1
AAY32254
ID AAY32254 standard; Peptide, 16 AA.
XX AAY32254;
AC AC
XX 15-FEB-2000 (first entry)
DT Light chain CDR L1 of mouse anti-CD23 MAB C11.
DE CD23; FCER11; IGE receptor; monoclonal antibody; C11; mouse;
XX monoclinal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy.
XX Mus musculus.
OS WO9958679-A1.
PN 18-NOV-1999.
XX 07-MAY-1999; 99WO-GB01434.
XX 09-MAY-1998; 98GB-0009839.
XX (GLAXO) GLAXO GROUP LTD.
XX

PI Bonney JMF, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 DR WPI; 2000-053101/04.
 DR N-PSDB; AA234739.
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis -
 PT
 XX
 XX Claim 1; Page 40; 81pp; English.
 XX
 CC This sequence represents complementarity determining region 1
 CC (CDR L1) of the light chain of murine anti-CD23 (FCER1I) monoclonal
 CC antibody C11 (see also AAY32262). The invention provides altered
 CC antibodies, such as chimeric or humanised antibodies, which comprise
 CC sufficient of the amino acid sequences of C11 light and heavy chain
 CC CDRs (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies
 CC are used to block soluble CD23 formation for treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 81; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 1 RSSKSLLYKDGKTYLN 16
 RESULT 2
 AA06969
 ID AAE06969 standard; Protein; 100 AA.
 AC
 AC AAE06969;
 DT 16-OCT-2001 (first entry)
 DE Mouse germline kappa light chain variable (VK) region, 167/24.
 KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VK; kappa light chain variable region.
 XX
 OS MIB sp.
 XX
 XX WO200157226-A1.
 FN
 PD 09-AUG-2001.
 XX
 PF 02-FEB-2001; 2001WO-US03537.
 XX
 PR 03-FEB-2000; 2000US-0497625.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Larosa GS, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;

XX WPI; 2001-489888/53.
 XX Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 FT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT
 XX
 XX Disclosure; Page 151; 183pp; English.
 XX
 CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherosclerosis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is mouse germline kappa light chain variable
 CC (VK) region, 167/24.
 XX
 SQ Sequence 100 AA;
 Query Match 100.0%; Score 81; DB 22; Length 100;
 Best Local Similarity 100.0%; Pred. No. 3.9e-06;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 24 RSSKSLLYKDGKTYLN 39
 RESULT 3
 AA32262
 ID AAY32262 standard; Protein; 116 AA.
 AC
 AC AAY32262;
 DT 15-FEB-2000 (first entry)
 DE Humanised anti-CD23 MAb C11 light chain variable region.
 DE
 DE CD23; FCER1I; IgE receptor; monoclonal antibody; C11; mouse; human;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes;
 KW B-cell malignancy; therapy.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT 1..23
 FT Region /note= "framework region 1"
 FT 24..39

RESULT 5
AAW39818
ID AAW39818 standard; peptide; 16 AA.
XX AC AAW39818;
XX DT 16-JUN-1998 (first entry)
XX DE Light chain CDR1 of catalytic antibody 6A12.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
overdose; addiction.
XX OS Mus sp.
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US10965.
XX PR 25-JUN-1996; 96US-0672345.
XX PA (UYCO) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX PS Claim 13; Page 81; 147pp; English.
XX CC AAW39818-20 represent the sequences of the light chain complementarity
CC determining regions (CDRs) of the catalytic antibody 6A12, which is able
CC to degrade cocaine. A series of cocaine transition state analogues
CC (TSAs) were prepared and used to immunise mice for production of
CC hybridomas. Catalytic antibodies were identified by their capacity to
CC release 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was
CC identified using TSA1, which is an immunogenic conjugate of a phosphate
CC monoster transition state analogue. Antibody 6A12 has a per minute Kcat
CC of 0.072. The antibodies reduce the concentration of cocaine in a
CC subject, and are used particularly for the treatment of an overdose. They
CC are also used for treating addiction (by reducing the in vivo
CC concentration that can be achieved).
XX SQ Sequence 16 AA;
Query Match 95.1%; Score 77; DB 19; Length 16;
Best Local Similarity 93.8%; Pred. No. 2.4e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSSKSLLYDKGTYLN 16
DB 1 RSSKSLLYEDGKTYLN 16
RESULT 6
AAW39882
ID AAW39882 standard; Protein; 113 AA.
XX AC AAW39882;
XX DT 16-JUN-1998 (first entry)
XX DE Light chain of the catalytic antibody 2A10.
XX

KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
overdose; addiction.
XX OS Mus sp.
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US10965.
XX PR 25-JUN-1996; 96US-0672345.
XX PA (UYCO) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX PS Disclosure; Fig 21; 147pp; English.
XX CC The present sequence represents the light chain of a catalytic antibody
CC which is capable of degrading cocaine. A series of cocaine transition
CC state analogues (TSAs) were prepared and used to immunise mice for
CC production of hybridomas. Catalytic antibodies were identified by their
CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
CC antibodies reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved).
XX SQ Sequence 113 AA;
Query Match 95.1%; Score 77; DB 19; Length 113;
Best Local Similarity 93.8%; Pred. No. 2.1e-05;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSSKSLLYDKGTYLN 16
DB 24 RSSKSLLYEDGKTYLN 39
RESULT 7
AAW39804
ID AAW39804 standard; protein; 113 AA.
XX AC AAW39804;
XX DT 16-JUN-1998 (first entry)
XX DE Variable domain of the Kappa light chain of catalytic antibody 2A10.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
overdose; addiction.
XX OS Mus sp.
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US10965.

PR 25-JUN-1996; 96US-0672345.
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX Landry DW;
XX WPI; 1998-077166/07.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
XX Claim 16; Pages 73-74; 147pp; English.
XX
XX AA39801-05 represent the amino acid sequences of the variable domain
CC of the Kappa light chain of catalytic antibodies which are able to
CC degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC were prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release
CC 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AA39809
CC represents the heavy chain) was identified using T9A1, which is an
CC immunogenic conjugate of a phosphate monoester transition state
CC analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies
CC reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used
CC for treating addiction (by reducing the in vivo concentration that can
CC be achieved).
XX
XX Sequence 113 AA;
XX
XX Query Match 95.1%; Score 77; DB 19; Length 113;
XX Best Local Similarity 93.8%; Pred. No. 2.1e-05; Indels 0; Gaps 0;
XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSSKSLLYKDGKTYLN 16
DB 24 RSSKSLLYEDGKTYLN 39
|||||:|||||
RESULT 8
AAR12232
ID AAR12232 standard; Protein; 131 AA.
XX
XX AAR12232;
XX 19-AUG-1991 (first entry)
XX
XX Mouse MAb 2E12 L chain V region.
XX
XX HIV-1; chimera.
XX
XX Mus sp.
XX
XX WO9107494-A.
XX
XX 30-MAY-1991.
XX
XX 13-NOV-1990; 90WO-US06627.
XX
XX 13-NOV-1989; 89US-0433703.
XX (XOMA-) XOMA CORP.
XX Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
XX WPI; 1991-178106/24.
XX N-PSDB; AAQ12012.
XX
XX New chimeric mouse human antibodies - used in treatment, diagnosis
XX and prophylaxis of HIV infections.
XX
XX Disclosure; Fig 1; 108pp; English.

XX The mouse VL gene product may be used to produce chimeric mouse-
CC human Abs against HIV-1 comprising human Ig constant regions and
CC murine variable regions. These novel sequence are useful in
CC treatment, diagnosis and prophylaxis of HIV infections, and may be
CC produced by a bacterial, yeast or mammalian expression system.
XX
XX Sequence 131 AA;
XX
XX Query Match 93.8%; Score 76; DB 12; Length 131;
XX Best Local Similarity 93.8%; Pred. No. 3.7e-05; Indels 0; Gaps 0;
XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSSKSLLYKDGKTYLN 16
DB 44 RSSKSLLYKDGKTYLS 59
|||||:|||||
RESULT 9
AAR12354
ID AAR12354 standard; Protein; 132 AA.
XX
XX AAR12354;
XX 15-AUG-1991 (first entry)
XX
XX Light (kappa) chain variable region of murine 2E12
XX immunoglobulin.
XX
XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
XX
XX Mus musculus.
XX
XX WO9107493-A.
XX
XX 30-MAY-1991.
XX
XX 13-NOV-1990; 90WO-US06615.
XX
XX 13-NOV-1989; 89US-0433730.
XX (XOMA-) XOMA CORP.
XX (GREC) GREEN CROSS CORP.
XX
XX Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
XX WPI; 1991-178044/24.
XX N-PSDB; AAQ12056.
XX
XX New chimeric mouse-human antibodies - used to detect, kill and
XX remove HIV-1 antigen from sample
XX
XX Disclosure; fig 1; 107pp; English.
XX
XX This is the light (kappa) - chain variable (V) region of a mouse
XX monoclonal antibody (MAb), 2E12, and is specific for an HIV-1
XX viral antigen. It is used in the construction of a chimeric MAb
XX comprising heavy and light chains having murine V regions and human
XX C regions. The chimeric MABs are more effective than murine MAB
XX 2E12 since they have an increased compatibility in humans. The
XX heavy and light chain V-regions are joined by manipulating their
XX respective joining (J) regions, to generate restriction enzyme
XX recognition sites. The chimeric MABs can be used as immuno-
XX conjugates, in association with e.g. toxins for HIV treatment.
XX They can also be used in diagnosis of HIV.
XX See also AAQ12057-63.
XX Sequence 132 AA;
XX
XX Query Match 93.8%; Score 76; DB 12; Length 132;
XX Best Local Similarity 93.8%; Pred. No. 3.7e-05; Indels 0; Gaps 0;
XX Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RSSKSLLYKDGKTYLN 16

```

Db 44 RSSKSLLYKDGKTYLS S9
|||||
RESULT 10
AAW39815
ID AAW39815 standard; peptide; 16 AA.
XX
AC AAW39815;
XX
DT 16-JUN-1998 (first entry)
XX
DE Light chain CDR1 of catalytic antibody 3B9.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
PN WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US10965.
XX
PR 25-JUN-1996; 96US-0672345.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Landry DW;
XX
DR WPI; 1998-077166/07.
XX
PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
PS Claim 11; Page 80; 147pp; English.
XX
CC AAW39815-17 represent the sequences of the light chain complementarity
CC determining regions (CDRs) of the catalytic antibody 3B9, which is able
CC to degrade cocaine. A series of cocaine transition state analogues
CC (TSAs) were prepared and used to immunise mice for production of
CC hybridomas. Catalytic antibodies were identified by their capacity to
CC release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was
CC identified using TSA1, which is an immunogenic conjugate of a phosphate
CC monoester transition state analogue. Antibody 3B9 has a per minute Kcat
CC of 0.11. The antibodies reduce the concentration of cocaine in a subject,
CC and are used particularly for the treatment of an overdose. They are also
CC used for treating addiction (by reducing the in vivo concentration that
CC can be achieved).
XX
SQ Sequence 16 AA;
Query Match 92.6%; Score 75; DB 19; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 RSSKSLLYKDGKTYLN 16
DB 1 RSSRSLLYRDGKTYLN 16
|||||
RESULT 11
AAW39824
ID AAW39824 standard; peptide; 16 AA.
XX
AC AAW39824;
XX
DT 16-JUN-1998 (first entry)
XX

```

```

XX
DE Light chain CDR1 of catalytic antibody 12H1.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
PN WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US10965.
XX
PR 25-JUN-1996; 96US-0672345.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Landry DW;
XX
DR WPI; 1998-077166/07.
XX
PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
PS Claim 17; Page 83; 147pp; English.
XX
CC AAW39824-26 represent the sequences of the light chain complementarity
CC determining regions (CDRs) of the catalytic antibody 12H1, which is able
CC to degrade cocaine. A series of cocaine transition state analogues
CC (TSAs) were prepared and used to immunise mice for production of
CC hybridomas. Catalytic antibodies were identified by their capacity to
CC release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was
CC identified using TSA2, and has a per minute Kcat of 0.16. The antibodies
CC reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved).
XX
SQ Sequence 16 AA;
Query Match 92.6%; Score 75; DB 19; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 RSSKSLLYKDGKTYLN 16
DB 1 RSSRSLLYRDGKTYLN 16
|||||
RESULT 12
AAW39886
ID AAW39886 standard; Protein; 113 AA.
XX
AC AAW39886;
XX
DT 18-JUN-1998 (first entry)
XX
DE Light chain of the catalytic antibody 6A12.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
PN WO9749800-A1.
XX

```


CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release
 CC 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody (AAW39807
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state
 CC analogue. Antibody 6A12 has a per minute Kcat of 0.072. The antibodies
 CC reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can
 CC be achieved).

XX SQ Sequence 113 AA;

Query Match 92.6%; Score 75; DB 19; Length 113;
 Best Local Similarity 87.5%; Pred. No. 4.6e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
 |||:||||:|||||
 DB 24 RSSRSLLYRDGKTYLN 39

RESULT 15

AAW39803
 ID AAW39803 standard; protein; 113 AA.

XX AC AAW39803;

XX DT 16-JUN-1998 (first entry)

XX DE Variable domain of the kappa light chain of catalytic antibody 12H1.

XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

XX OS MUB SP.

XX PN WO9749800-A1.

XX PD 31-DEC-1997.

XX PF 25-JUN-1997; 97WO-US10965.

XX PR 25-JUN-1996; 96US-0672345.

XX PA (UYCO) UNIV COLUMBIA NEW YORK.

XX PI Landry DW;

XX DR WPI; 1998-077166/07.

XX DR P-PSDB; AAW09802.

XX PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding

XX PS Claim 18; Page 73; 147pp; English.

XX CC AAW39801-05 represent the amino acid sequences of the variable domain
 CC of the kappa light chain of catalytic antibodies which are able to
 CC degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release
 CC 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808
 CC represents the heavy chain) was identified using TSA2, and has a per
 CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine
 CC in a subject, and are used particularly for the treatment of an
 CC overdose. They are also used for treating addiction (by reducing the in
 CC vivo concentration that can be achieved).

SQ Sequence 113 AA;

Query Match 92.6%; Score 75; DB 19; Length 113;
 Best Local Similarity 87.5%; Pred. No. 4.6e-05;
 Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16

|||:||||:|||||

DB 24 RSSRSLLYRDGKTYLN 39

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	81	100.0	100	10	US-09-840-459-32
2	55	80.2	112	10	US-09-840-459-55
3	64	79.0	93	10	US-09-305-243-61
4	64	79.0	100	9	US-10-194-975-75
5	64	79.0	100	9	US-10-194-975-76
6	64	79.0	100	10	US-09-840-459-23
7	64	79.0	100	10	US-09-840-459-24
8	64	79.0	112	10	US-09-840-459-56
9	64	79.0	112	10	US-09-840-459-66
10	64	79.0	132	12	US-10-006-773-11
11	64	79.0	222	9	US-09-479-614-26
12	64	79.0	242	9	US-09-479-614-20
13	64	79.0	253	9	US-09-880-748-1964
14	61	75.3	112	10	US-09-840-459-70
15	60	74.1	112	10	US-09-840-459-62
16	59	72.8	100	10	US-09-840-459-22
17	59	72.8	111	10	US-09-835-087-2
18	59	72.8	111	10	US-09-809-739-13
19	59	72.8	111	10	US-09-840-459-11

20	59	72.8	111	10	US-09-840-459-59	Sequence 59, Appl
21	59	72.8	112	9	US-10-032-482-8	Sequence 8, Appl
22	59	72.8	112	10	US-09-772-120-6	Sequence 6, Appl
23	59	72.8	112	10	US-09-840-459-54	Sequence 54, Appl
24	59	72.8	112	10	US-09-840-459-58	Sequence 58, Appl
25	59	72.8	113	10	US-09-840-459-63	Sequence 63, Appl
26	59	72.8	244	9	US-09-880-748-1991	Sequence 1991, Ap
27	59	72.8	535	9	US-09-968-851-38	Sequence 38, Appl
28	59	71.6	100	9	US-10-194-975-78	Sequence 78, Appl
29	58	71.6	112	10	US-09-840-459-60	Sequence 60, Appl
30	58	71.6	113	10	US-09-840-459-64	Sequence 64, Appl
31	58	71.6	113	10	US-09-840-459-65	Sequence 65, Appl
32	57	70.4	112	10	US-09-840-459-67	Sequence 67, Appl
33	56	69.1	112	10	US-09-840-459-69	Sequence 69, Appl
34	55	67.9	16	10	US-09-835-087-14	Sequence 14, Appl
35	55	67.9	100	10	US-09-840-459-21	Sequence 21, Appl
36	55	67.9	112	10	US-09-835-087-1	Sequence 1, Appl
37	55	67.9	112	10	US-09-835-087-3	Sequence 3, Appl
38	55	67.9	112	10	US-09-835-087-4	Sequence 4, Appl
39	55	67.9	112	10	US-09-835-087-5	Sequence 5, Appl
40	55	67.9	112	10	US-09-835-087-6	Sequence 6, Appl
41	55	67.9	112	10	US-09-835-087-7	Sequence 7, Appl
42	55	67.9	112	10	US-09-809-739-11	Sequence 11, Appl
43	55	67.9	112	10	US-09-809-739-14	Sequence 14, Appl
44	55	67.9	112	10	US-09-809-739-15	Sequence 15, Appl
45	55	67.9	112	10	US-09-809-739-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larrosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran H.
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; *TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-840-459-32

Query Match 100.0%; Score 81; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYKDGKTYLN 16

Db 24 RSSKSLLYKDGKTYLN 39

RESULT 2

Thu Apr 24 09:13:30 2003

us-09-674-716b-3.open.rapb

;; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
;; FILE REFERENCE: 1855.1052-012
;; CURRENT APPLICATION NUMBER: US/09/840,459
;; PRIOR FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: PCT/US01/03537
;; PRIOR FILING DATE: 2001-02-02
;; PRIOR APPLICATION NUMBER: 09/497,625
;; PRIOR FILING DATE: 2000-02-03
;; PRIOR APPLICATION NUMBER: 09/359,193
;; PRIOR FILING DATE: 1999-07-22
;; PRIOR APPLICATION NUMBER: 09/121,781
;; PRIOR FILING DATE: 1998-07-23
;; NUMBER OF SEQ ID NOS: 107
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 23
;; LENGTH: 100
;; TYPE: PRT
;; ORGANISM: Mus musculus
US-09-840-459-23

Query Match 79.0%; Score 64; DB 10; Length 100;
Best Local Similarity 75.0%; Pred. No. 0.0017;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
:|||||:|||||
Db 24 KSSQSLLYSNGKTYLN 39

RESULT 7

US-09-840-459-24
; Sequence 24, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Newman, Walter
; APPLICANT: Horvath, Christopher
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
; NAME/KEY: VARIANT
; LOCATION: (1)...(100)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-840-459-24

Query Match 79.0%; Score 64; DB 10; Length 100;
Best Local Similarity 75.0%; Pred. No. 0.0017;
Matches 12; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
:|||||:|||||
Db 24 KSSQSLLYSNGKTYLN 39

RESULT 8

US-09-840-459-56
; Sequence 56, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-56

Query Match 79.0%; Score 64; DB 10; Length 112;
Best Local Similarity 75.0%; Pred. No. 0.0019;
Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
:|||||:|||||
Db 24 RSSQSLVYSDGNTYLN 39

RESULT 9

US-09-840-459-66
; Sequence 66, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 66
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens

Search completed: April 22, 2003, 13:11:11
Job time : 17.8571 secs

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; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 70
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-70

Query Match      75.3%; Score 61; DB 10; Length 112;
Best Local Similarity 68.8%; Pred.No. 0.006;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 RSSKSLLYKDGKTYLN 16
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Db 24 RSSQSLVPSDGNLYLN 39

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RESULT 15
US-09-840-459-62
; Sequence 62, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 62
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-840-459-62

Query Match      74.1%; Score 60; DB 10; Length 112;
Best Local Similarity 68.8%; Pred.No. 0.0087;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 RSSKSLLYKDGKTYLN 16
|||:|||||
Db 24 RSSQSLVPSDGNLYLN 39

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GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:46:53 ; Search time 3.5 Seconds
(without alignments)
82.953 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	100.0	112	1 KV2A MOUSE	P01626 mus musculus
2	31	100.0	113	1 KV2C MOUSE	P01628 mus musculus
3	31	100.0	120	1 KV2E MOUSE	P01627 mus musculus
4	27	87.1	104	1 YHGB BACSU	P38048 bacillus su
5	27	87.1	234	1 YHKO YEAST	P40011 saccharomyc
6	27	87.1	760	1 MCMW SCHPO	O75001 schizosacch
7	27	87.1	845	1 CC47 YEAST	P38132 saccharomyc
8	27	87.1	1401	1 WIS4 SCHPO	O14299 schizosacch
9	26	83.9	193	1 RS3A SULTO	Q97558 sulfolobus
10	26	83.9	341	1 NU2M DROME	P03896 drosophila
11	26	83.9	341	1 NU2M DROME	P03896 drosophila
12	26	83.9	1453	1 CALL1 MOUSE	P11087 mus musculus
13	26	83.9	1460	1 CALL1 CANFA	O9X817 canis famil
14	26	83.9	1464	1 CALL1 HUMAN	P02452 homo sapien
15	25	80.6	212	1 AG11 WHEAT	P10968 triticum ae
16	25	80.6	212	1 AG1 HORVU	P15312 hordeum vul
17	25	80.6	463	1 D2DR FUGRU	P53453 fugu rubrip
18	25	80.6	565	1 TP6B AERPE	Q9ye64 aeropyrum p
19	25	80.6	664	1 ALOX PTCAN	P04841 pichia angu
20	25	80.6	778	1 YFK8 YEAST	P43610 saccharomyc
21	25	80.6	887	1 YAY5 SCHPO	Q10213 schizosacch
22	24	77.4	176	1 Y059 NPVOP	O10316 orgyia pseu
23	24	77.4	228	1 EBP CAVPO	Q60490 cavia porce
24	24	77.4	230	1 EBP MOUSE	P70245 mus musculus
25	24	77.4	250	1 PP26 BRUME	Q57099 bruceella me
26	24	77.4	259	1 PP26 BRUAB	Q44642 bruceella ab
27	24	77.4	312	1 YG37 YEAST	P53275 saccharomyc
28	24	77.4	339	1 G3P MYCTU	O06822 mycobacteri
29	24	77.4	443	1 FBL4 CRIGR	O55058 cricetulus
30	24	77.4	443	1 FBL4 HUMAN	O95967 homo sapien
31	24	77.4	443	1 FBL4 MOUSE	Q9wv79 mus musculu
32	24	77.4	463	1 SAHH CAUCR	Q9abh0 caulobacter
33	24	77.4	543	1 NFL_HUMAN	P07196 homo sapien

34	24	77.4	548	1 NFL_PIG	P02547 sus scrofa
35	24	77.4	584	1 PARF PARTE	P47244 paramecium
36	24	77.4	636	1 CAI3 RAT	P13941 rattus norv
37	24	77.4	766	1 METE YEAST	P05694 saccharomyc
38	24	77.4	859	1 ALR1 YEAST	Q08269 saccharomyc
39	24	77.4	909	1 Y4GI RHISN	P55465 rhizobium s
40	24	77.4	925	1 YBK4 YEAST	P38164 saccharomyc
41	24	77.4	1359	1 STH1 YEAST	P32597 saccharomyc
42	24	77.4	1373	1 HRP1 SCHPO	Q9u825 schizosacch
43	24	77.4	1388	1 HRP3 SCHPO	O14139 schizosacch
44	24	77.4	1420	1 APX XENLA	Q01613 xenopus lae
45	24	77.4	1464	1 CAI3_MOUSE	P08121 mus musculu

ALIGNMENTS

RESULT 1
KV2A_MOUSE
ID KV2A_MOUSE STANDARD; PRT; 112 AA.
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
RP SEQUENCE.
RX MEDLINE=79000273; PubMed=99160;
RA Rudnikoff S., Potter M.;
RT "Kappa Chain variable region from M167, a phosphorylcholine binding
myeloma protein.";
RL Biochemistry 17:2703-2707(1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY
CHAIN HAS ALSO BEEN DETERMINED.
CC PIR; A01908; KVM516.
DR HSP; P80362; 1WTL.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IG; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 123 93
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD640B9726 CRC64;
Query Match 100.0%; Score 31; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 2
KV2C_MOUSE
ID KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

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DE IG kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT "Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
CC PIR: A01910; KVM51.
DR HSSP: P80362; LWT.
DR InterPro: IPR003006; IG MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT SIGNAL 1 23
FT CHAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 55 LMSTRAS 61

RESULT 3
KV2B_MOUSE STANDARD; PRT; 120 AA.
AC P01627;
AT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-II region VKAPPA167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82002223; PubMed=6791832;
RA Seising E., Storb U.;
RT "Somatic mutation of immunoglobulin light-chain variable-region
RT genes.";
RL Cell 25:47-58(1981).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: J00562; AAA39032.1; -
DR AFBL: K02415; AAA39051.1; -
DR PIR: A01909; KVM567.
DR HSSP: P80362; LWT.
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DR InterPro: IPR003006; IG MHC.
DR InterPro: IPR003596; IG_v.
DR Pfam: PF00047; IG; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 120
FT DOMAIN 21 43
FT DOMAIN 44 59
FT DOMAIN 60 74
FT DOMAIN 75 81
FT DOMAIN 82 113
FT DOMAIN 114 120
FT DISULFID 43 113
FT SEQUENCE 120 AA; 638571F0E4DE3E8 CRC64;

Query Match 100.0%; Score 31; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 75 LMSTRAS 81

RESULT 4
YHGB_BACSU STANDARD; PRT; 104 AA.
ID YHGB_BACSU
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yhgb.
GN YHGB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RA Noback M.A., Terpestra P., Holsappel S., Venema G., Bron S.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritze C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rev M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche S., Rose M., Sadaie Y.,
RA Sato T., Scanlan E.J., Schleich S., Schroeter R., Scofield P.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Taconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoehi A., Tanaka T., Terpetra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Yamane K., Yasumoto K., Yata K.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
```


RA Yoshida K., Yoshikawa H.F., Zunstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
RT *subtilis*.";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-67 FROM N.A.
RC STRAIN=168;
RX MEDLINE=93328693; PubMed=8335642;
RA Popham D.L., Setlow P.;
RT "Cloning, nucleotide sequence, and regulation of the *Bacillus*
RT *subtilis* pbpF gene, which codes for a putative class A
RT high-molecular-weight penicillin-binding protein.";
RL J. Bacteriol. 175:4870-4876(1993).
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CC -----
CC EMBL; Y14083; CAA74515.1; -;
DR EMBL; Z99109; CAB12849.1; -;
DR EMBL; L10630; AAB71940.2; -;
DR PIR; C40614; C40614.
DR Subtilisin; EG10426; yhgB.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 104 AA; 11998 MW; 6B44CD77B52FD968 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 104;
Best Local Similarity 85.7%; Pred. No. 3.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 38 LMSTRCS 44

RESULT 5
YER0_YEAST
ID YER0_YEAST STANDARD; PRT; 234 AA.
AC P40011;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 25.6 kDa protein in NTF2-SRP1 intergenic region.
GN YER010C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Dietrich F.S., Mullen J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
CC EMBL; U18778; AAB64543.1; -;
DR

DR SGD; S0000812; YER010C.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25563 MW; EC109F224240F980 CRC64;

Query Match 87.1%; Score 27; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 6
Db 102 LMSTRAS 107

RESULT 6
MCM7_SCHPO
ID MCM7_SCHPO STANDARD; PRT; 760 AA.
AC O75001; P87302;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA replication licensing factor mcm7 (Minichromosome maintenance
DE protein 7).
GN MCM7 OR SPBC25D12.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=011;
RA Liang D.T., Forsburg S.L.;
RT "Fission yeast mcm7+ is an essential gene required for normal DNA
RT replication.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Mosatl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas R., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of *Schizosaccharomyces pombe*.";
RL Nature 415:871-880(2002).
RN [3]
RP SEQUENCE OF 367-466 FROM N.A.
RC STRAIN=972;
RX MEDLINE=98031880; PubMed=9366552;
RA Adachi Y., Usukura J., Yanagida M.;
RT "A globular complex formation by Nda1 and the other five members of
RT the MCM protein family in fission yeast.";
RL Genes Cells 2:467-479(1997).

CC -!- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE MCM FAMILY.
CC
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CC
CC EMBL; AF070481; AAC33693.1; -
CC EMBL; AL031158; CAA20099.1; -
CC EMBL; AJ000065; CAA03898.1; -
CC InterPro; IPR001208; MCM.
CC Pfam; PF00493; MCM; 1.
CC ProDom; PD001041; MCM; 1.
CC SMART; SM00350; MCM; 1.
CC PROSITE; PS00847; MCM 1; 1.
CC PROSITE; PS0051; MCM 2; 1.
CC Transcription regulation; DNA-binding; Nuclear protein;
CC DNA replication; Cell cycle; ATP-binding.
CC DOMAIN 353 559 MCM.
CC NP_BIND 403 410 ATP (POTENTIAL).
CC NP_BIND 457 457 V -> I (IN REF. 3).
CC CONFLICT 457 457
CC SEQUENCE 760 AA; 85622 MW; 2141F9FCB0BAA34 CRC64;
CC
CC Query Match 87.1%; Score 27; DB 1; Length 760;
CC Best Local Similarity 100.0%; Pred. No. 29;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 2 MSTRAS 7
CC DB 243 MSTRAS 248
CC
CC RESULT 7
CC ID CC47_YEAST STANDARD; PRT; 845 AA.
CC AC F38132;
CC DT 01-OCT-1994 (Rel. 30, Created)
CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE DNA replication licensing factor CDC47 (Cell division control protein
CC 47).
CC DE CDC47 OR YER202W OR YBR1441.
CC OS Saccharomyces cerevisiae (Baker's yeast).
CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
CC OX NCBI_TaxID=4932;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RA Dalton S.;
CC RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=S288c;
CC RX MEDLINE=93377417; PubMed=8368014;
CC RA Bussereau F., Mallet L., Gallion L., Jacquet M.;
CC RT "A 12.8 kb segment, on the right arm of chromosome II from
CC Saccharomyces cerevisiae including part of the DUK1,2 gene, contains
CC five putative new genes."
CC RL Yeast 9:797-806 (1993).
CC CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: BELONGS TO THE MCM FAMILY.
CC
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CC

CC EMBL; U14730; AAA86309.1; -
CC EMBL; Z21487; CAA79689.1; -
CC EMBL; Z36071; CAA85166.1; -
CC PIR; S34027; S34027.
CC SGD; S0000406; CDC47.
CC InterPro; IPR001208; MCM.
CC Pfam; PF00493; MCM; 1.
CC ProDom; PD001041; MCM; 1.
CC SMART; SM00350; MCM; 1.
CC PROSITE; PS00847; MCM 1; 1.
CC PROSITE; PS0051; MCM 2; 1.
CC Transcription regulation; DNA-binding; Nuclear protein;
CC DNA replication; Cell cycle; ATP-binding.
CC DOMAIN 410 617 MCM.
CC NP_BIND 460 467 ATP (POTENTIAL).
CC NP_BIND 552 552 G -> V (IN REF. 2).
CC CONFLICT 556 558 TLN -> NFG (IN REF. 2).
CC CONFLICT 574 574 Y -> I (IN REF. 2).
CC SEQUENCE 845 AA; 94942 MW; ADA66C719D96DB4A CRC64;
CC
CC Query Match 87.1%; Score 27; DB 1; Length 845;
CC Best Local Similarity 100.0%; Pred. No. 33;
CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 2 MSTRAS 7
CC DB 300 MSTRAS 305
CC
CC RESULT 8
CC ID WIS4_SCHPO STANDARD; PRT; 1401 AA.
CC AC O14299; P87062; Q92384;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE MAP kinase kinase kinase wis4 (EC 2.7.1.-) (MAP kinase kinase kinase
CC wisk1) (MAP kinase kinase kinase wisk1).
CC DE WIS4 OR WAK1 OR WIKI OR SPAC9G1.02.
CC GN Schizosaccharomyces pombe (Fission yeast).
CC OS Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
CC OC Schizosaccharomycetales; Schizosaccharomycetaceae;
CC OC Schizosaccharomycetes.
CC OX NCBI_TaxID=4896;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=98026892; PubMed=9321395;
CC RA Samejima I., Mackie S., Fantes P.A.;
CC RT "Multiple modes of activation of the stress-responsive MAP kinase
CC pathway in fission yeast."
CC RL EMBO J. 16:6162-6170 (1997).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=972;
CC RX MEDLINE=21848401; PubMed=11859360;
CC RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
CC RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
CC RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
CC RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
CC RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
CC RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
CC RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
CC RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
CC RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
CC RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
CC RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
CC RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
CC RA Woodward J., Volkart G., Aert R., Robben J., Grymprez B.,
CC RA Weltjens I., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
CC RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
CC RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
CC Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Goffeau A., Cadieu B., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garçon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of *Schizosaccharomyces pombe*.";
 RN Nature 415:871-880(2002).
 RN [3]
 RP SEQUENCE OF 96-1401 FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=97282620; PubMed=9136929;
 RA Shieh J.C., Wilkinson M., Buck V., Morgan B., Makino K.,
 RA Millar J.B.A.;
 RT "The Mca4 response regulator coordinately controls the stress-
 RT activated Wsk1-Wsk1-Styl MAP kinase pathway and fission yeast cell
 RT cycle.";
 RL Genes Dev. 11:1008-1022(1997).
 RN [4]
 RP SEQUENCE OF 457-543 FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=97331762; PubMed=9188094;
 RA Shiozaki K., Shiozaki M., Russell P.;
 RT "Mca4 mitotic catastrophe suppressor regulates the fission yeast cell
 RT cycle through the Wsk1-Wsk1-Spc1 kinase cascade.";
 RL Mol. Biol. Cell 8:409-419(1997).
 CC -!- FUNCTION: INVOLVED IN A SIGNAL TRANSDUCTION PATHWAY THAT IS
 CC ACTIVATED IN UNDER CONDITIONS OF HEAT SHOCK, OXIDATIVE STRESS OR
 CC LIMITED NUTRITION. UNLIKE WSK1, IT IS NOT ACTIVATED BY CHANGES IN
 CC THE OSMOLARITY OF THE EXTRACELLULAR ENVIRONMENT. ACTIVATES THE
 CC WSK1 MAP KINASE KINASE BY PHOSPHORYLATION.
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC MAP KINASE KINASE SUBFAMILY.
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 DR EMBL; Z98763; CAB11500.1; -;
 DR EMBL; Y07750; CAA69030.1; ALT_INIT.
 DR EMBL; Y11989; CAA72718.1; -;
 DR EMBL; U81521; AAB39762.1; -;
 DR HSP; P24941; 1CXP.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR002290; Ser_thr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
 DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 1037 1306 PROTEIN KINASE.
 FT NP_BIND 1043 1051 ATP (BY SIMILARITY).
 FT BINDING 1066 1066 ATP (BY SIMILARITY).
 FT ACT_SITE 1161 1161 BY SIMILARITY.
 FT CONFLICT 484 485 RL -> SP (IN REF. 3).
 FT CONFLICT 1346 1346 D -> V (IN REF. 1).
 SQ SEQUENCE 1401 AA; 160537 MW; 529A989D2B627F3D CRC64;

Query Match 87.1%; Score 27; DB 1; Length 1401;
 Best Local Similarity 85.7%; Pred. No. 58;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 |||||
 DB 81 LMSTRAS 87

RESULT 9
 RS3A_SULTO STANDARD; PRT; 193 AA.
 ID RS3A_SULTO
 AC Q975F8;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S3Ae.
 GN RPS3AE OR S70453.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermophilic
 RT Crenarchaeon, *Sulfolobus tokodaii* strain 7.";
 RL DNA Res. 8:123-140(2001).
 CC -!- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL; AP000982; BAB65443.1; -;
 DR InterPro; IPR001593; Ribosomal_S3AE.
 DR Pfam; PF01015; Ribosomal_S3AE; 1.
 DR ProDom; PD003035; Ribosomal_S3AE; 1.
 DR PROSITE; PS01191; RIBOSOMAL_S3AE; FALSE_NEG.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 193 AA; 22180 MW; 78A94B87B961D751 CRC64;
 Query Match 83.9%; Score 26; DB 1; Length 193;
 Best Local Similarity 71.4%; Pred. No. 12;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 :|||:
 DB 142 ILSTRAS 148

RESULT 10
 NU2M_DROME STANDARD; PRT; 341 AA.
 ID NU2M_DROME
 AC P03896;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NADH-ubiquinone oxidoreductase chain 2 (EC 1.6.5.3).
 GN ND2.
 OS Drosophila melanogaster (Fruit fly).
 OG Mitochondrion.
 OC Rukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Sphingroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96423163; PubMed=8825764;
 RA Lewis D.L., Farr C.L., Kaguni L.S.;

```

RT "Drosophila melanogaster mitochondrial DNA: completion of the
RT nucleotide sequence and evolutionary Comparisons.";
RL Insect Mol. Biol. 4:263-278(1995).
[2]
RN SEQUENCE OF 56-341 FROM N.A.
RX MEDLINE=83245048; PubMed=6408489;
RA de Bruijn M.H.L.;
RT "Drosophila melanogaster mitochondrial DNA, a novel organization and
RT genetic code.";
RL Nature 304:234-241(1983).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
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DR EMBL; U37541; AAC47811.1; -.
DR EMBL; J01404; AAB59238.1; -.
DR PIR; A00419; OXFF2M
DR FlyBase; FBgn0013680; mt:ND2.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
DR Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
KW OXIDOREDUCTASE; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 341 AA; 39773 MW; 2B8E9528C28007D8 CRC64;

Query Match 83.9%; Score 26; DB 1; Length 341;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 51 LMSTAS 57

RESULT 11
NU2M DROVA
ID NU2M DROVA STANDARD; PRT; 341 AA.
AC P03895;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 2 [EC 1.6.5.3].
GN ND2.
OS Drosophila yakuba (Fruit fly).
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7245;
[1]
RN SEQUENCE FROM N.A.
RX STRAIN=2317.6 Ivory Coast;
RA MEDLINE=86089137; PubMed=3001325;
RT Clary D.O., Wolstenholme D.R.;
RT "The mitochondrial DNA molecular of Drosophila yakuba: nucleotide
RT sequence, gene organization, and genetic code.";
RL J. Mol. Evol. 22:252-271(1985).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=84041489; PubMed=6314262;
RA Clary D.O., Wolstenholme D.R.;
RT "Genes for cytochrome c oxidase subunit I, URF2, and three tRNAs in
RT Drosophila mitochondrial DNA.";
RL Nucleic Acids Res. 11:6859-6872(1983).
[3]
RN SEQUENCE OF 1-56 FROM N.A.

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RX MEDLINE=83090428; PubMed=6294611;
RA Clary D.O., Goddard J.M., Martin S.C., Fauron C.M.-R.,
RA Wolstenholme D.R.;
RT "Drosophila mitochondrial DNA: a novel gene order.";
RL Nucleic Acids Res. 10:6619-6637(1982).
[4]
RN SEQUENCE OF 1-56 FROM N.A.
RX MEDLINE=88011348; PubMed=3116271;
RA Clary D.O., Wolstenholme D.R.;
RT "Drosophila mitochondrial DNA: conserved sequences in the A + T-rich
RT region and supporting evidence for a secondary structure model of the
RT small ribosomal RNA.";
RL J. Mol. Evol. 25:116-125(1987).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
DR EMBL; X03240; CAA26985.1; -.
DR EMBL; X05915; CAA29342.1; -.
DR PIR; A00418; OXFF2Y.
DR PIR; A25797; A25797.
DR FlyBase; FBgn0013184; Dyak\mt:ND2.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
DR Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
KW OXIDOREDUCTASE; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ SEQUENCE 341 AA; 39495 MW; 56117DE50BE9D4AF CRC64;

Query Match 83.9%; Score 26; DB 1; Length 341;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 51 LMSTAS 57

RESULT 12
CALL MOUSE
ID CALL MOUSE STANDARD; PRT; 1453 AA.
AC P11087; Q60635;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Collagen alpha 1(I) chain precursor.
DE COL1A1 OR COLA1.
GN COL1A1 OR COLA1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N;
RX MEDLINE=96033240; PubMed=8535610;
RA Li S.W., Khillan J., Prockop D.J.;
RT "The complete cDNA coding sequence for the mouse pro alpha 1(I) chain
RT of type I procollagen.";
RL Matrix Biol. 14:593-595(1995).
[2]
RN SEQUENCE OF 518-1128 FROM N.A.
RX MEDLINE=86137403; PubMed=3641523;
RA French B.T., Lee W.-H., Maul G.G.;
RT "Nucleotide sequence of a cDNA clone for mouse pro alpha 1(I)
RT collagen protein.";
RL Gene 39:311-312(1985).

```

[3] SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
 RP MEDLINE=831517109; PubMed=6298597;
 RA Monson J.M., Friedman J., McCarthy B.J.;
 RT "DNA sequence analysis of a mouse pro alpha 1 (I) procollagen gene:
 FT evidence for a mouse B1 element within the gene";
 RL Mol. Cell. Biol. 2:1362-1371(1982).
 [4]
 RP SEQUENCE OF 735-878 AND 1005-1058 FROM N.A.
 RX MEDLINE=831517109; PubMed=6219867;
 RA Monson J.M., McCarthy B.J.;
 RT "Identification of a Balb/c mouse pro alpha 1(I) procollagen gene:
 FT evidence for insertions or deletions in gene coding sequences";
 RL DNA 1:59-69(1981).
 [5]
 RP SEQUENCE OF 1442-1453 FROM N.A.
 RX MEDLINE=88124276; PubMed=3340560;
 RA Mooslechner K., Harbers K.;
 RT "Two mRNAs of mouse pro alpha 1(I) collagen gene differ in the size
 of the 3'-untranslated region";
 RL Nucleic Acids Res. 16:773-773(1988).
 CC -!- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
 (FIBRILLAR FORMING COLLAGEN).
 CC -!- SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.
 CC -!- TISSUE SPECIFICITY: FORMS THE FIBRILS OF TENDON, LIGAMENTS AND
 BONES. IN BONES THE FIBRILS ARE MINERALIZED WITH CALCIUM
 HYDROXYAPATITE.
 CC -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
 UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
 CC -!- SIMILARITY: CONTAINS 1 VFEC DOMAIN.
 CC
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 CC
 CC EMBL; U08020; AAA88912.1; -
 DR EMBL; X15896; AAA33904.1; -
 DR EMBL; M14423; AAA37333.1; -
 DR EMBL; M17491; AAA37334.1; -
 DR EMBL; X06753; CAA29927.1; -
 DR EMBL; K03036; AAA37332.1; -
 DR EMBL; K03029; AAA37332.1; JOINED.
 DR EMBL; K03030; AAA37332.1; JOINED.
 DR EMBL; K03031; AAA37332.1; JOINED.
 DR EMBL; K03032; AAA37332.1; JOINED.
 DR EMBL; K03033; AAA37332.1; JOINED.
 DR EMBL; K03034; AAA37332.1; JOINED.
 DR EMBL; K03035; AAA37332.1; JOINED.
 DR PIR; A23982; A23982.
 DR MGD; MGI:88467; Collagen.
 DR InterPro; IPR000087; Collagen.
 DR InterPro; IPR000885; Fib collagen_C.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01391; Collagen_18.
 DR Pfam; PF01410; COLFI; 1.
 DR ProDom; PD000007; Collagen; 1.
 DR ProDom; PD002078; Fib collagen_C; 1.
 DR SMART; SM00038; COLFI; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS01208; VWF; 1.
 DR Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Glycoprotein; Collagen; Signal.
 FT SIGNAL 1 22
 FT PROPEP 23 151 AMINO-TERMINAL PROPEPTIDE.
 FT CHAIN 152 1207 COLLAGEN ALPHA 1(I) CHAIN.
 FT PROPEP 1208 1453 CARBOXYL-TERMINAL PROPEPTIDE.
 FT DOMAIN 29 87 VWF.
 FT DOMAIN 152 167 NONHELICAL REGION (N-TERMINAL).
 FT DOMAIN 168 1181 TRIPLE-HELICAL REGION.

FT DOMAIN 1182 1207 NONHELICAL REGION (C-TERMINAL).
 FT CARBOHYD 56 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1354 1354 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT SITE 734 736 CELL ATTACHMENT SITE (POTENTIAL).
 FT SITE 1082 1084 CELL ATTACHMENT SITE (POTENTIAL).
 FT CONFLICT 1450 1450 A -> V (IN REF. 5).
 SQ SEQUENCE 1453 AA; 137944 MW; 3B802E535DF81808 CRC64;
 Query Match 83.9%; Score 26; DB 1; Length 1453;
 Best Local Similarity 85.7%; Pred. No. 1.le-02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 DB 1346 LMSTRAS 1352
 RESULT 13
 ID CAN1 CANFA STANDARD; PRT; 1460 AA.
 AC Q9X5J7.
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DE 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Collagen alpha 1(I) chain precursor.
 GN COL1A1.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Skin;
 RA Campbell B.G., Wootton J.A.M., McLeod J.N., Minor R.R.;
 RT "Sequence of normal canine COL1A1 cDNA";
 Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: TYPE I COLLAGEN IS A MEMBER OF GROUP I COLLAGEN
 (FIBRILLAR FORMING COLLAGEN).
 CC -!- SUBUNIT: TRIMERS OF ONE ALPHA 2(I) AND TWO ALPHA 1(I) CHAINS.
 CC -!- PTM: PROLINES AT THE THIRD POSITION OF THE TRIPEPTIDE REPEATING
 UNIT (G-X-Y) ARE HYDROXYLATED IN SOME OR ALL OF THE CHAINS.
 CC -!- SIMILARITY: CONTAINS 1 VFEC DOMAIN.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF153062; AAD34619.1; -
 DR InterPro; IPR000087; Collagen.
 DR InterPro; IPR000885; Fib collagen_C.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01391; Collagen; 18.
 DR Pfam; PF01410; COLFI; 1.
 DR ProDom; PD000007; Collagen; 1.
 DR ProDom; PD002078; Fib collagen_C; 1.
 DR SMART; SM00038; COLFI; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS01208; VWF; 1.
 DR Extracellular matrix; Connective tissue; Repeat; Hydroxylation;
 KW Glycoprotein; Collagen; Signal.
 FT SIGNAL 1 22
 FT PROPEP 23 157 AMINO-TERMINAL PROPEPTIDE.
 FT CHAIN 158 1214 COLLAGEN ALPHA 1(I) CHAIN.
 FT PROPEP 1215 1460 CARBOXYL-TERMINAL PROPEPTIDE.
 FT DOMAIN 34 52 VWF.
 FT DOMAIN 158 174 NONHELICAL REGION (N-TERMINAL).
 FT DOMAIN 175 1188 TRIPLE-HELICAL REGION.
 FT DOMAIN 1189 1214 NONHELICAL REGION (C-TERMINAL).
 FT DOMAIN 741 743 CELL ATTACHMENT SITE (POTENTIAL).

FT SITE 1089 1091 CELL ATTACHMENT SITE (POTENTIAL).
 FT CARBOHYD 1361 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 1460 AA; 138762 NW; 58E3674D2B570697 CRC64;
 Query Match 83.9%; Score 26; DB 1; Length 1460;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
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 Db 1353 LMSTRAS 1359

RESULT 14
 CALL HUMAN
 ID CALL_HUMAN STANDARD; PRT; 1464 AA.
 AC P02452; Q15176; Q14037;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Collagen alpha 1(I) chain precursor.
 GN COL1A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 1-472 FROM N.A.
 RX MEDLINE=89025644; PubMed=3178743;
 RA Tromp G., Kuivaniemi H., Stacey A., Shikata H., Baldwin C.T.,
 Jaenisch R., Prockop D.J.;
 RT "Structure of a full-length cDNA clone for the prepro alpha 1(I)
 chain of human type I procollagen.";
 RL Biochem. J. 253:919-922(1988).
 RN [2]
 RP SEQUENCE OF 1-181 FROM N.A.
 RX MEDLINE=84270697; PubMed=6462220;
 RA Chu M.-L., de Wet W.J., Bernard M.P., Ding J.-F., Morabito M.,
 Myers J., Williams C., Ramirez F.;
 RT "Human pro alpha 1(I) collagen gene structure reveals evolutionary
 conservation of a pattern of introns and exons.";
 RL Nature 310:337-340(1984).
 RN [3]
 RP SEQUENCE OF 162-301.
 RC TISSUE=Skin;
 RX MEDLINE=71038625; PubMed=5529814;
 RA Click E.M., Bornstein P.;
 RT "Isolation and characterization of the cyanogen bromide peptides from
 the alpha 1 and alpha 2 chains of human skin collagen.";
 RL Biochemistry 9:4699-4706(1970).
 RN [4]
 RP SEQUENCE OF 263-268.
 RC TISSUE=Skin;
 RX MEDLINE=71001508; PubMed=4319110;
 RA Morgan P.H., Jacobs H.G., Segrest J.P., Cunningham L.W.;
 RT "A comparative study of glycopeptides derived from selected
 vertebrate collagens. A possible role of the carbohydrate in fibril
 formation.";
 RL J. Biol. Chem. 245:5042-5048(1970).
 RN [5]
 RP SEQUENCE OF 425-1464 FROM N.A.
 RX MEDLINE=84080385; PubMed=6689127;
 RA Bernard M.P., Chu M.-L., Myers J.C., Ramirez F., Eikenberry E.F.,
 Prockop D.J.;
 RT "Nucleotide sequences of complementary deoxyribonucleic acids for the
 pro alpha 1 chain of human type I procollagen. Statistical evaluation
 of structures that are conserved during evolution.";
 RL Biochemistry 22:5213-5223(1983).
 RN [6]
 RP SEQUENCE OF 1229-1454 FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=88124208; PubMed=3340531;
 RA Mackelae J.K., Raassina M., Virta A., Vuorio E.;

RT "Human pro alpha 1(I) collagen: cDNA sequence for the C-propeptide
 domain.";
 RL Nucleic Acids Res. 16:349-349(1988).
 RN [7]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=88097389; PubMed=3480516;
 RA Bornstein P., McKay J., Morishima J.K., Devarayalu S., Gelinas R.E.;
 RT "Regulatory elements in the first intron contribute to
 transcriptional control of the human alpha 1(I) collagen gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8869-8873(1987).
 RN [8]
 RP SEQUENCE OF 1-34 FROM N.A.
 RX MEDLINE=85130970; PubMed=2857713;
 RA Chu M.-L., de Wet W.J., Bernard M.P., Ramirez F.;
 RT "Fine structural analysis of the human pro-alpha 1 (I) collagen gene.
 Promoter structure, Alu repeats, and polymorphic transcripts.";
 RL J. Biol. Chem. 260:2315-2320(1985).
 RN [9]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=88033098; PubMed=2822714;
 RA Roesouw C.M.S., Vergeer W.P., du Plooy S.J., Bernard M.P., Ramirez F.,
 de Wet W.J.;
 RT "DNA sequences in the first intron of the human pro-alpha 1(I)
 collagen gene enhance transcription.";
 RL J. Biol. Chem. 262:15151-15157(1987).
 RN [10]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=91184577; PubMed=2010058;
 RA Kuivaniemi H., Tromp G., Prockop D.J.;
 RT "Mutations in collagen genes: causes of rare and some common diseases
 in humans.";
 RL FASEB J. 5:2052-2060(1991).
 RN [11]
 RP REVIEW ON VARIANTS.
 RX MEDLINE=97255959; PubMed=9101290;
 RA Kuivaniemi H., Tromp G., Prockop D.J.;
 RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
 associated collagen (type IX), and network-forming collagen (type X)
 cause a spectrum of diseases of bone, cartilage, and blood vessels.";
 RL Hum. Mutat. 9:300-315(1997).
 RN [12]
 RP REVIEW ON OI VARIANTS.
 RX MEDLINE=91374476; PubMed=1895312;
 RA Byers P.H., Wallis G.A., Willing M.C.;
 RT "Osteogenesis imperfecta: translation of mutation to phenotype.";
 RL J. Med. Genet. 28:433-442(1991).
 RN [13]
 RP REVIEW ON OI VARIANTS.
 RX MEDLINE=97169389; PubMed=9016532;
 RA Dalgleish R.;
 RT "The human type I collagen mutation database.";
 RL Nucleic Acids Res. 25:181-187(1997).
 RN [14]
 RP VARIANT OI-II CYS-1166.
 RX MEDLINE=86287390; PubMed=3016737;
 RA Cohn D.H., Byers P.H., Steinmann B., Gelinas R.E.;
 RT "Lethal osteogenesis imperfecta resulting from a single nucleotide
 change in one human pro alpha 1(I) collagen allele.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:6045-6047(1986).
 RN [15]
 RP VARIANT OI-II ARG-569.
 RX MEDLINE=87222295; PubMed=3108247;
 RA Bateman J.F., Chan D., Walkers I.D., Rogers J.G., Cole W.G.;
 RT "Lethal perinatal osteogenesis imperfecta due to the substitution of
 arginine for glycine at residue 391 of the alpha 1(I) chain of type I
 collagen.";
 RL J. Biol. Chem. 262:7021-7027(1987).
 RN [16]
 RP VARIANT OI-II CYS-926.
 RX MEDLINE=88033031; PubMed=3667599;
 RA Vogel B.E., Minor R.R., Freund M., Prockop D.J.;
 RT "A point mutation in a type I procollagen gene converts glycine 748
 of the alpha 1 chain to cysteine and destabilizes the triple helix in

RT a lethal variant of osteogenesis imperfecta.";
 RL J. Biol. Chem. 262:14737-14744(1987).
 RN [17]
 RP VARIANT OI-II ARG-842.
 RX MEDLINE=88298828; PubMed=3403550;
 RA Bateman J.F., Lamané S.R., Dahl H.H., Chan D., Cole W.G.;
 RT "Substitution of arginine for glycine-664 in the collagen alpha 1(I)
 chain in lethal perinatal osteogenesis imperfecta. Demonstration of
 the peptide defect by in vitro expression of the mutant cDNA.";
 RL J. Biol. Chem. 263:11627-11630(1988).
 RN [18]
 RP VARIANT OI CYS-1195.
 RX MEDLINE=89218628; PubMed=3244312;
 RA Labhard M.E., Wirtz M.K., Pope F.M., Nicholls A.C., Hollister D.W.;
 RT "A cysteine for glycine substitution at position 1017 in an alpha
 1(I) chain of type I collagen in a patient with mild dominantly
 inherited osteogenesis imperfecta.";
 RL Mol. Biol. Med. 5:197-207(1988).
 RN [19]
 RP VARIANT OI-II VAL-434.
 RX MEDLINE=89255493; PubMed=2470760;
 RA Patterson E., Smiley E., Bonadio J.;
 RT "RNA sequence analysis of a perinatal lethal osteogenesis imperfecta
 mutation.";
 RL J. Biol. Chem. 264:10083-10087(1989).
 RN [20]
 RP VARIANT OI-IV SER-1010.
 RX MEDLINE=89308591; PubMed=2745420;
 RA Marini J.C., Grange D.K., Gottesman G.S., Lewis M.B., Koepf D.A.;
 RT "Osteogenesis imperfecta type IV. Detection of a point mutation in
 one alpha 1(I) collagen allele (COL1A1) by RNA/RNA hybrid analysis.";
 RL J. Biol. Chem. 264:11893-11900(1989).
 RN [21]
 RP VARIANTS OI-II ALA-1106; VAL-1151; ARG-1154 AND VAL-1184.
 RX MEDLINE=89380165; PubMed=2777764;
 RA Lamané S.R., Dahl H.-H.M., Cole W.G., Bateman J.F.;
 RT "Characterization of point mutations in the collagen COL1A1 and
 COL1A2 genes causing lethal perinatal osteogenesis imperfecta.";
 RL J. Biol. Chem. 264:15809-15812(1989).
 RN [22]
 RP VARIANT OI SER-1022.
 RX MEDLINE=90062068; PubMed=2511192;
 RA Pack M., Constantinou C.D., Kalia K., Nielsen K.B., Prockop D.J.;
 RT "Substitution of serine for alpha 1(I)-glycine 844 in a severe
 variant of osteogenesis imperfecta minimally destabilizes the triple
 helix of type I procollagen. The effects of glycine substitutions on
 thermal stability are either position of amino acid specific.";
 RL J. Biol. Chem. 264:19694-19699(1989).
 RN [23]
 RP VARIANT OI-II CYS-1082.
 RX MEDLINE=89109573; PubMed=2913053;
 RA Constantinou C.D., Nielsen K.B., Prockop D.J.;
 RT "A lethal variant of osteogenesis imperfecta has a single base
 mutation that substitutes cysteine for glycine 904 of the alpha 1(I)
 chain of type I procollagen. The asymptomatic mother has an
 unidentified mutation producing an overmodified and unstable type I
 procollagen.";
 RL J. Clin. Invest. 83:574-584(1989).
 RN [24]
 RP VARIANTS OI CYS-272; CYS-704 AND CYS-896.
 RX MEDLINE=90009313; PubMed=2794057;
 RA Starman B.J., Eyre D., Charbonneau H., Harrylock M., Weis M.A.,
 RA Weiss L., Graham J.M., Byers P.H.;
 RT "Osteogenesis imperfecta. The position of substitution for glycine by
 cysteine in the triple helical domain of the pro alpha 1(I) chains of
 type I collagen determines the clinical phenotype.";
 RL J. Clin. Invest. 84:1206-1214(1989).
 RN [25]
 RP VARIANT OI-II CYS-422.

Query Match 83.9%; Score 26; DB 1; Length 1464;
 Best Local Similarity 85.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LMSTRAS 7
 Db 1357 LMSTEAS 1363
 |||||
 AG11 WHEAT STANDARD; PRT; 212 AA.
 AC P10958;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Agglutinin isolectin 1 precursor (WGA1) (Isolectin A).
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91370843; PubMed=2491677;
 RA Smith J.J., Raikhel N.V.;
 RT "Nucleotide sequences of cDNA clones encoding wheat germ agglutinin
 isolectins A and D.";
 RL Plant Mol. Biol. 13:601-603(1989).
 RN [2]
 RP SEQUENCE OF 27-197.
 RC TISSUE=Germ;
 RX MEDLINE=89279931; PubMed=2499688;
 RA Wright C.S., Raikhel N.V.;
 RT "Sequence variability in three wheat germ agglutinin isolectins:
 products of multiple genes in polyploid wheat.";
 RL J. Mol. Evol. 28:327-336(1989).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE=91039324; PubMed=2231724;
 RA Wright C.S.;
 RT "2.2-A resolution structure analysis of two refined
 N-acetylneuramyl-lactose-wheat germ agglutinin isolectin
 complexes.";
 RL J. Mol. Biol. 215:635-651(1990).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE=90064507; PubMed=2585496;
 RA Wright C.S.;
 RT "Comparison of the refined crystal structures of two wheat germ
 isolectins.";
 RL J. Mol. Biol. 209:475-487(1989).
 CC -1- FUNCTION: N-ACETYL-D-GLUCOSAMINE / N-ACETYL-D-NEURAMINIC ACID
 BINDING LECTIN
 CC -1- SUBUNIT: HOMODIMER, U-SHAPED.
 CC -1- MISCELLANEOUS: THE 4 SITES PROPOSED FOR BINDING TO CARBOHYDRATES
 (N-ACETYL-D-GLUCOSAMINE) OF RECEPTOR MOLECULES ARE ON THE SURFACE
 OF THE AGGLUTININ MOLECULE.
 CC -1- SIMILARITY: THERE ARE THREE VARIANTS OF WGA; VARIABILITY AMONG
 THEM IS OBSERVED AT A TOTAL OF 10 POSITIONS.
 CC -1- SIMILARITY: CONTAINS 4 CHITIN-BINDING DOMAINS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M25536; AAA34256.1; -.
 DR PIR; S09623; S09623.
 DR PIR; S07289; S07289.
 DR PDB; 7WGA; 15-OCT-90.
 DR PDB; 1WGC; 15-OCT-90.
 DR PDB; 2CWG; 31-JAN-94.

DR InterPro; IPR001002; Chitin_binding_1.
DR Pfam; PF00187; Chitin_bind_1; 4.
DR PRINTS; PR00451; CHITINBINDING.
DR ProDom; PD000609; Chitin_binding_1; 4.
DR SMART; SM00270; ChtBD1; 4.
DR PROSITE; PS00026; CHITIN_BINDING; 4.
KW Lectin; Repeat; Chitin-binding; 3D-structure; Signal.
FT SIGNAL 1 26
FT CHAIN 27 197 AGGLUTININ ISOLECTIN 1.
FT PROPEP 198 212
FT DOMAIN 27 69 CHITIN-BINDING 1.
FT DOMAIN 70 112 CHITIN-BINDING 2.
FT DOMAIN 113 155 CHITIN-BINDING 3.
FT DOMAIN 156 197 CHITIN-BINDING 4.
FT DISULFID 29 44
FT DISULFID 38 50
FT DISULFID 43 57
FT DISULFID 61 66
FT DISULFID 72 87
FT DISULFID 81 93
FT DISULFID 86 100
FT DISULFID 104 109
FT DISULFID 115 130
FT DISULFID 124 136
FT DISULFID 129 143
FT DISULFID 147 152
FT DISULFID 158 173
FT DISULFID 167 179
FT DISULFID 172 186
FT DISULFID 190 195
FT CONFLICT 63 63
FT STRAND 30 30
FT HELIX 31 33
FT TURN 34 35
FT STRAND 36 37
FT HELIX 39 41
FT STRAND 43 44
FT TURN 46 47
FT STRAND 50 52
FT HELIX 54 57
FT TURN 59 60
FT STRAND 71 71
FT HELIX 74 76
FT TURN 77 78
FT HELIX 82 84
FT STRAND 86 87
FT TURN 89 90
FT STRAND 92 95
FT HELIX 97 100
FT TURN 102 103
FT STRAND 106 106
FT STRAND 114 114
FT STRAND 116 116
FT HELIX 117 119
FT TURN 120 121
FT STRAND 122 122
FT HELIX 125 127
FT STRAND 129 130
FT TURN 132 133
FT STRAND 135 138
FT HELIX 140 143
FT TURN 145 146
FT STRAND 149 149
FT STRAND 157 157
FT STRAND 159 159
FT HELIX 160 162
FT TURN 163 164
FT STRAND 165 165
FT HELIX 168 170
FT STRAND 172 173
FT TURN 175 176
FT STRAND 178 181
FT HELIX 183 186

N -> D (IN REF. 2 AND 3).

FT TURN 188 189
SQ SEQUENCE 212 AA; 21239 MW; EC7B6F007DDC15EB CRC64;
Query Match 80.6%; Score 25; DB 1; Length 212;
Best Local Similarity 83.3%; Pred.No. 24;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LMSTRA 6
Db 3 MMSTRA 8
Search completed: April 22, 2003, 12:51:47
Job time : 5.5 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:48:24 ; Search time 6.875 Seconds
(without alignments)
97.882 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:.*
1: Pir1:.*
2: Pir2:.*
3: Pir3:.*
4: Pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	74	G30538	Ig kappa chain V r
2	31	100.0	112	KVMS16	Ig kappa chain V r
3	31	100.0	113	KVMS51	Ig kappa chain V r
4	31	100.0	120	KVMS67	Ig kappa chain pre
5	27	87.1	104	E69832	conserved hypother
6	27	87.1	234	S50468	hypothetical prote
7	27	87.1	342	C81451	flagellar motor sw
8	27	87.1	409	E86017	probable beta-keto
9	27	87.1	409	E91171	probable beta-keto
10	27	87.1	760	T39991	minichromosome mai
11	27	87.1	842	T16198	hypothetical prote
12	27	87.1	845	S34027	replication licens
13	27	87.1	1401	T39925	MAP kinase kinase
14	26	83.9	112	E95905	hypothetical prote
15	26	83.9	113	D96028	probable transcrip
16	26	83.9	341	QXFF2Y	NADH2 dehydrogenas
17	26	83.9	810	C70791	probable pona, pro
18	26	83.9	1453	S21626	collagen alpha 1(I
19	26	83.9	1464	CGHUI5	collagen alpha 1(I
20	25	80.6	177	TS1460	hypothetical prote
21	25	80.6	212	S99623	agglutinin isolect
22	25	80.6	212	T05936	agglutinin isolect
23	25	80.6	326	T26647	hypothetical prote
24	25	80.6	341	T39105	WD repeat protein
25	25	80.6	390	E98925	protein T22H9.4 [i
26	25	80.6	511	C56849	dopamine receptor-
27	25	80.6	532	AF0453	malate synthase (E
28	25	80.6	565	B72660	probable type II D
29	25	80.6	627	B75867	conserved hypother

ALIGNMENTS

RESULT 1

G30538
Ig kappa chain V region (253.15E2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 10-Feb-1989 #sequence_revision 10-Feb-1989 #text_change 16-Aug-1996
C:Accession: G30538
R:Clafin, J.L.; Berry, J.
J. Immunol. 141, 4012-4019, 1988
A:Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneu
A:Reference number: A30534; MUID:89035545; PMID:3141511
A:Accession: G30538
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-74 <CIA>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 100.0%; Score 31; DB 2; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q% 1 LMSTRAS 7
Db 24 LMSTRAS 30

RESULT 2

KVMS16
Ig kappa chain V region (M167) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
C:Accession: A01908
R:Rudikoff, S.; Potter, M.
Biochemistry 17, 2703-2707, 1978
A:Title: kappa-chain variable region from M167, a phosphorylcholine binding myeloma pro:
A:Reference number: A01908; MUID:79000273; PMID:99160
A:Accession: A01908
A:Molecule type: protein
A:Residues: 1-112 <RUD>
C:Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q% 1 LMSTRAS 7

Db 55 LMSTRAS 61
|||||

RESULT 3

KVMS51
Ig kappa chain V region (M511) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000

C/Accession: A01910

R/Appella, E.

Mol. Immunol. 17, 711-718, 1980

A/Title: Amino acid sequence of the light chain variable region of M511, a phosphorylated

A/Reference number: A01910; MUID:81052016; PMID:6776396

A/Accession: A01910

A/Molecule type: Protein

A/Residues: 1-113 <APP>

C/Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer

F:16-95/Domain: immunoglobulin homology <IMM>

F:23-93/Disulfide bonds: #status predicted

Query Match 100.0%; Score 37; DB 1; Length 113;

Best Local Similarity 100.0%; Pred. No. 1.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7

|||||

Db 55 LMSTRAS 61

RESULT 4

KVMS67

Ig kappa chain precursor V region (VK167) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000

C/Accession: A01909

R/Seising, E.; Storb, U.

Cell 25, 47-58, 1981

A/Title: Somatic mutation of immunoglobulin light-chain variable-region genes.

A/Reference number: A01909; MUID:82002223; PMID:6791832

A/Accession: A01909

A/Molecule type: DNA

A/Residues: 1-120 <SEL>

A/Note: the sequence was determined from the germline gene

C/Genetics:

A/Introns: 17/1

C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>

F:36-115/Domain: immunoglobulin homology <IMM>

F:43-113/Disulfide bonds: #status predicted

Query Match 100.0%; Score 31; DB 1; Length 120;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7

|||||

Db 75 LMSTRAS 81

RESULT 5

E69832

conserved hypothetical protein yhgB - Bacillus subtilis

N/Alternate names: hypothetical protein Y (pbpf 5' region)

C/Species: Bacillus subtilis

C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999

C/Accession: E69832; C40614

R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galler

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Huilo, M.F

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon

A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Togato, V.; Uchiyama

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.

A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A/Reference number: A69580; MUID:98044033; PMID:9384377

A/Accession: E69832

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-104 <KUN>

A/Cross-references: GB:Z99109; GB:AL009126; NID:G2633260; PIDN:CAB12849.1; PID:el183011,

A/Experimental source: strain 168

R/Popham, D.L.; Setlow, P.

J. Bacteriol. 175, 4870-4876, 1993

A/Title: Cloning, nucleotide sequence, and regulation of the Bacillus subtilis pbpf gene

A/Reference number: A40614; MUID:93328693; PMID:8335642

A/Accession: C40614

A/Molecule type: DNA

A/Residues: 1-67 <POP>

A/Cross-references: GB:L10630

C/Genetics:

A/Gene: yhgB

Query Match 87.1%; Score 27; DB 2; Length 104;

Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7

|||||

Db 38 LMSTRCS 44

RESULT 6

S50468

hypothetical protein YER010c - yeast (Saccharomyces cerevisiae)

C/Species: Saccharomyces cerevisiae

C/Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 19-Apr-2002

C/Accession: S50468

R/Dietrich, F.S.

submitted to the EMBL Data Library, December 1994

A/Description: The sequence of S. cerevisiae cosmid 9537, 9581, 9495, 9867, and lambda

A/Reference number: S50433

A/Accession: S50468

A/Molecule type: DNA

A/Residues: 1-234 <DIE>

A/Cross-references: EMBL:U18778; NID:G603592; PID:G603602; GSPDB:GN000005; MIPS:YER010c

C/Genetics:

A/Gene: MIPS:YER010c

A/Cross-references: SGD:S0000812

A/Map position: 5R

Query Match 87.1%; Score 27; DB 2; Length 234;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 6

|||||

Db 102 LMSTRAS 107

RESULT 7

A;Cross-references: EMBL:U42834; NID:g1125756; PID:g1125758; PIDN:AAA83583.1; CESP:F28B4
 C;Genetics:
 A;Gene: CESP:F28B4.2
 A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2
 C;Superfamily: CDC25-type guanine nucleotide exchange activator homology
 F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
 Query Match 87.1%; Score 27; DB 2; Length 842;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTRAS 7
 |||||
 Db 650 MSTRAS 655
 RESULT 12
 S34027
 replication licensing factor MCM7 [validated] - yeast (Saccharomyces cerevisiae)
 N;Alternate names: cell division control protein CDC47; protein YBR1441; protein YBR202w
 C;Species: Saccharomyces cerevisiae
 C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000
 C;Accession: S34027; S46074; S34925; S56049
 R;Jacquet, M.
 submitted to the EMBL Data Library, January 1993
 A;Reference number: S34022
 A;Accession: S34027
 A;Molecule type: DNA
 A;Residues: 1-845 <JAC>
 A;Cross-references: EMBL:Z21487; NID:g311665; PIDN:CAA79689.1; PID:g311678
 R;Bussereau, F.; Demolis, N.; Jacquet, M.; Mallet, L.
 submitted to the Protein Sequence Database, August 1994
 A;Reference number: S46054
 A;Accession: S46074
 A;Molecule type: DNA
 A;Residues: 1-845 <BUS>
 A;Cross-references: EMBL:Z36071; NID:g536576; PIDN:CAA85166.1; PID:g536577; GSPDB:GN0000
 R;Bussereau, F.; Mallet, L.; Gaillon, L.; Jacquet, M.
 Yeast 9, 797-806, 1993
 A;Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome II
 A;Reference number: S34925; MUID:93377417; PMID:8368014
 A;Accession: S34925
 A;Molecule type: DNA
 A;Residues: 407-620 <BUS>
 A;Cross-references: EMBL:Z21487
 R;Dalton, S.
 submitted to the EMBL Data Library, September 1994
 A;Description: Cdc47 and Cdc54 belong to a family of proteins essential for initiation o
 A;Reference number: S56049
 A;Accession: S56049
 A;Molecule type: DNA
 A;Residues: 1-551, 'G', 553-555, 'TLN', 559-573, 'Y', 575-845 <DAL>
 A;Cross-references: EMBL:U14730; NID:g508168; PIDN:AAA86309.1; PID:g508169
 C;Comment: The complex of six MCM proteins is one of several proteins that must be bound
 phosphorylated and dissociate from the chromatin.
 C;Genetics:
 A;Gene: SGD:CDC47; MIPS:YBR202w
 A;Cross-references: SGD:S0000406; MIPS:YBR202w
 A;Map position: 2R
 C;Complex: The predominant form is a heterohexamer of MCM2 (PIR:S45757), MCM3 (PIR:A3637
 component of replication licensing factor.
 C;Function:
 A;Description: MCM7 is a component of the replication licensing factor that permits DNA
 C;Superfamily: replication licensing factor MCM7; MCM homology
 C;Keywords: cell cycle control; DNA replication initiation; heterohexamer; nucleus; phos
 F;227-719/Domain: MCM homology <MCM>
 Query Match 87.1%; Score 27; DB 1; Length 845;
 Best Local Similarity 100.0%; Pred. No. 94;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTRAS 7
 |||||

Db 300 MSTRAS 305
 RESULT 13
 T39225
 MAP kinase kinase kinase - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000
 C;Accession: T39225
 R;Churcher, C.M.; Gentles, S.; Barrrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, August 1997
 A;Reference number: Z21837
 A;Accession: T39225
 A;Status: preliminary; translated from GB/EMBL/DBBJ
 A;Molecule type: DNA
 A;Residues: 1-1401 <CHU>
 A;Cross-references: EMBL:Z98763; PIDN:CAB11500.1; GSPDB:GN00066; SPDB:SPAC9G1.02
 A;Experimental source: strain 972h-; cosmid c9G1
 C;Genetics:
 A;Gene: SPDB:SPAC9G1.02
 A;Map position: 1
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
 Query Match 87.1%; Score 27; DB 2; Length 1401;
 Best Local Similarity 85.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 |||||
 Db 81 LMSTRAS 87
 RESULT 14
 E95905
 hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) megaplasmid pSymb
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C;Accession: E95905
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1.683-kb pSymb megaplasmid from the N2-fixing endo
 A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: E95905
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-112 <KUR>
 A;Cross-references: GB:AL591985; PIDN:CAC48909.1; PID:g15140382; GSPDB:GN00167
 A;Experimental source: strain 1021, megaplasmid pSymb
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 heault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: SMB20530
 A;Genome: plasmid
 Query Match 83.9%; Score 26; DB 2; Length 112;
 Best Local Similarity 71.4%; Pred. No. 22;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 :|||||
 Db 5 IMSTRAS 11
 RESULT 15
 D96028
 probable transcription activator of the pca operon, LysR family protein [imported] - Sin

C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: D96028
 R:Finan, T.M.; Weidner, S.; Wong, K.; Ruhmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-fixing endo
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: D96028
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-313 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CAC49892.1; PID:gl5141380; GSPDB:GN00167
 A:Experimental source: Strain 1021, megaplasmid pSymb
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebaud, P.; Vandenberg, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: pcaQ; SMb20580
 A:Genome: plasmid

Query Match 83.9%; Score 26; DB 2; Length 313;
 Best Local Similarity 85.7%; Pred. No. 63;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
 Db 199 LMPTRAS 205

Search completed: April 22, 2003, 12:54:47
 Job time : 8.875 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:47:43 ; Search time 14 Seconds
(without alignments)
103.024 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	87.1	342	16 Q9PII0	Q9pi10 campylobact
2	27	87.1	409	16 Q8X5U5	Q8x5u5 escherichia
3	27	87.1	860	5 Q19852	Q19852 caenorhabdi
4	27	87.1	1024	11 Q9ESJ5	Q9esj5 mus musculu
5	27	87.1	1049	2 Q9XBP6	Q9xbp6 myxococcus
6	26	83.9	112	16 Q92W36	Q92w36 rhizobium m
7	26	83.9	284	4 Q16050	Q16050 homo sapien
8	26	83.9	287	6 Q95ND8	Q95nd8 bos taurus
9	26	83.9	313	16 Q92TL9	Q92tl9 rhizobium m
10	26	83.9	325	11 Q60785	Q60785 mus musculu
11	26	83.9	338	8 Q9MF00	Q9mfg0 cochliomyia
12	26	83.9	338	8 Q9B2J6	Q9b2j6 chrysomya c
13	26	83.9	340	8 Q9XMP1	Q9xmp1 ceratitis c
14	26	83.9	341	8 Q9MD59	Q9md59 drosophila
15	26	83.9	341	8 Q9MD83	Q9md83 drosophila
16	26	83.9	341	8 Q9MD72	Q9md72 drosophila

17	26	83.9	341	8 Q9MJC9	Q9mjc9 drosophila
18	26	83.9	341	8 Q9MGP1	Q9mcp1 drosophila
19	26	83.9	341	8 Q9MGN7	Q9mgn7 drosophila
20	26	83.9	341	8 Q9MGN2	Q9mgn2 drosophila
21	26	83.9	341	8 Q9MGL3	Q9mgl3 drosophila
22	26	83.9	481	13 Q90TJ1	Q90tj1 brachydanio
23	26	83.9	589	11 Q99LL6	Q99ll6 mus musculu
24	26	83.9	810	16 Q69650	Q69650 mycobacteri
25	26	83.9	1260	5 Q9GY27	Q9gy27 leishmania
26	26	83.9	1453	11 Q63079	Q63079 rattus norv
27	26	83.9	1461	4 Q76045	Q76045 homo sapien
28	25	80.6	135	2 Q8RQ37	Q8rq37 bacillus ce
29	25	80.6	149	8 Q8WA98	Q8wa98 narceus ann
30	25	80.6	177	10 Q9LFF8	Q9lff8 arabidopsis
31	25	80.6	211	16 Q8VKC3	Q8vkc3 mycobacteri
32	25	80.6	263	7 Q9MX44	Q9mx44 ginglymosto
33	25	80.6	290	16 Q9F3E2	Q9f3e2 streptomyce
34	25	80.6	326	5 Q9XW66	Q9xw66 caenorhabdi
35	25	80.6	341	3 Q9UT39	Q9ut39 schizosacch
36	25	80.6	367	5 Q8SXA7	Q8sxa7 drosophila
37	25	80.6	383	5 Q9VNI7	Q9vni7 drosophila
38	25	80.6	390	5 Q9TXN8	Q9txn8 caenorhabdi
39	25	80.6	400	10 Q9LUQ7	Q9luq7 arabidopsis
40	25	80.6	508	12 Q9E234	Q9e234 helicoverpa
41	25	80.6	510	12 Q99GU9	Q99gu9 helicoverp
42	25	80.6	511	13 Q9PSA7	Q9psa7 fugu rubrip
43	25	80.6	532	16 Q8ZAR5	Q8zar5 yersinia pe
44	25	80.6	536	9 Q94MR7	Q94mr7 bacterioph
45	25	80.6	581	1 Q9P9C2	Q9p9c2 uncultured

ALIGNMENTS

RESULT 1

ID Q9PII0 PRELIMINARY; PRT; 342 AA.
AC Q9PII0;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Flagellar motor switch protein.
GN FLIG OR CJO319.
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCCTC 11168;
RX MEDLINE=20150912; PubMed=10688204;
RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whithead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni
reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; AL139074; CAB72786.1; -.
DR HSSP; Q9WY63; 1QC7.
DR InterPro; IPR000090; Flg_Motor_Flag.
DR Pfam; PF01706; Flig-C; 1.
DR PRINTS; PR00954; FLGMOTORFLIG.
DR TIGRFAMs; TIGR00207; flig; 1.
KW Complete proteome.
SQ SEQUENCE 342 AA; 38429 MW; ED4D214417C1524C CRC64;

Query Match 87.1%; Score 27; DB 16; Length 342;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTRAS 7

Db 289 MSTRAS 294
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RESULT 2
Q8X5U5 PRELIMINARY; PRT; 409 AA.
AC Q8X5U5;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative beta-ketoacyl-ACP synthase (Putative 3-oxoacyl-(acyl-carrier-
DE protein) synthase II).
DE Z4866 OR EC54311.
GN
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
ON NCBI_TaxID=83334;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074935; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glaesner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfal G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimallanta E.T., Potamouis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533 (2001).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kuzokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
RN [3]
SEQUENCE FROM N.A.
RC EMBL; AE005571; AKG58601.1; -.
DR EMBL; AP002565; BAB37764.1; -.
DR InterPro; IPR000794; Ketoacyl-synt.
DR Pfam; PF00109; ketoacyl-synt; 1.
DR Pfam; PF02801; ketoacyl-synt C; 1.
DR PROSITE; PS00606; B_KETOACYL_SYNTHASE; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 409 AA; 44148 MW; A4DAB0AF11ED883 CRC64;

Query Match 87.1%; Score 27; DB 16; Length 409;
Best Local Similarity 100.0%; Pred. NO. 81;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTRAS 7
Db 77 MSTRAS 82
|||||

RESULT 3
Q19852 PRELIMINARY; PRT; 860 AA.
AC Q19852;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 96.1 kDa protein.
GN F28B4.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
ON NCBI_TaxID=6239;
RN [1]

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SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018 (1998).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Leimbach D.;
RT "The sequence of C. elegans cosmid F28B4.";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX Waterston R.;
RT "Direct Submission.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U42834; AAA83583.2; -.
DR HSSP; O61193; IRLP.
DR InterPro; IPR000651; RasGEFN.
DR InterPro; IPR001895; RasGEF_CDC25.
DR InterPro; IPR000159; RA_domain.
DR Pfam; PF00788; RA; 1.
DR Pfam; PF00617; RasGEF; 1.
DR Pfam; PF00618; RasGEFN; 1.
DR SMART; SM00314; RA; 1.
DR SMART; SM00147; RasGEF; 1.
DR SMART; SM00229; RasGEFN; 1.
DR PROSITE; PS00720; GDS_CDC25; 1.
KW Hypothetical protein.
SQ SEQUENCE 860 AA; 96122 MW; 16089524FBC65CA5 CRC64;

Query Match 87.1%; Score 27; DB 5; Length 860;
Best Local Similarity 100.0%; Pred. NO. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MSTRAS 7
Db 668 MSTRAS 673
|||||

RESULT 4
Q9ESJ5 PRELIMINARY; PRT; 1024 AA.
AC Q9ESJ5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glur-delta2 phlic-protein.
GN GRID2IP OR DELPHILIN.
OS Mus musculus (Mouse).
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX Miyagi Y., Yamashita T., Okuda K., Mishina M., Kawamoto S.;
RT "Delphinin: A novel PDZ-containing protein associates with the Glur-
RT delta2 subunit.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF099933; AAG31020.1; -.
DR HSSP; P29476; IQAV.
DR MGD; MGI:2176213; Grid2ip.
DR InterPro; IPR003104; FH2.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR002965; P_rich_extensn.
DR Pfam; PF02181; FH2; 1.
DR Pfam; PF00595; PD2; 1.
DR PRINTS; PR01217; PRICHEXTENS.
DR SMART; SM00498; FH2; 1.

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DR SMART; SM00228; PDZ; 1.
DR PROSITE; PS50106; PDZ; 1.
SQ SEQUENCE 1024 AA; 112578 MW; E318AFDE02F846A CRC64;

Query Match      87.1%; Score 27; DB 11; Length 1024;
Best Local Similarity 85.7%; Pred.No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
   |:|||||
Db 53 LVSTRAS 59

RESULT 5
Q9XBP6 PRELIMINARY; PRT; 1049 AA.
ID AC Q9XBP6;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Serine/threonine kinase PKN8.
GN PKN8.
OS Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxID=34;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DZF1;
RA Inouye S., Jain R., Ueki T., Nariya H., Xu C., Hsu M.,
RA Munoz-Dorado J., Farez-Vidal E., Inouye M.;
RT "Sequence Analysis of 13 Eukaryotic-like Protein Ser/Thr Kinases of
RT Myxococcus xanthus, a Developmental Bacterium and Significance of
RT Their Coexistence with Protein His Kinases";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR DR EMBL; AF159691; AAD42856.1; -.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00515; TPR; 5.
DR PRODOM; PFD000001; Euk_pkinase; 1.
DR SMART; SM00028; TPR; 3.
DR PROSITE; PS00107; PROTEIN KINASE_ATP; UNKNOWN_1.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
KW ATP-binding; Kinase; Transferase.
SQ SEQUENCE 1049 AA; 114313 MW; 7752862DAA25338C CRC64;

Query Match      87.1%; Score 27; DB 2; Length 1049;
Best Local Similarity 85.7%; Pred.No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
   |:|||||
Db 1002 LMEIRAS 1008

RESULT 6
Q92W36 PRELIMINARY; PRT; 112 AA.
ID AC Q92W36;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-WAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein RB0509.
GN RB0509 OR SMB20530.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymb (megaplasmid 2).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;

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RESULT 8
O95ND8      Q95ND8      PRELIMINARY;      PRT;      287 AA.
AC      Q95ND8;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      Pro alpha 1(I) collagen (Fragment).
GN      COL1A1.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Grosse-Hovest L., Brem G.;
RT      "Bos taurus pro alpha 1(I) collagen gene, exon 49.";
RL      Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ312109; CAC38832.1; -.
DR      EMBL; AJ312110; CAC38832.1; JOINED.
DR      EMBL; AJ312111; CAC38832.1; JOINED.
DR      EMBL; AJ312112; CAC38832.1; JOINED.
DR      InterPro; IPR000087; Collagen.
DR      InterPro; IPR000885; Fib_collagen_C.
DR      Pfam; PF01410; COLFI; 1.
DR      ProDom; PD002078; Fib_collagen_C; 1.
KW      Collagen.
FT      NON_TER.
SQ      SEQUENCE      287 AA; 31698 MW; A9122CAEB7DC3DAE CRC64;

Query Match      83.9%; Score 26; DB 6; Length 287;
Best Local Similarity      85.7%; Pred. No. 1.1e+02;
Matches      6; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 LMSTRAS 7
DB      180 LMSTAS 186

RESULT 9
O92TL9      Q92TL9      PRELIMINARY;      PRT;      313 AA.
AC      Q92TL9;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Putative transcriptional activator of the pca operon, LysR family
DE      protein.
GN      PCQA OR RB1492 OR SWE20580
OS      Rhizobium meliloti (Sinorhizobium meliloti).
OG      Plasmid pSymB (megaplasmid 2).
OC      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC      Rhizobiaceae; Sinorhizobium.
NCBI_TaxID=382;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      FINAN T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA      Vorhoefer F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA      Golding B., Puehler A.;
RT      "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
RT      fixing endosymbiont Sinorhizobium meliloti.";
RL      Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
DR      EMBL; AL603647; CAC49892.1; -.
DR      InterPro; IPR000847; HTH_LysR.
DR      Pfam; PF00126; HTH 1; 1.
DR      Pfam; PF03466; LysR_subst.
DR      PROSITE; PS00044; HTH_LYSR_FAMILY; UNKNOWN_1.

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KW      Plasmid; Hypothetical protein; Complete proteome.
SQ      SEQUENCE      313 AA; 33832 MW; 4787BC1BE5476709 CRC64;

Query Match      83.9%; Score 26; DB 16; Length 313;
Best Local Similarity      85.7%; Pred. No. 1.2e+02;
Matches      6; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 LMSTRAS 7
DB      199 LMPTRAS 205

RESULT 10
O60785      Q60785      PRELIMINARY;      PRT;      325 AA.
AC      Q60785;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Alpha-1 type I procollagen (Fragment).
GN      COL1A1.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Lu Z., Laptiev A.V., Prockop D.J.;
RT      "The nucleotide sequence of cDNA for the last 5 exons and 3'-
RT      untranslated region of murine type I(1) procollagen.";
RL      Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR      EMBL; U03419; AAA03475.1; -.
DR      MGD; MGI:88467; Colla1.
DR      InterPro; IPR000087; Collagen.
DR      InterPro; IPR000885; Fib_collagen_C.
DR      Pfam; PF01410; COLFI; 1.
DR      Pfam; PF01391; Collagen; 1.
DR      ProDom; PD002078; Fib_collagen_C; 1.
DR      SMART; SM00038; COLFI; 1.
KW      Collagen.
FT      NON_TER.
SQ      SEQUENCE      325 AA; 35229 MW; A5A21E74DFDE3EF1 CRC64;

Query Match      83.9%; Score 26; DB 11; Length 325;
Best Local Similarity      85.7%; Pred. No. 1.2e+02;
Matches      6; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      1 LMSTRAS 7
DB      218 LMSTAS 224

RESULT 11
O9MFQ0      Q9MFQ0      PRELIMINARY;      PRT;      338 AA.
AC      Q9MFQ0;
DT      01-OCT-2000 (TREMBLrel. 15, Created)
DT      01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT      01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE      NADH subunit 2.
OS      Cochliomyia hominivorax (Primary screw-worm).
OG      Mitochondrion.
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Cecidoidea; Calliphoridae; Cochliomyia.
NCBI_TaxID=115425;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=20485491; PubMed=11029671;
RA      Lessinger A.C., Martins Junqueira A.C., Lemos T.A., Kemper E.L.,
RA      da Silva F.R., Vettore A.L., Arruda P., Azeredo-Espin A.M.;
RT      "The mitochondrial genome of the primary screwworm fly Cochliomyia
RT      hominivorax (Diptera: Calliphoridae).";

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RL Insect Mol. Biol. 9:521-529(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Lessinger A.C., Junqueira A.C.M., Lemos T.A., Kemper E.L.,
RA Vettore A.L., da Silva F.R., Arruda P., Azeredo-Espin A.M.L.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AF260826; AAF78613.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 338 AA; 39337 MW; E6501A86D02439D0 CRC64;

Query Match      83.9%; Score 26; DB 8; Length 338;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 50 LMSTEAS 56

RESULT 12
Q9B2J6 PRELIMINARY; PRT; 338 AA.
AC Q9B2J6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH subunit 2.
GN ND2.
OS Chrysomya chloropyga.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestroidea; Calliphoridae; Chrysomya.
OX NCBI_TaxID=142978;
RN [1]
RP SEQUENCE FROM N.A.
RA Junqueira A.C.M.;
RL "The complete mitochondrial genome of the Chrysomya putoria.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AF352790; AAK21318.1; -.
DR InterPro; IPR003917; NADHUB_oxred2.
DR Pfam; PF00361; oxidored_q1.
DR PRINTS; PR01436; NADHDHGNASE2.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 338 AA; 39228 MW; ABD5B1B5A5A46A23 CRC64;

Query Match      83.9%; Score 26; DB 8; Length 338;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 50 LMSTEAS 56

RESULT 13
Q9XMP1 PRELIMINARY; PRT; 340 AA.
AC Q9XMP1;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase (ubiquinone) chain 2 (EC 1.6.5.3).
GN NDH-U1.
OS Ceratitis capitata (Mediterranean fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
```

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OC Tephritoidea; Tephritidae; Ceratitis.
OX NCBI_TaxID=7213;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=2025575; PubMed=10762421;
RA Spanos L., Koutroumbas G., Kotsyfakis M., Louis C.;
RT "The complete sequence of the mitochondrial genome of the Medfly,
RT Ceratitis capitata."
RL Insect Mol. Biol. 9:139-144(2000).
CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AJ242872; CAB45088.1; -.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 340 AA; 39231 MW; F4C646E1C5E3F4F CRC64;

Query Match      83.9%; Score 26; DB 8; Length 340;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 50 LMSTEAS 56

RESULT 14
Q9MDS9 PRELIMINARY; PRT; 341 AA.
AC Q9MDS9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NADH dehydrogenase subunit 2.
OS Drosophila simulans (Fruit fly).
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7240;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=RU35, C167, DSW, DSR, MD106, MD225, AND SC00;
RA Ballard J.W.O.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
DR EMBL; AF200845; AAF77447.1; -.
DR EMBL; AF200839; AAF77369.1; -.
DR EMBL; AF200840; AAF77382.1; -.
DR EMBL; AF200841; AAF77395.1; -.
DR EMBL; AF200842; AAF77408.1; -.
DR EMBL; AF200843; AAF77421.1; -.
DR EMBL; AF200844; AAF77434.1; -.
DR FlyBase; FBgn0012880; Desim\mt.ND2.
DR InterPro; IPR001750; Oxidored_q1.
DR Pfam; PF00361; oxidored_q1; 1.
KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
SQ SEQUENCE 341 AA; 39734 MW; 8C42C96FF977A173 CRC64;

Query Match      83.9%; Score 26; DB 8; Length 341;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 51 LMSTEAS 57

RESULT 15
Q9MD83 PRELIMINARY; PRT; 341 AA.
AC Q9MD83;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE NADH dehydrogenase subunit 2.
 OS Drosophila simulans (Fruit fly), and
 OS Drosophila mauritiana (Fruit fly).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Prorygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephyroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7240, 7226;
 RN [1]

RP SEQUENCE FROM N.A.
 RC SPECIES=D.simulans, and D.mauritiana; STRAIN=VARIOUS STRAINS;
 RA Ballard J.W.O.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases
 CC -|- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
 DR EMBL; AF200854; AAF77564.1; -;
 DR EMBL; AF200831; AAF77265.1; -;
 DR EMBL; AF200846; AAF77460.1; -;
 DR EMBL; AF200847; AAF77473.1; -;
 DR EMBL; AF200848; AAF77486.1; -;
 DR EMBL; AF200849; AAF77499.1; -;
 DR EMBL; AF200850; AAF77512.1; -;
 DR EMBL; AF200851; AAF77525.1; -;
 DR EMBL; AF200852; AAF77538.1; -;
 DR EMBL; AF200853; AAF77551.1; -;
 DR FlyBase; FBgn0012512; Dmau\mt:ND2.
 DR FlyBase; FBgn0012880; Dsim\mt:ND2.
 DR InterPro; IPR001750; Oxidored_q1.
 DR Pfam; PF00361; oxidored_q1; 1_
 DR Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 KW Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
 SQ SEQUENCE 341 AA; 39649 MW; 27BAE96F482BC088 CRC64;

Query Match 83.9%; Score 26; DB 8; Length 341;
 Best Local Similarity 85.7%; Pred. NO. 1.3e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 Db 51 LMSTEAS 57

Search completed: April 22, 2003, 12:53:48
 Job time : 17 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:45:19 ; Search time 17.75 Seconds
(without alignments)
52.550 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 22: /SID32/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
- 23: /SID32/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	7	19	AAW39819
2	31	100.0	7	19	AAW39822
3	31	100.0	7	19	AAW39825
4	31	100.0	7	21	AAW32255
5	31	100.0	100	22	AAE06969
6	31	100.0	113	19	AAW39886
7	31	100.0	113	19	AAW39882
8	31	100.0	113	19	AAW39802
9	31	100.0	113	19	AAW39803
10	31	100.0	113	19	AAW39804

11	11	100.0	116	21	AAW32262	Humanised anti-CD2
12	31	100.0	145	21	AAW32261	Mouse anti-CD23 MA
13	28	90.3	7	19	AAW39816	Light chain CDR2 o
14	28	90.3	113	19	AAW39801	Variable domain of
15	28	90.3	274	19	AAW39899	Single chain Fv re
16	27	87.1	7	19	AAW39876	Light chain CDR2 o
17	27	87.1	68	22	AAU64213	Protonibacterium
18	27	87.1	123	22	AAU54742	Protonibacterium
19	27	87.1	131	12	AAU12332	Mouse Mab 2E12 L c
20	27	87.1	132	12	AAU12354	Light (kappa) chai
21	27	87.1	140	22	AAU95756	Human reproductive
22	27	87.1	409	22	ABB52717	Escherichia coli p
23	26	83.9	77	22	AAU39838	Protonibacterium
24	26	83.9	115	22	ABB27906	Human peptide #557
25	26	83.9	115	22	ABB33078	Peptide #584 encod
26	26	83.9	115	22	ABB18546	Protein #545 encod
27	26	83.9	115	22	AAU53875	Human brain expres
28	26	83.9	115	22	AAU66263	Human bone marrow
29	26	83.9	115	22	AAU14133	Peptide #567 encod
30	26	83.9	115	22	AAU26539	Peptide #553 encod
31	26	83.9	115	22	AAU01871	Human peptide enco
32	26	83.9	115	23	ABG35910	Novel human diagno
33	26	83.9	134	22	ABG10627	Novel human diagno
34	26	83.9	250	18	AAU12845	Pro-alpha(I) chai
35	26	83.9	441	22	AAU75593	Human colon cancer
36	26	83.9	449	21	AAU43439	Myobacterium tube
37	26	83.9	810	22	AAU81232	Novel human diagno
38	26	83.9	980	22	ABG3181	Novel human diagno
39	26	83.9	980	22	ABG10626	Novel human diagno
40	26	83.9	1341	16	AAU71701	Collagen alpha 1 (
41	26	83.9	1341	21	AAU96122	Collagen type I al
42	26	83.9	1341	23	ABB80733	Collagen type I-al
43	26	83.9	1341	23	ABB09625	Amino acid sequenc
44	26	83.9	1341	23	AAU16475	Human collagen alp
45	26	83.9	1411	21	AAU56800	Human preproalpha

ALIGNMENTS

RESULT 1	AAW39819	standard; peptide; 7 AA.
ID	AAW39819	standard; peptide; 7 AA.
XX	AAW39819	
AC	AAW39819	
XX	AAW39819	
DT	16-JUN-1998	(first entry)
XX	16-JUN-1998	
DE	Light chain CDR2 of catalytic antibody 6A12.	
XX	Variable domain; lambda light chain; catalytic antibody; degradation;	
KW	cocaine; cocaine transition state analogue; TSA; benzoic acid;	
KW	phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;	
KW	overdose; addiction.	
OS	Mus sp.	
XX	Mus sp.	
PN	WO9749800-A1.	
XX	WO9749800-A1.	
PD	31-DEC-1997.	
XX	31-DEC-1997.	
PF	25-JUN-1997;	97WO-US10985.
XX	25-JUN-1997;	
PR	25-JUN-1996;	96US-0672345.
XX	25-JUN-1996;	
PA	(UYCO) UNIV COLUMBIA NEW YORK.	
XX	(UYCO) UNIV COLUMBIA NEW YORK.	
PI	Landry DW;	
XX	Landry DW;	
DR	WPI; 1998-077166/07.	
XX	WPI; 1998-077166/07.	
PT	New catalytic antibodies able to decompose cocaine, single-chain	
PT	analogues - used to treat cocaine overdose and addiction, required	

PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding

PS Claim 13; Page 81; 147pp; English.

XX AAW39818-20 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 6A12, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was
 CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 6A12 has a per minute Kcat
 CC of 0.072. The antibodies reduce the concentration of cocaine in a
 CC subject, and are used particularly for the treatment of cocaine in an
 CC are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved).

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 1 LMSTRAS 7

RESULT 2

AAW39822

ID AAW39822 standard; peptide; 7 AA.

AC AAW39822;

XX 16-JUN-1998 (first entry)

DT Light chain CDR2 of catalytic antibody 2A10.

DE Variable domain; lambda light chain; catalytic antibody; degradation;

XX cocaine; cocaine transition state analogue; TSA; benzoic acid;

XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

XX overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US10965.

XX 25-JUN-1996; 96US-0672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain

XX analogues - used to treat cocaine overdose and addiction, required

XX in far smaller doses than antibodies that antagonise cocaine by

XX simply binding

XX Claim 15; Page 82; 147pp; English.

XX AAW39821-23 represent the sequences of the light chain complementarity

XX determining regions (CDRs) of the catalytic antibody 2A10, which is able

XX to degrade cocaine. A series of cocaine transition state analogues

XX (TSAs) were prepared and used to immunise mice for production of

XX hybridomas. Catalytic antibodies were identified by their capacity to

XX release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was

CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 2A10 has a per minute Kcat
 CC of 0.011. The antibodies reduce the concentration of cocaine in a
 CC subject, and are used particularly for the treatment of cocaine in an
 CC are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved).

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 1 LMSTRAS 7

RESULT 3

AAW39825

ID AAW39825 standard; peptide; 7 AA.

XX AAW39825;

XX 16-JUN-1998 (first entry)

DT Light chain CDR2 of catalytic antibody 12H1.

DE Variable domain; lambda light chain; catalytic antibody; degradation;

XX cocaine; cocaine transition state analogue; TSA; benzoic acid;

XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

XX overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US10965.

XX 25-JUN-1996; 96US-0672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain

XX analogues - used to treat cocaine overdose and addiction, required

XX in far smaller doses than antibodies that antagonise cocaine by

XX simply binding

XX Claim 17; Page 83; 147pp; English.

XX AAW39824-26 represent the sequences of the light chain complementarity

XX determining regions (CDRs) of the catalytic antibody 12H1, which is able

XX to degrade cocaine. A series of cocaine transition state analogues

XX (TSAs) were prepared and used to immunise mice for production of

XX hybridomas. Catalytic antibodies were identified by their capacity to

XX release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was

XX identified using TSA2, and has a per minute Kcat of 0.16. The antibodies

XX reduce the concentration of cocaine in a subject, and are used

XX particularly for the treatment of cocaine in an overdose. They are also used for

XX treating addiction (by reducing the in vivo concentration that can be

XX achieved).

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 31; DB 21; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels

The patent discloses a humanised antibody or its antigen-binding fragment, having binding specificity for CC-chemokine receptor 2 (CCR2), comprising an antigen binding region of non-human origin and at least a portion of an immunoglobulin of human origin. The humanised antibodies are useful for inhibiting the interaction of a cell expressing CCR2. They are useful for inhibiting or treating HIV infection. The proteins of the invention are useful for inhibiting leukocyte trafficking, for treating CCR2-mediated disorders such as inflammatory disorder, autoimmune disorders such as rheumatoid arthritis and multiple sclerosis, atherogenesis and atherosclerosis, and for inhibiting restenosis. They are useful in therapy or diagnosis, and in the manufacture of a medicament for treating CCR2 mediated disease. They are also useful for treating allergy, anaphylaxis, malignancy, chronic and acute inflammation, histamine and IgE-mediated allergic reaction, shock, stenosis, allograft rejection, fibrotic disease, asthma, inflammatory glomerulopathies, acquired immune deficiency syndrome (AIDS), restenosis associated with vascular intervention, including angioplasty and/or stent placement in a mammal. Humanised antibodies are also useful for inhibiting narrowing of the lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of a vessel in a mammal, preferably associated with vascular intervention. The present sequence is mouse germline kappa light chain variable (VK) region, 167/24.

XX


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OS Mus sp.
XX WO9749800-A1.
XX 31-DEC-1997.
XX 25-JUN-1997; 97WO-US10965.
XX 25-JUN-1996; 96US-0672345.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX Landry DW;
XX WPI; 1998-077166/07.
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX Claim 14; Page 72; 147pp; English.
XX AA39801-05 represent the amino acid sequences of the variable domain
CC of the kappa light chain of catalytic antibodies which are able to
CC degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC were prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release
CC 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody (AAW39807
CC represents the heavy chain) was identified using TSA1, which is an
CC immunogenic conjugate of a phosphate monoester transition state
CC analogue. Antibody 6A12 has a per minute Kcat of 0.072. The antibodies
CC reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used
CC for treating addiction (by reducing the in vivo concentration that can
CC be achieved).
XX SQ Sequence 113 AA;
Query Match 100.0%; Score 31; DB 19; Length 113;
Best Local Similarity 100.0%; Pred. NO. 6.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMSTRAS 7
DB 55 LMSTRAS 61
RESULT 9
AAW39803
ID AA39803 standard; protein; 113 AA.
XX AC AAW39803;
XX 16-JUN-1998 (first entry)
XX Variable domain of the Kappa light chain of catalytic antibody 12H1.
XX Variable domain; lambda light chain; catalytic antibody; degradation;
XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX overdose; addition.
XX Mus sp.
XX WO9749800-A1.
XX 31-DEC-1997.
XX 25-JUN-1997; 97WO-US10965.
XX 25-JUN-1996; 96US-0672345.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX Landry DW;
XX WPI; 1998-077166/07.
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX Claim 18; Page 73; 147pp; English.
XX AA39801-05 represent the amino acid sequences of the variable domain
CC of the kappa light chain of catalytic antibodies which are able to
CC degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC were prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release
CC 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808
CC represents the heavy chain) was identified using TSA2, and has a per
CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine
CC in a subject, and are used particularly for the treatment of an
CC overdose. They are also used for treating addiction (by reducing the in
CC vivo concentration that can be achieved).
XX SQ Sequence 113 AA;
Query Match 100.0%; Score 31; DB 19; Length 113;
Best Local Similarity 100.0%; Pred. NO. 6.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMSTRAS 7
DB 55 LMSTRAS 61
RESULT 10
AAW39804
ID AA39804 standard; protein; 113 AA.
XX AC AAW39804;
XX 16-JUN-1998 (first entry)
XX Variable domain of the Kappa light chain of catalytic antibody 2A10.
XX Variable domain; lambda light chain; catalytic antibody; degradation;
XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX overdose; addition.
XX Mus sp.
XX WO9749800-A1.
XX 31-DEC-1997.
XX 25-JUN-1997; 97WO-US10965.
XX 25-JUN-1996; 96US-0672345.
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX Landry DW;
XX WPI; 1998-077166/07.
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
```

Claim 16; Pages 73-74; 147pp; English.

PS AAW39801-05 represent the amino acid sequences of the variable domain
 CC of the Kappa light chain of catalytic antibodies which are able to
 CC degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release
 CC 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state
 CC analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies
 CC reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can
 CC be achieved).

XX Sequence 113 AA;
 SQ Query Match 100.0%; Score 31; DB 19; Length 113;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 DB 55 LMSTRAS 61
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RESULT 11
 AAY32262
 ID AAY32262 standard; Protein; 116 AA.
 AC AAY32262;
 XX 15-FEB-2000 (first entry)
 DT Humanised anti-CD23 Mab C11 light chain variable region.
 DE
 XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes;
 KW B-cell malignancy; therapy.

XX Homo sapiens.
 OS Synthetic.
 XX

Key Location/Qualifiers
 FT Region 1..23 "framework region 1"
 FT Region 24..39 "framework region 1"
 FT Region 40..54 "framework region 2"
 FT Region 55..61 "framework region 2"
 FT Region 62..93 "framework region 3"
 FT Region 94..102 "framework region 3"
 FT Region 103..113 "framework region 4"
 FT Region "framework region 4"
 FT

WO958679-A1.
 XX
 XX 18-NOV-1999.
 PD
 XX 07-MAY-1999; 99WO-GB01434.
 PF
 XX

PR 09-MAY-1998; 98GB-0009839.
 XX (GLAX) GLAXO GROUP LTD.
 PA
 XX Bonnefoy JWP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 PI
 XX MPI; 2000-053101/04.
 DR N-PSDB; AAZ34747.
 XX
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis -
 PT
 XX Claim 9; Fig 3; 81pp; English.
 PS
 XX This sequence represents the light chain variable region (VL) of
 CC humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of
 CC a human framework (H5IGKVII) and the light chain complementarity
 CC determining regions (see AAY32254-56) of murine antibody C11. The
 CC DNA was constructed by splice overlap PCR. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies, which
 CC comprise sufficient of the amino acid sequences of the C11 light
 CC and heavy chain complementarity determining regions to render them
 CC capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble
 CC CD23 formation in human therapy, for the treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis,
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.

XX Sequence 116 AA;
 SQ Query Match 100.0%; Score 31; DB 21; Length 116;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 DB 55 LMSTRAS 61
 |||||

RESULT 12
 AAY32261
 ID AAY32261 standard; Protein; 145 AA.
 AC AAY32261;
 XX 15-FEB-2000 (first entry)
 DT Mouse anti-CD23 Mab C11 light chain variable region.
 DE
 XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes;
 KW B-cell malignancy; therapy.

XX Mus musculus.
 OS
 XX Key Location/Qualifiers
 FT Region 55..70
 FT "note= "CDR LI"

FT Region 83..92
FT /note= "CDR L2"
FT 125..134
FT /note= "CDR L3"
XX
XX
PN WO9558679-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-GB01434.
XX
XX 09-MAY-1998; 98GB-0009839.
XX
XX (GLAX) GLAXO GROUP LTD.
XX
XX Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX WPI; 2000-053101/04.
XX N-PSDB; AA234746.
XX
XX Cell receptor specific antibodies useful for treating e.g. arthritis,
XX diabetes, multiple sclerosis and psoriasis -
XX Claim 8; Fig 2; 81pp; English.
XX
XX This sequence represents the light chain variable region (VL) of
XX murine anti-CD23 (FCER11) monoclonal antibody C11. The invention
XX provides altered antibodies, such as chimeric or humanised
XX antibodies (see AAY32262 and AAY32263), which comprise sufficient of
XX the amino acid sequences of the C11 light and heavy chain
XX complementarity determining regions (see AAY32254-59) to render them
XX capable of binding to the CD23 type II molecule expressed on
XX haematopoietic cells. The antibodies are used to block soluble
XX CD23 formation in human therapy, for the treatment of arthritis,
XX lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
XX diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
XX syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
XX colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
XX asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
XX eczema, graft-versus-host disease, COPD, sinusitis, bronchitis
XX (particularly chronic bronchitis) or diabetes (particularly type 1
XX diabetes), and B-cell malignancies (claimed). They are also useful
XX for studying interactions between CD23 and various ligands and
XX determining the binding agents.
XX
SQ Sequence 145 AA;

Query Match 100.0%; Score 31; DB 21; Length 145;
Best Local Similarity 100.0%; Pred. NO. 8.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 86 LMSTRAS 92

RESULT 13
AAW39816
ID AAW39816 standard; peptide; 7 AA.
XX
XX AAW39816;
XX
XX 16-JUN-1998 (first entry)
XX
XX Light chain CDR2 of catalytic antibody 3B9.
XX
XX Variable domain; lambda light chain; Catalytic antibody; degradation;
XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX overdose; addiction.
XX
XX Mus sp.
XX
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US10965.
XX
XX 25-JUN-1996; 96US-0672345.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX WPI; 1998-077166/07.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
XX analogues - used to treat cocaine overdose and addiction, required
XX in far smaller doses than antibodies that antagonise cocaine by
XX simply binding
XX Claim 11; Page 80; 147pp; English.
XX
XX AAW39815-17 represent the sequences of the light chain complementarity
XX determining regions (CDRs) of the catalytic antibody 3B9, which is able
XX to degrade cocaine. A series of cocaine transition state analogues
XX (TSAs) were prepared and used to immunise mice for production of
XX hybridomas. Catalytic antibodies were identified by their capacity to
XX release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was
XX identified using TSA1, which is an immunogenic conjugate of a phosphate
XX monoester transition state analogue. Antibody 3B9 has a per minute Kcat
XX of 0.11. The antibodies reduce the concentration of cocaine in a subject,
XX and are used particularly for the treatment of an overdose. They are also
XX used for treating addiction (by reducing the in vivo concentration that
XX can be achieved).
XX
SQ Sequence 7 AA;

Query Match 90.3%; Score 28; DB 19; Length 7;
Best Local Similarity 85.7%; Pred. No. 7.8e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 1 LMSTRSS 7

RESULT 14
AAW39801
ID AAW39801 standard; protein; 113 AA.
XX
XX AAW39801;
XX
XX 16-JUN-1998 (first entry)
XX
XX Variable domain of the Kappa light chain of catalytic antibody 3B9.
XX
XX Variable domain; lambda light chain; catalytic antibody; degradation;
XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX overdose; addiction.
XX
XX Mus sp.
XX
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US10965.
XX
XX 25-JUN-1996; 96US-0672345.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX PI

PN WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US10965.
XX
XX 25-JUN-1996; 96US-0672345.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX WPI; 1998-077166/07.
XX
XX New catalytic antibodies able to decompose cocaine, single-chain
XX analogues - used to treat cocaine overdose and addiction, required
XX in far smaller doses than antibodies that antagonise cocaine by
XX simply binding
XX Claim 11; Page 80; 147pp; English.
XX
XX AAW39815-17 represent the sequences of the light chain complementarity
XX determining regions (CDRs) of the catalytic antibody 3B9, which is able
XX to degrade cocaine. A series of cocaine transition state analogues
XX (TSAs) were prepared and used to immunise mice for production of
XX hybridomas. Catalytic antibodies were identified by their capacity to
XX release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was
XX identified using TSA1, which is an immunogenic conjugate of a phosphate
XX monoester transition state analogue. Antibody 3B9 has a per minute Kcat
XX of 0.11. The antibodies reduce the concentration of cocaine in a subject,
XX and are used particularly for the treatment of an overdose. They are also
XX used for treating addiction (by reducing the in vivo concentration that
XX can be achieved).
XX
SQ Sequence 7 AA;

Query Match 90.3%; Score 28; DB 19; Length 7;
Best Local Similarity 85.7%; Pred. No. 7.8e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 1 LMSTRSS 7

RESULT 14
AAW39801
ID AAW39801 standard; protein; 113 AA.
XX
XX AAW39801;
XX
XX 16-JUN-1998 (first entry)
XX
XX Variable domain of the Kappa light chain of catalytic antibody 3B9.
XX
XX Variable domain; lambda light chain; catalytic antibody; degradation;
XX cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX overdose; addiction.
XX
XX Mus sp.
XX
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US10965.
XX
XX 25-JUN-1996; 96US-0672345.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
XX Landry DW;
XX
XX PI

XX WPI; 1998-077166/07.
 DR P-PSDB; AAV09791.
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX Claim 12; Pages 71-72; 147pp; English.
 PS
 XX AA039801-05 represent the amino acid sequences of the variable domain
 CC of the kappa light chain of catalytic antibodies which are able to
 CC degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release
 CC 3H-benzoic acid from 3H-phenyl cocaine. The 389 antibody (AAW39806
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state
 CC analogue. Antibody 389 has a per minute Kcat of 0.11. The antibodies
 CC reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can
 CC be achieved).
 XX
 SQ Sequence 113 AA;
 Query Match 90.3%; Score 28; DB 19; Length 113;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 Db 55 LMSTRSS 61
 RESULT 15
 AA039899
 ID AA039899 standard; Protein; 274 AA.
 XX
 AC AA039899;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Single chain Fv region of the catalytic antibody 389.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 32..37 "complementarity determining region 1 of the
 FT heavy chain"
 FT Region 52..67 "complementarity determining region 2 of the
 FT heavy chain"
 FT Region 99..106 "complementarity determining region 3 of the
 FT heavy chain"
 FT Region 120..134 "complementarity determining region 1 of the
 FT heavy chain"
 FT Region 159..174 "complementarity determining region 2 of the
 FT heavy chain"
 FT Region 186..192 "complementarity determining region 3 of the
 FT heavy chain"
 FT Region 225..233 "complementarity determining region 1 of the
 FT heavy chain"
 FT Region 255..263 "complementarity determining region 2 of the
 FT heavy chain"

FT Region 259..263 light chain"
 FT /note= "Flag epitope sequence"
 XX
 XX WO9749800-A1.
 XX 31-DEC-1997.
 PD
 XX 25-JUN-1997; 97WO-US10965.
 XX 25-JUN-1996; 96US-0672345.
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX Landry DW;
 XX WPI; 1998-077166/07.
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX Disclosure; Fig 27; 147pp; English.
 XX
 CC The present sequence represents the single chain Fv region of the
 CC monoclonal catalytic antibody 389, which is capable of degrading
 CC cocaine. A series of cocaine transition state analogues (TSAs) were
 CC prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release
 CC 3H-benzoic acid from 3H-phenyl cocaine. The antibodies reduce the
 CC concentration of cocaine in a subject, and are used particularly for
 CC the treatment of an overdose. They are also used for treating addiction
 CC (by reducing the in vivo concentration that can be achieved).
 XX
 SQ Sequence 274 AA;
 Query Match 90.3%; Score 28; DB 19; Length 274;
 Best Local Similarity 85.7%; Pred. No. 91;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LMSTRAS 7
 Db 186 LMSTRSS 192
 Search completed: April 22, 2003, 12:51:12
 Job time : 18.75 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:53:59 ; Search time 7.375 Seconds
(without alignments)
76.055 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pap.*
- 2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pap.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pap.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pap.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pap.*
- 6: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pap.*
- 7: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pap.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pap.*
- 9: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pap.*
- 10: /cgn2_6/ptodata/1/pubaa/US09_PUBCOMB.pap.*
- 11: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pap.*
- 12: /cgn2_6/ptodata/1/pubaa/US10_PUBCOMB.pap.*
- 13: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pap.*
- 14: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	100	10	US-09-840-459-32
2	26	83.9	115	10	US-09-864-761-33844
3	26	83.9	449	10	US-09-925-301-884
4	26	83.9	810	9	US-09-712-363-281
5	26	83.9	1464	9	US-10-060-036-159
6	24	77.4	32	10	US-09-864-761-45487
7	24	77.4	108	10	US-09-764-877-1708
8	24	77.4	114	9	US-10-083-357-784
9	24	77.4	274	9	US-09-866-050A-336
10	24	77.4	295	9	US-09-829-936A-31
11	24	77.4	295	9	US-09-829-936A-31
12	24	77.4	297	9	US-10-005-057A-5
13	24	77.4	305	9	US-09-738-626-4088
14	24	77.4	309	10	US-09-908-711-788
15	24	77.4	433	10	US-09-925-302-691
16	24	77.4	442	9	US-09-829-936A-16
17	24	77.4	443	9	US-10-028-072-318
18	24	77.4	443	9	US-10-121-049-318
19	24	77.4	443	9	US-10-123-904-318

20	24	77.4	443	9	US-10-140-470-318	Sequence 318, App
21	24	77.4	443	9	US-10-175-746-318	Sequence 318, App
22	24	77.4	443	9	US-10-176-921-318	Sequence 318, App
23	24	77.4	443	9	US-10-176-921-318	Sequence 318, App
24	24	77.4	443	9	US-10-137-865-318	Sequence 318, App
25	24	77.4	443	9	US-10-140-474-318	Sequence 318, App
26	24	77.4	443	9	US-10-142-431-318	Sequence 318, App
27	24	77.4	443	9	US-10-143-114-318	Sequence 318, App
28	24	77.4	443	9	US-10-140-002-318	Sequence 318, App
29	24	77.4	443	9	US-10-142-419-318	Sequence 318, App
30	24	77.4	443	9	US-09-829-936A-22	Sequence 22, Appl
31	24	77.4	443	9	US-10-123-262-318	Sequence 318, App
32	24	77.4	443	9	US-10-142-423-318	Sequence 318, App
33	24	77.4	443	9	US-10-121-050-318	Sequence 318, App
34	24	77.4	443	9	US-10-141-755-318	Sequence 318, App
35	24	77.4	443	9	US-10-143-032-318	Sequence 318, App
36	24	77.4	443	9	US-10-123-108-318	Sequence 318, App
37	24	77.4	443	9	US-10-123-236-318	Sequence 318, App
38	24	77.4	443	9	US-10-123-261-318	Sequence 318, App
39	24	77.4	443	9	US-10-140-921-318	Sequence 318, App
40	24	77.4	443	9	US-10-140-928-318	Sequence 318, App
41	24	77.4	443	9	US-10-121-045-318	Sequence 318, App
42	24	77.4	443	9	US-10-123-292-318	Sequence 318, App
43	24	77.4	443	9	US-10-123-903-318	Sequence 318, App
44	24	77.4	443	9	US-10-124-819-318	Sequence 318, App
45	24	77.4	443	9	US-10-124-822-318	Sequence 318, App

ALIGNMENTS

RESULT 1
US-09-840-459-32
; Sequence 32, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: Larosa, Gregory J.
; APPLICANT: Horvath, Christopher
; APPLICANT: Newman, Walter
; APPLICANT: Jones, S. Tarran
; APPLICANT: O'Brien, Siobhan H.
; APPLICANT: O'Keefe, Theresa
; TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND
; FILE REFERENCE: 1855.1052-012
; CURRENT APPLICATION NUMBER: US/09/840,459
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: PCT/US01/03537
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/497,625
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/359,193
; PRIOR FILING DATE: 1999-07-22
; PRIOR APPLICATION NUMBER: 09/121,781
; PRIOR FILING DATE: 1998-07-23
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-840-459-32

Query Match 100.0%; Score 31; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 2

US-09-864-761-33844
; Sequence 33844, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, David R.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33844
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC007786.1
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96
; OTHER INFORMATION: SWISSPROT HIT: P04885, EVALU 3.60e+00
; OTHER INFORMATION: EST_HUMAN HIT: AA306055.1, EVALU 6.60e-01
US-09-864-761-33844

Query Match 83.9%; Score 26; DB 10; Length 115;
Best Local Similarity 71.4%; Pred. No. 42;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 LMSTRAS 7
; :|||
Db 62 MMTTRAS 68
RESULT 3
US-09-925-301-884
; Sequence 884, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 884
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-884

Query Match 83.9%; Score 26; DB 10; Length 449;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
; :|||
Db 342 LMSTEAS 348

RESULT 4
US-09-712-363-281
; Sequence 281, Application US/09712363
; Patent No. US20020164588A1
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, David
; APPLICANT: Rotstein, Sergio H.
; APPLICANT: Marcotte, Edward M.
; TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
; FILE REFERENCE: 07419-032001
; CURRENT APPLICATION NUMBER: US/09/712,363
; CURRENT FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/US00/02246
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,531
; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: 60/117,844
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/118,206,
; PRIOR FILING DATE: 1999-02-01
; PRIOR APPLICATION NUMBER: 60/126,593
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/134,093
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/134,092
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/165,124
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/165,086
; PRIOR FILING DATE: 1999-11-12
; NUMBER OF SEQ ID NOS: 292
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281
; LENGTH: 810

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; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-281

Query Match      83.9%; Score 26; DB 9; Length 810;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 38 LMSNRAS 44

RESULT 5
US-10-060-036-159
; Sequence 159, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-159

Query Match      83.9%; Score 26; DB 9; Length 1464;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 1357 LMSTRAS 1363

RESULT 6
US-09-864-761-45487
; Sequence 45487, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-281

Query Match      83.9%; Score 26; DB 9; Length 810;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 38 LMSNRAS 44

RESULT 5
US-10-060-036-159
; Sequence 159, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-159

Query Match      83.9%; Score 26; DB 9; Length 1464;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 1357 LMSTRAS 1363

RESULT 6
US-09-864-761-45487
; Sequence 45487, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-281

Query Match      83.9%; Score 26; DB 9; Length 810;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 38 LMSNRAS 44

RESULT 5
US-10-060-036-159
; Sequence 159, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-159

Query Match      83.9%; Score 26; DB 9; Length 1464;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 1357 LMSTRAS 1363

RESULT 6
US-09-864-761-45487
; Sequence 45487, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-281

Query Match      83.9%; Score 26; DB 9; Length 810;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 38 LMSNRAS 44

RESULT 5
US-10-060-036-159
; Sequence 159, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Benson, Darin R.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Persing, David H.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; FILE REFERENCE: 210121.566
; CURRENT APPLICATION NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 159
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-036-159

Query Match      83.9%; Score 26; DB 9; Length 1464;
Best Local Similarity 85.7%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 1357 LMSTRAS 1363

RESULT 6
US-09-864-761-45487
; Sequence 45487, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aecmca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667

; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-712-363-281

Query Match      83.9%; Score 26; DB 9; Length 810;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 38 LMSNRAS 44

RESULT 5
US-10-060-036-159
; Sequence 159,
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; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(425)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-005-057A-5

Query Match 77.4%; Score 24; DB 9; Length 297;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRA 6
|:|:|
Db 66 LMSTRA 71

RESULT 13
US-09-738-626-4088
; Sequence 4088, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4088
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; US-09-738-626-4088

Query Match 77.4%; Score 24; DB 9; Length 305;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|:|:|
Db 246 VMSSRAS 252

RESULT 14
US-09-908-711-78
; Sequence 78, Application US/09908711
; Patent No. US20020045230A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA128
; CURRENT APPLICATION NUMBER: US/09/908,711

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; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US01/01360
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,867
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01344
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,892
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01345
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,888
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01329
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,905
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01354
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,891
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01339
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,869
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01340
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,874
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01334
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,898
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01320
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,853
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01349
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,902
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01239
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,870
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01348
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,882
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01347
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,896
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01307
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,864
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01341
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,856
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01336
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,868
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US01/01312
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07

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; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 78
; LENGTH: 309
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (4)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-908-711-78

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Query Match      77.4%; Score 24; DB 10; Length 309;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LMSTRAS 7
|:|:|
Db 202 LLSRRAS 208

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RESULT 15

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US-09-925-302-691
; Sequence 691, Application US/09925302
; Patent No. US20020044941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 691
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-691

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Query Match      77.4%; Score 24; DB 10; Length 433;
Best Local Similarity 85.7%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 LMSTRAS 7
|:|:|
Db 413 LMSYRAS 419

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Search completed: April 22, 2003, 13:11:12
Job time : 8.375 secs

J. Immunol. 141, 4012-4019, 1988
 A;Title: Genetics of the phosphocholine-specific antibody response to Streptococcus pneumoniae
 A;Reference number: A30534; UID:85035545; PMID:3141511
 A;Accession: G30538
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-74 <CLA>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 87.5%; Score 42; DB 2; Length 74;
 Best Local Similarity 88.9%; Pred. No. 0.16;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||
 Db 63 QQLVEYPLT 71

RESULT 3
 KWS16
 Ig kappa chain V region (M167) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 16-Aug-1996
 C;Accession: A01908
 R;Rudikoff, S.; Potter, M.
 Biochemistry 17, 2703-2707, 1978
 A;Title: Kappa-Chain variable region from M167, a phosphorylcholine binding myeloma protein
 A;Reference number: A01908; UID:7900273; PMID:99160
 A;Accession: A01908
 A;Molecule type: protein
 A;Residues: 1-112 <RUD>
 C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger oligomers.
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer
 F;16-95/Domain: immunoglobulin homology <IMM>
 F;23-93/Disulfide bonds: #status predicted

Query Match 87.5%; Score 42; DB 1; Length 112;
 Best Local Similarity 88.9%; Pred. No. 0.24;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||
 Db 94 QQLVEYPLT 102

RESULT 4
 KWS1
 Ig kappa chain V region (M511) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change 21-Jan-2000
 C;Accession: A01910
 R;Appella, E.
 Mol. Immunol. 17, 711-718, 1980
 A;Title: Amino acid sequence of the light chain variable region of M511, a phosphorylcholine binding myeloma protein
 A;Reference number: A01910; UID:81052016; PMID:6776396
 A;Accession: A01910
 A;Molecule type: protein
 A;Residues: 1-113 <APP>
 C;Comment: This chain was isolated from a myeloma protein that binds phosphorylcholine.
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger oligomers.
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer
 F;16-95/Domain: immunoglobulin homology <IMM>
 F;23-93/Disulfide bonds: #status predicted

Query Match 87.5%; Score 42; DB 1; Length 113;
 Best Local Similarity 88.9%; Pred. No. 0.24;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||
 Db 94 QQLVEYPLT 102

RESULT 5
 KWS67
 Ig kappa chain precursor V region (VK167) - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 21-Jan-2000
 C;Accession: A01909
 R;Selsing, E.; Storb, U.
 Cell 25, 47-58, 1981
 A;Title: Somatic mutation of immunoglobulin light-chain variable-region genes.
 A;Reference number: A01909; UID:82002223; PMID:6791832
 A;Accession: A01909
 A;Molecule type: DNA
 A;Residues: 1-120 <SEL>
 A;Note: the sequence was determined from the germline gene
 C;Genetics:
 A;Introns: 17/1
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger oligomers.
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-120/Product: Ig kappa chain V region (VK167) #status predicted <MAT>
 F;36-113/Domain: immunoglobulin homology <IMM>
 F;43-113/Disulfide bonds: #status predicted

Query Match 77.1%; Score 37; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
 |||||
 Db 114 QQLVEYP 120

RESULT 6
 A85363
 probable calmodulin-binding protein [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 C;Accession: A85363
 R;anonymus, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Harbor Laboratory
 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A;Reference number: A85001; UID:20083488; PMID:10617198
 A;Accession: A85363
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-467 <SPO>
 A;Cross-references: GB:NC_001268; NID:g7270002; PIDN:CAB79818.1; GSPDB:GN00140
 C;Genetics:
 A;Gene: AT4G31000
 A;Map position: 4

Query Match 77.1%; Score 37; DB 2; Length 467;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPF 8
 |||||
 Db 334 QQLIEYPF 341

RESULT 7
 S36277
 Ig lambda chain V region (clone alpha-FOG1-G8) - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000

C;Accession: S36277
 R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
 EMBO J. 12, 725-734, 1993
 A;Title: Human anti-self antibodies with high specificity from phage display libraries.
 A;Reference number: S36256; MUID:93178448; PMID:7679990
 A;Accession: S36277
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-108 <GRI>
 A;Cross-references: EMBL:Z18829; NID:q33417; PIDN:CAA79281.1; PID:g939910
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 36; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 4;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||: |||
 Db 89 QQLISYPLT 97

RESULT 8
 T38148
 phosphatidyl synthase - fission yeast (Schizosaccharomyces pombe)
 C;Species: Schizosaccharomyces pombe
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C;Accession: T38148
 R;Pearson, D.; Church, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
 submitted to the EMBL Data Library, September 1997
 A;Reference number: Z21774
 A;Accession: T38148
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-570 <PEA>
 A;Cross-references: EMBL:Z99295; PIDN:CAB16578.1; GSPDB:GN00066; SPDB:SPAC22A12.08C
 A;Experimental source: strain 972h-; cosmid c22A12
 C;Genetics:
 A;Gene: SPDB:SPAC22A12.08C
 A;Map position: 1
 A;Introns: 43/2; 62/2; 227/2; 483/1

Query Match 75.0%; Score 36; DB 2; Length 570;
 Best Local Similarity 77.8%; Pred. No. 23;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||: |||
 Db 547 QQLVEYSPT 555

RESULT 9
 B29775
 Ig kappa chain precursor V region (mouse 24.1) - shrew mouse
 C;Species: Mus pahari
 C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 21-Jan-2000
 C;Accession: B29775
 R;Jouvin-Marche, E.; Rudikoff, S.
 Immunogenetics 24, 191-201, 1986
 A;Title: Evolution of a V-kappa gene family.
 A;Reference number: A91751; MUID:87006895; PMID:3093373
 A;Accession: B29775
 A;Molecule type: DNA
 A;Residues: 1-120 <JOU>
 A;Cross-references: GB:M1553; NID:gl97470; PIDN:AAA39037.1; PID:gl97471
 A;Note: this sequence was determined from the germline gene
 C;Genetics:
 A;Introns: 17/1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-120/Product: Ig kappa chain V region 24.1 #status predicted <MAT>

F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 35; DB 2; Length 120;
 Best Local Similarity 85.7%; Pred. No. 7.2;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
 |||: |||
 Db 114 QQLVEYP 120

RESULT 10

A86371

hypothetical protein F508.25 - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001

C;Accession: A86371

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

A;Authors: Salzberg, S.L.; Schwartz, J.C.; Davis, R.W.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Venter, J.C.; Venter, J.C.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: A86371

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-480 <STO>

A;Cross-references: GB:AE005172; NID:g4056452; PIDN:AAC98025.1; GSPDB:GN00141

C;Genetics:

A;Map position: 1

Query Match 72.9%; Score 35; DB 2; Length 480;

Best Local Similarity 85.7%; Pred. No. 31;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 QQLVEYPF 8

|||: |||

Db 269 QQLVEYPF 275

RESULT 11

D82100

mesJ protein VC2242 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C;Species: Vibrio cholerae

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C;Accession: D82100

R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;

chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A;Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82100

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-440 <HEI>

A;Cross-references: GB:AE004296; GB:AE003852; NID:g9656799; PIDN:AAF95386.1; GSPDB:GN001

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics:

A;Gene: VC2242

A;Map position: 1

C;Superfamily: hypothetical protein HI0404

Query Match 70.8%; Score 34; DB 2; Length 440;

Best Local Similarity 75.0%; Pred. No. 46;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPF 8

Db 10 QQLARYPF 17
||| |||

RESULT 12

D89903
hypothetical protein Sali131 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89903
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogino, A.; Mizukami, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89903
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-586 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701099; PIDN:BAB42384.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Gene: Sali131
C:Superfamily: Halobacterium halobium 2-oxoacid ferredoxin oxidoreductase; 2-oxoacid ferredoxin

Query Match 70.8%; Score 34; DB 2; Length 586;
Best Local Similarity 75.0%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QLVVEYPT 9
||| |||

Db 109 QLELPPT 116

RESULT 13

S76367
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76367
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis sp.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76367
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-722 <KAN>
A:Cross-references: EMBL:D84000; GB:AB001339; NID:g1001484; PIDN:BAA10219.1; PID:g100159
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: glycine-tRNA ligase beta chain

Query Match 70.8%; Score 34; DB 2; Length 722;
Best Local Similarity 85.7%; Pred. No. 78;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYP 7
||| |||

Db 254 QQLVEYP 260

RESULT 14

T01906
hypothetical protein T12H20.3 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 24-Mar-1999
C:Accession: T01906
R:Cotton, M.; Graves, T.; Sutterer, C.; Modde, T.
submitted to the EMBL Data Library, July 1998

A:Description: The sequence of A. thaliana T12H20.
A:Reference number: Z14453
A:Accession: T01906
A>Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1074 <COT>
A:Cross-references: EMBL:AF080119; NID:g3600029; PID:g3600033
A:Experimental source: cultivar Columbia
C:Genetics:
A:Map position: 4
A:Note: T12H20.3

Query Match 70.8%; Score 34; DB 2; Length 1074;
Best Local Similarity 71.4%; Pred. No. 12e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QLVVEYPT 8
||| |||

Db 853 QLVVEYPT 859

RESULT 15

I26317
IG kappa chain V region (H158-89H4) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: I26317
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: I26317
A:Molecule type: DNA
A:Residues: 1-112 <CAT>

A:Experimental source: strain Balb/c
A:Note: this sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 68.8%; Score 33; DB 2; Length 112;
Best Local Similarity 75.0%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QLVVEYPT 9
||| |||

Db 95 QLVVEYPT 102

Search completed: April 22, 2003, 12:54:49
Job time : 10.8393 secs

GenCore version 5.1.4_p5_4578
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QM protein - protein search, using sw model

Run on: April 22, 2003, 12:46:53 ; Search time 4.5 Seconds
(without alignments)
82.953 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEVPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	89.6	383	1	CYB APILI
2	42	87.5	112	1	KV2A MOUSE
3	42	87.5	113	1	KV2C MOUSE
4	37	77.1	120	1	KV2B MOUSE
5	36	75.0	379	1	CYB AKOJE
6	36	75.0	379	1	CYB AKOTO
7	36	75.0	381	1	CYB SIGHI
8	34	70.8	722	1	SYGB SYNXY3
9	33	68.8	452	1	CN17_DICDI
10	33	68.8	561	1	LCFA_ECOLI
11	33	68.8	664	1	SYGB_AQUAE
12	33	68.8	792	1	ATX1_MOUSE
13	33	68.8	816	1	ATX1_HUMAN
14	32	66.7	295	1	BIEA RAT
15	32	66.7	296	1	BIEA HUMAN
16	32	66.7	374	1	Y006 BORBU
17	32	66.7	379	1	CYB BOLAM
18	32	66.7	673	1	2145 HUMAN
19	31	64.6	130	1	MSRR_PASMU
20	31	64.6	168	1	CRACA
21	31	64.6	178	1	YP20_BACLI
22	31	64.6	222	1	TYST_METJA
23	31	64.6	366	1	HNLS_SORBI
24	31	64.6	379	1	CYB ALCAA
25	31	64.6	379	1	CYB AMBCI
26	31	64.6	379	1	CYB AMWHA
27	31	64.6	379	1	CYB ARCGZ
28	31	64.6	379	1	CYB CAPCA
29	31	64.6	379	1	CYB CAPPY
30	31	64.6	379	1	CYB CEREL
31	31	64.6	379	1	CYB CERNI
32	31	64.6	379	1	CYB CHAMA
33	31	64.6	379	1	CYB DAMDA

34 31 64.6 379 1 CYB_EUTDO Q9tf32 eutamias do
35 31 64.6 379 1 CYB_GLASA O48372 glaucomyx s
36 31 64.6 379 1 CYB_HYDIN O47930 hydrotapes
37 31 64.6 379 1 CYB_SAISC Q35930 saimiri sci
38 31 64.6 379 1 CYB_SCINI Q35895 sciurus nig
39 31 64.6 379 1 CYB_SPEAR Q9tf51 spermophilu
40 31 64.6 379 1 CYB_SPMO Q9tf31 spermophilu
41 31 64.6 379 1 CYB_SPERI P49341 spermophilu
42 31 64.6 380 1 CYB_HUMAN P00156 homo sapien
43 31 64.6 380 1 CYB_LATCH O03176 latimeria c
44 31 64.6 380 1 CYB_MICAR Q36922 microtus ar
45 31 64.6 380 1 CYB_MICLO P56731 microtus lo

ALIGNMENTS

RESULT 1
CYB APILI STANDARD; PRT; 383 AA.
AC P34845;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cytochrome B.
GN COB OR CYTB.
OS Apis mellifera ligustica (Common honeybee).
OG Mitochondrion.
OC Insecta; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC Aculeata; Apoidea; Apidae; Apis.
OX NCBI_TaxID=7469;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thorax;
RX MEDLINE=92261310; PubMed=1533894;
RA Crozier R.H., Crozier Y.C.;
RT "The cytochrome b and ATPase genes of honeybee mitochondrial DNA."; [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Thorax;
RX MEDLINE=93114603; PubMed=8417993;
RA Crozier R.H., Crozier Y.C.;
RT "The mitochondrial genome of the honeybee Apis mellifera: complete sequence and genome organization."; Genetics 133:97-117(1993).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS.
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
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CC -----
CC EMBL: L06178; AAB96809.1; -
CC EMBL: M87052; -; NOT_ANNOTATED_CDS.
CC PIR: C43622; C43622.
CC IncerPro: IPR000179; Cyt_b_b6.
CC Pfam: PF000032; cytochrome_b_c1.
CC Pfam: PF000032; cytochrome_b_c1.
CC PROSITE: PS00192; CYTOCHROME_B_HEME; 1.
CC PROSITE: PS00193; CYTOCHROME_B_QQ; 1.
CC

```

KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
KW Heme.
FT METAL 85 85 IRON 1 (HEME B562 AXIAL LIGAND) .
FT METAL 99 99 IRON 2 (HEME B566 AXIAL LIGAND) .
FT METAL 184 184 IRON 2 (HEME B562 AXIAL LIGAND) .
FT METAL 198 198 IRON 1 (HEME B566 AXIAL LIGAND) .
SQ SEQUENCE 383 AA; 45256 MW; A140A05B6053C2D5 CRC64;

Query Match 89.6%; Score 43; DB 1; Length 383;
Best Local Similarity 77.8%; Pred. No. 0.32;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 341 QQLVEYPPT 349

RESULT 2
KV2A_MOUSE STANDARD; PRT; 112 AA.
AC P01626;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MOPC 167.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A01910; KVM51.
DR HSP; P80362; IWT.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12349 MW; A58EDF56404B9726 CRC64;

Query Match 87.5%; Score 42; DB 1; Length 112;
Best Local Similarity 88.9%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 94 QQLVEYPPT 102

RESULT 3
KV2C_MOUSE STANDARD; PRT; 113 AA.
AC P01628;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

```

```

DE Ig kappa chain V-II region MOPC 511.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81052016; PubMed=6776396;
RA Appella E.;
RT Amino acid sequence of the light chain variable region of M511, a
RT phosphorylcholine-binding murine myeloma protein.";
RL Mol. Immunol. 17:711-718(1980).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A01910; KVM51.
DR HSP; P80362; IWT.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; EFB0DC4DA2BD3450 CRC64;

Query Match 87.5%; Score 42; DB 1; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 94 QQLVEYPPT 102

RESULT 4
KV2B_MOUSE STANDARD; PRT; 120 AA.
AC P01627;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region VKAPPA167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82002223; PubMed=6791832;
RA Selsing E.; Storb U.;
RT Somatic mutation of immunoglobulin light-chain variable-region
RT genes.";
RL Cell 25:47-58(1981).
CC
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CC -----
CC EMBL; J00562; AAA39032.1; --
CC EMBL; K02415; AAA39051.1; --
CC FIR; A01909; KVM567.
CC HSP; P80362; IWT.

```


DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig V.
 DR SMART; PF00047; Ig 1.
 DR SMART; SM00406; IGV 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 120 IG KAPPA CHAIN V-II REGION VKAPPAL67.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 44 59 FRAMEWORK-2.
 FT DOMAIN 60 74 FRAMEWORK-2.
 FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 82 113 FRAMEWORK-3.
 FT DOMAIN 114 120 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 113 BY SIMILARITY.
 SQ SEQUENCE 120 AA; 13280 MW; 638B571F0E4DE3E8 CRC64;
 Query Match 77.1%; Score 37; DB 1; Length 120;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEYP 7
 Db 114 QQLVEYP 120
 RESULT 5
 CYB AKOJO
 ID CYB AKOJO STANDARD; PRT; 379 AA.
 AC P21715;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome B.
 GN MTCYB OR COB OR CYTB.
 OS Akodon jelskii.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Akodon.
 OX NCBI_TaxID=10079;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Smith M.F.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 1-267 FROM N.A.
 RC TISSUE=Liver;
 RA Smith M.F.; Patton J.L.;
 RL "The diversification of South American murid rodents: evidence from mitochondrial DNA sequence data for the akodontine tribe.";
 RL Biol. J. Linn. Soc. Lond. 50:149-177(1993).
 [3]
 RP SEQUENCE OF 1-133 FROM N.A.
 RC STRAIN=MVZ catalog 173073, 173074, 173083, and 173084; TISSUE=Liver;
 RX MEDLINE=91163325; PubMed=2002767;
 RA Smith M.F.; Patton J.L.;
 RL "Variation in mitochondrial cytochrome b sequence in natural populations of South American akodontine rodents (Muridae; Sigmodontinae).";
 RL Mol. Biol. Evol. 8:85-103(1991).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
 CC COUPLED TO ATP SYNTHESIS
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
 CC BOUND TO THE PROTEIN.
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
 CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
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 CC -----
 DR EMBL; M35714; AAA16998.2; ALT_TERM.
 DR EMBL; M35715; AAA31630.1; -.
 DR EMBL; M35716; AAA31629.1; -.
 DR PIR; C41824; C41824.
 DR InterPro; IPR000179; Cyt_b_b6.
 DR Pfam; PF00032; cytochrome b_n; 1.
 DR PROSITE; PS00193; CYTOCHROME B_N; 1.
 DR PROSITE; PS00192; CYTOCHROME B_HEME; 1.
 KW Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
 KW Heme.
 FT METAL 83 83 IRON 1 (HEME B562 AXIAL LIGAND).
 FT METAL 97 97 IRON 2 (HEME B566 AXIAL LIGAND).
 FT METAL 182 182 IRON 2 (HEME B562 AXIAL LIGAND).
 FT METAL 196 196 IRON 1 (HEME B566 AXIAL LIGAND).
 FT VARIANT 118 118 V -> I (IN STRAINS 173083 AND 173084).
 FT VARIANT 122 122 T -> A (IN STRAINS 173083 AND 173084).
 SQ SEQUENCE 379 AA; 42529 MW; F9F012A46671D59A CRC64;
 Query Match 75.0%; Score 36; DB 1; Length 379;
 Best Local Similarity 87.5%; Pred. No. 8;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 QQLVEYPFT 9
 Db 341 QPVEYPFT 348
 RESULT 6
 CYB AKOTO
 ID CYB AKOTO STANDARD; PRT; 379 AA.
 AC P21721;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Cytochrome B.
 GN MTCYB OR COB OR CYTB.
 OS Akodon torques.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 OC Akodon.
 OX NCBI_TaxID=10079;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Smith M.F.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 [2]
 RP SEQUENCE OF 1-267 FROM N.A.
 RC TISSUE=Liver;
 RA Smith M.F.; Patton J.L.;
 RL "The diversification of South American murid rodents: evidence from mitochondrial DNA sequence data for the akodontine tribe.";
 RL Biol. J. Linn. Soc. Lond. 50:149-177(1993).
 [3]
 RP SEQUENCE OF 1-133 FROM N.A.
 RC STRAIN=MVZ catalog 171720, 171721, 174053, and 174054; TISSUE=Liver;
 RX MEDLINE=91163325; PubMed=2002767;
 RA Smith M.F.; Patton J.L.;
 RL "Variation in mitochondrial cytochrome b sequence in natural populations of South American akodontine rodents (Muridae; Sigmodontinae).";
 RL Mol. Biol. Evol. 8:85-103(1991).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
 CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
 CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

COUPLED TO ATP SYNTHESIS.
 -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.
 -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.
 -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

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 EMBL; M35700; AAA1897.2; -.
 EMBL; M35701; AAA31624.1; -.
 EMBL; M35702; AAA31625.1; -.
 PIR; G23725; G23725.
 InterPro; IPR000179; Cyt b b6.
 Pfam; PF00032; cytochrome_b_c1.
 Pfam; PF00033; cytochrome_b_n; 1.
 PROSITE; PS00193; CYTOCHROME_B_QQ; 1.
 PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
 Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
 Heme.
 METAL 83 IRON 1 (HEME B562 AXIAL LIGAND).
 METAL 97 IRON 2 (HEME B566 AXIAL LIGAND).
 METAL 182 IRON 1 (HEME B562 AXIAL LIGAND).
 METAL 196 IRON 2 (HEME B566 AXIAL LIGAND).
 VARIANT 108 108 V -> A (IN STRAINS 174053 AND 174054).
 VARIANT 115 115 V -> I (IN STRAINS 174053 AND 174054).
 SEQUENCE 379 AA; 42611 MW; 4C94CF8A92CCC34F CRC64;

Query Match 75.0%; Score 36; DB 1; Length 379;
 Best Local Similarity 87.5%; Pred. No. 8;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVVEYPT 9
 | |||||
 Db 341 QVVEYPT 348

RESULT 7
 CYB_SIGHI STANDARD; PRT; 381 AA.
 AC Q9XNU6;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cytochrome B.
 GN MTCYB OR COB OR CVTB.
 OS Sigmmodon hispidus (Hispid cotton rat).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmmodontinae;
 OC Sigmmodon.
 OC NCBI_TaxID=42415;
 [1]
 SEQUENCE FROM N.A.
 RA Smith M.P., Patton J.L.;
 RT "Phylogenetic relationships and the radiation of sigmodontine rodents in South America: evidence from cytochrome b.";
 RL J. Mammal. Evol. 6:89-128(1999).
 CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS.
 CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN.
 CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

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 EMBL; AF108702; AAD45484.1; -.
 InterPro; IPR000179; Cyt b b6.
 Pfam; PF00032; cytochrome_b_c1.
 Pfam; PF00033; cytochrome_b_n; 1.
 PROSITE; PS00192; CYTOCHROME_B_QQ; 1.
 PROSITE; PS00193; CYTOCHROME_B_QQ; 1.
 Electron transport; Mitochondrion; Respiratory chain; Transmembrane;
 Heme.
 METAL 83 IRON 1 (HEME B562 AXIAL LIGAND).
 METAL 97 IRON 2 (HEME B566 AXIAL LIGAND).
 METAL 182 IRON 1 (HEME B562 AXIAL LIGAND).
 METAL 196 IRON 2 (HEME B566 AXIAL LIGAND).
 SEQUENCE 381 AA; 42965 MW; 0472259421B38284 CRC64;

Query Match 75.0%; Score 36; DB 1; Length 381;
 Best Local Similarity 87.5%; Pred. No. 8;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVVEYPT 9
 | |||||
 Db 341 QVVEYPT 348

RESULT 8
 SYGB_SYNY3 STANDARD; PRT; 722 AA.
 AC Q55690;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) (Glycine--tRNA ligase beta chain) (GLYRS).
 DE GLYS OR SLR0220.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 OC NCBI_TaxID=1148;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiyama M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64k to 92k of the genome.";
 RL DNA Res. 2:153-166(1995).
 CC -1- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate + Glycyl-tRNA(Gly).
 CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.

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 EMBL; D64000; BAA10219.1; -.
 InterPro; IPR002311; tRNA_synth_2f.
 Pfam; PF02092; tRNA_synth_2f; 1.
 PRINTS; PR01045; TRNASYNTHGB.

DR TIGRfams; TIGR00211; glyS; 1.
 DR PROSITE; PS00861; AA TRNA_LIGASE_II_GLYAB; 1.
 KW Aminoacyl-tRNA synthetase; Protein Biosynthesis; Ligase; ATP-binding;
 SQ SEQUENCE 722 AA; 80051 MW; F7085BA5A23436D7 CRC64;
 Query Match 70.8%; Score 34; DB 1; Length 722;
 Best Local Similarity 85.7%; Pred. No. 38;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEYP 7
 :|||||
 Db 254 EQLVEYP 260
 :|||||
 RESULT 9
 ID_CN17 D1CDI STANDARD; PRT; 452 AA.
 AC P12019;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 3',5'-cyclic-nucleotide phosphodiesterase precursor (EC 3.1.4.17)
 DE (PDEase) (3':5'-CNP).
 GN PDEA.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
 OX NCBI_TaxID=44689;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87057386; PubMed=3023365;
 RA Lacombe M.-L., Podgorski G.J., Franke J., Kessin R.H.;
 RT "Molecular cloning and developmental expression of the cyclic
 RT nucleotide phosphodiesterase gene of Dictyostelium discoideum.";
 RL J. Biol. Chem. 261:16811-16817(1986).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89384622; PubMed=2779573;
 RA Podgorski G.J., Franke J., Faure M., Kessin R.H.;
 RT "The cyclic nucleotide phosphodiesterase gene of Dictyostelium
 RT discoideum utilizes alternate promoters and splicing for the
 RT synthesis of multiple mRNAs.";
 RL Mol. Cell. Biol. 9:3938-3950(1989).
 [3]
 RP SEQUENCE OF 1-69 FROM N.A.
 RX MEDLINE=87010528; PubMed=3020155;
 RA Podgorski G.J., Franke J., Kessin R.H.;
 RT "Isolation of a cDNA encoding a portion of the cyclic nucleotide
 RT phosphodiesterase of Dictyostelium discoideum.";
 RL J. Gen. Microbiol. 132:1043-1050(1986).
 CC -1- FUNCTION: TO MAINTAIN THE RESPONSIVENESS OF CELLS TO THE
 CC CHEMOTACTIC CAMP DURING THE AGGREGATION PHASE OF DEVELOPMENT.
 CC -1- CATALYTIC ACTIVITY: Nucleoside 3',5'-cyclic phosphate + H(2)O =
 CC nucleoside 5'-phosphate.
 CC -1- SIMILARITY: BELONGS TO THE CAMP PHOSPHODIESTERASE CLASS-II FAMILY.
 CC
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 CC
 DR EMBL; J02628; AAA68447.1; -.
 DR EMBL; M23449; AAA63168.1; -.
 DR EMBL; M15738; AAA33238.1; -.
 DR PIR; A25346; A25346.
 DR PIR; A32573; A32573.
 DR DictyDb; DD02009; pdeA.
 DR InterPro; IPR000396; Pdiesterase2.
 DR Pfam; PF02112; PDEase II; 1.
 DR PRINTS; PR00368; PDIESTERASE2.

DR ProDom; PD010003; Pdiesterase2; 2.
 DR PROSITE; PS00607; PDEASE_II; 1.
 KW Glycoprotein; Hydrolase; CAMP; Zinc; Signal.
 FT SIGNAL 1 23
 FT PROPEP 24 49
 FT CHAIN 50 452
 FT CARBOHYD 101 101
 FT CARBOHYD 141 141
 FT CARBOHYD 277 277
 FT CONFLICT 68 69
 SQ SEQUENCE 452 AA; 51093 MW; A8F3C190D4603BD1 CRC64;
 Query Match 68.8%; Score 33; DB 1; Length 452;
 Best Local Similarity 83.3%; Pred. No. 38;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 VEYFPT 9
 :|||||
 Db 266 IEYFPT 271
 :|||||
 RESULT 10
 ID_LCPA ECOLI STANDARD; PRT; 561 AA.
 AC P29212;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Long-chain-fatty-acid-CoA ligase (EC 6.2.1.3) (Long-chain acyl-CoA
 DE synthetase).
 GN FADD OR OLDD OR B1805.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=94150456; PubMed=8107670;
 RA Fulda M., Heinz E., Wolter F.P.;
 RT "The fadD gene of Escherichia coli K12 is located close to rnd at
 RT 39.6 min of the chromosomal map and is a new member of the
 RT AMP-binding protein family.";
 RL Mol. Gen. Genet. 242:241-249(1994).
 [2]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
 RC STRAIN=K12;
 RX MEDLINE=93094273; PubMed=1460045;
 RA Black P.N., Dirusso C.C., Metzger A.K., Heimert T.L.;
 RT "Cloning, sequencing, and expression of the fadD gene of Escherichia
 RT coli encoding acyl coenzyme A synthetase.";
 RL J. Biol. Chem. 267:25513-25520(1992).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97251358; PubMed=9097040;
 RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
 RA Isono K., Kasai H., Mizumura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Sivasubramanian S., Tagami H.,
 RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;

RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
 RL corresponding to the 40.1-50.0 min region on the linkage map."
 CC -1- FUNCTION: ESTERIFICATION, CONCOMITANT WITH TRANSPORT, OF EXOGENOUS
 CC LONG-CHAIN FATTY ACIDS INTO METABOLICALLY ACTIVE COA THIOESTERS
 CC FOR SUBSEQUENT DEGRADATION OR INCORPORATION INTO PHOSPHOLIPIDS.
 CC -1- CATALYTIC ACTIVITY: ATP + a long-chain carboxylic acid + CoA = AMP
 CC + diphosphate + an acyl-CoA.
 CC -1- COFACTOR: MAGNESIUM.
 CC -1- SUBUNIT: HOMODIMER (PROBABLE).
 CC -1- SUBCELLULAR LOCATION: PARTIALLY MEMBRANE-ASSOCIATED (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE ATP-DEPENDENT AMP-BINDING ENZYME
 CC FAMILY.
 CC -----
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 CC -----
 DR EMBL; X70994; CAAS0321.1; -
 DR EMBL; L02649; AAA23752.1; -
 DR EMBL; A5000275; AAC74875.1; -
 DR EMBL; D90823; BAA15600.1; -
 DR EMBL; D90824; BAA15609.1; -
 DR EMBL; D90825; BAA15614.1; -
 DR PIR; A45062; A45062.
 DR HSP; P08659; ILCI.
 DR EcoGene; EG11530; fadD.
 DR InterPro; IPR000873; AMP-bind.
 DR Pfam; PF0501; AMP-binding; 1.
 DR PROSITE; PS00455; AMP BINDING; 1.
 DR Ligase; Fatty acid metabolism; Magnesium; Membrane; Complete proteome.
 FT CONFLICT 34 51 ARYADQAPAFVNMGEVMTF -> GALRRSTVCVEYGGNDL
 (IN REF. 2).
 FT CONFLICT 468 490 NEIEDVVMCHQVCEVRAVGVPs ->
 TELKSSCSMWAYKSKRLAYLP (IN REF. 2).
 FT CONFLICT 496 496 A -> G (IN REF. 2).
 FT CONFLICT 555 561 GKVDNKA -> QSGQ (IN REF. 2).
 SQ SEQUENCE 561 AA; 62332 MW; 249B0AA54B3DBFA5 CRC64;
 Query Match 68.8%; Score 33; DB 1; Length 561;
 Best Local Similarity 55.6%; Pred. No. 47;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQLVEYVPT 9
 Db 293 KELAKVPT 301
 RESULT 11
 ID SYGB_AQUAE STANDARD; PRT; 664 AA.
 AC O67896;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Glycyl-tRNA synthetase beta chain (EC 6.1.1.14) (Glycine--tRNA ligase
 DE beta chain) (GLYRS).
 GN GLYS OR AQ.2141.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;
 OC Aquifex.
 CC NCBI_TaxID=63363;
 CC [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=VF5;
 RC MEDLINE=98196666; PubMed=9537320;
 RX Qeckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
 RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;

RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RL aeolicus.";
 CC -1- CATALYTIC ACTIVITY: ATP + glycine + tRNA (Gly) = AMP + diphosphate
 CC + glycyl-tRNA (Gly).
 CC -1- SUBUNIT: Tetramer of two alpha and two beta chains
 CC (by similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AE000775; AAC07870.1; -
 DR InterPro; IPR002311; tRNA synt 2f.
 DR Pfam; PF02092; tRNA synt 2f; 1.
 DR PRINTS; PR01045; TRNASYNTHGB.
 DR TIGRFAMs; TIGR00211; GLYS, 1.
 DR PROSITE; PS50861; AA-tRNA_LIGASE II GLYAB, 1.
 DR Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 SQ SEQUENCE 664 AA; 77523 MW; 7F7EF7A8F552E3DB CRC64;
 Query Match 68.8%; Score 33; DB 1; Length 664;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LVEYVPT 8
 Db 248 LVEYVPT 253
 RESULT 12
 ID ATX1_MOUSE STANDARD; PRT; 792 AA.
 AC P54254;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Ataxin-1 (Spinocerebellar ataxia type 1 protein).
 GN SCAL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CC NCBI_TaxID=10090;
 CC [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6 X CBA; TISSUE=Brain, Thymus, and Retina;
 RX MEDLINE=96381424; PubMed=8789437;
 RA Banfi S., Servadio A., Chung M.-Y., Capozzoli F., Duvick L.A.,
 RA Elde R., Zoghbi H.Y., Orr H.T.;
 RT "Cloning and developmental expression analysis of the murine homolog
 RT of the spinocerebellar ataxia type 1 gene (Scal).";
 RL Hum. Mol. Genet. 5:33-40(1996).
 CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED. IN BRAIN, THE PATTERN OF
 CC DISTRIBUTION IS LIMITED TO NEURONS POPULATIONS.
 CC -1- DEVELOPMENTAL STAGE: TRANSIENT EXPRESSION BURST IN PURKINJE CELLS
 CC AS THE CEREBELLAR CORTEX BECOMES FUNCTIONAL (POSTNATAL DAY 14),
 CC AND IN MESENCHYMAL CELLS OF THE DEVELOPING INTERVERTEBRAL DISCS OF
 CC THE SPINAL COLUMN.
 CC -1- POLYMORPHISM: THE MURINE POLY-GLN REGION IS VERY LIMITED IN
 CC COMPARISON TO THE HUMAN SCAL AND IS NOT POLYMORPHIC.
 CC -----
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CC -----
CC EMBL; X83542; CAAS5833.1; -.
CC MGD; MGI:104783; SCAL.
CC DR InterPro; IPR003652; Atax_HMG.
CC DR SMART; SM00536; AXH; 1.
CC FT DOMAIN 214 217 POLY-PRO.
CC SQ SEQUENCE 792 AA; 84052 MW; CA5F59C0013499DB CRC64;

Query Match 68.8%; Score 33; DB 1; Length 792;
Best Local Similarity 100.0%; Pred.No. 66;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVEYDF 8
| | | | |
DB 621 LVEYDF 626

RESULT 13
ATX1 HUMAN
ID ATX1 HUMAN STANDARD; PRT; 816 AA.
AC P54253; Q9UUG2;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ataxin-1 (Spinocerebellar ataxia type 1 protein).
GN SCAL OR ATX1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cerebellum, and Brain;
RX MEDLINE=95038938; PubMed=7951322;
RA Banfi S., Servadio A., Chung M.-Y., Kwiatkowski T.J. Jr., McCall A.E.,
RA Duvick L.A., Shen Y., Roth E.J., Orr H.T., Zoghbi H.Y.;
RT "Identification and characterization of the gene causing type 1
RT spinocerebellar ataxia";
RL Nat. Genet. 7:513-519(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Tubby B.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS ARE PRODUCED BY
CC -!- ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED THROUGHOUT THE BODY.
CC -!- POLYMORPHISM: THE POLY-GLN REGION OF SCAL IS HIGHLY POLYMORPHIC
CC (9 TO 39 REPEATS) IN THE NORMAL POPULATION AND IS EXPANDED TO
CC ABOUT 40-81 REPEATS IN SCAL PATIENTS. LONGER EXPANSIONS RESULT IN
CC EARLIER ONSET AND MORE SEVERE CLINICAL MANIFESTATIONS OF THE
CC DISEASE.
CC -!- DISEASE: DEFECTS IN SCAL ARE THE CAUSE OF SPINOCEREBELLAR ATAXIA
CC TYPE 1; ALSO KNOWN AS OLIVOPONTOCEREBELLAR ATROPHY 1 (OPCA 1).
CC SCAL IS AN AUTOSOMAL DOMINANT NEURODEGENERATIVE DISORDER
CC CHARACTERIZED BY PROGRESSIVE NEURONAL LOSS IN THE CEREBELLUM,
CC BRAIN STEM AND SPINOCEREBELLAR TRACTS. CLINICAL FEATURES ARE
CC CEREBELLAR ATAXIA, DYSPHAGIA, OPHTHALMOPARESIS, MUSCLE WASTING AND
CC NEUROPATHY. ONSET OF THE DISEASE USUALLY OCCURS IN THE THIRD OR
CC FOURTH DECADE OF LIFE AND DEATH OCCURS TEN TO TWENTY YEARS LATER.
CC -----
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CC -----
CC EMBL; X79204; CAAS5793.1; -.
CC EMBL; AL009031; CAAL5622.1; -.
CC Genew; HGNC:10548; SCAL.

DR MIM; 601556; -.
DR MIM; 164400; -.
DR InterPro; IPR003652; Atax_HMG.
DR SMART; SM00536; AXH; 1.
KW Polymorphism; Triplet repeat expansion; Alternative splicing.
FT DOMAIN 197 226 POLY-GLN.
SQ SEQUENCE 816 AA; 87051 MW; D49BA5DB423D0777 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 816;
Best Local Similarity 100.0%; Pred.No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVEYDF 8
| | | | |
DB 646 LVEYDF 651

RESULT 14
BIEA RAT
ID BIEA RAT STANDARD; PRT; 295 AA.
AC P46874;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Biliverdin reductase A precursor (EC 1.3.1.24) (Biliverdin-IX alpha-
DE reductase).
GN BLVRA OR BLVR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=92156147; PubMed=1371282;
RA Fakhrai H., Maines M.D.;
RT "Expression and characterization of a cDNA for rat kidney biliverdin
RT reductase. Evidence suggesting the liver and kidney enzymes are the
RT same transcript product";
RL J. Biol. Chem. 267:4023-4029(1992).
RN [2]
RP MUTAGENESIS.

RX MEDLINE=94291657; PubMed=8020496;
RA McCoubrey W.K. Jr., Maines M.D.;
RT "Site-directed mutagenesis of cysteine residues in biliverdin
RT reductase. Roles in substrate and cofactor binding";
RL Eur. J. Biochem. 222:597-603(1994).
CC -!- FUNCTION: CONVERTS BILIVERDIN TO BILIRUBIN; DISPLAYS TWO DISTINCT
CC PH OPTIMA USING A DIFFERENT COFACTOR AT EACH PH: NADH AT THE LOWER
CC PH 6.7-6.9 RANGE AND NADPH AT PH 8.5-8.7. NADPH, HOWEVER, IS THE
CC PROBABLE COFACTOR IN BIOLOGICAL SYSTEMS.
CC -!- CATALYTIC ACTIVITY: Bilirubin + NAD(P)(+) = biliverdin + NAD(P)H.
CC -!- COFACTOR: BINDS ONE ZINC ION.
CC -!- PATHWAY: FINAL STEP IN HEME METABOLISM.
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: TO E. COLI YHHX.

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CC -----
CC EMBL; M81681; AAA40830.1; -.
CC InterPro; IPR000683; GFO IDH MCA; 1.
CC Pfam; PF01408; GFO IDH MCA; 1.
KW Oxidoreductase; NAD; NADP; Zinc.
FT PROPEP 1 2
FT CHAIN 3 295 BILIVERDIN REDUCTASE A.
FT DOMAIN 11 16 POLY-VAL.

```

FT METAL          279      279      ZINC (POTENTIAL).
FT METAL          280      280      ZINC (POTENTIAL).
FT METAL          291      291      ZINC (POTENTIAL).
FT METAL          292      292      ZINC (POTENTIAL).
FT MUTAGEN        73       73       C->A: LOSS OF ACTIVITY.
FT MUTAGEN        73       73       C->A: REDUCED ACTIVITY.
FT MUTAGEN        280      280      C->A: REDUCED ACTIVITY.
FT MUTAGEN        291      291      C->A: REDUCED ACTIVITY.
SQ SEQUENCE       295 AA; 33565 MW; 219C8EA96C150588 CRC64;

Query Match      66.7%; Score 32; DB 1; Length 295;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVEYPT 9
Db 94 LVEYPT 100

RESULT 15
BIEA_HUMAN
ID BIEA_HUMAN STANDARD; PRT; 296 AA.
AC P53004;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Biliverdin reductase A precursor (EC 1.3.1.24) (Biliverdin-IX alpha-
DE reductase).
GN BLVRA OR BLVR OR BVR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=96202961; PubMed=8631357;
RA Maines M.D., Polevoda B.V., Huang T.-J., McCoubrey W.K. Jr.;
RT "Human biliverdin IXalpha reductase is a zinc-metalloprotein.
RT Characterization of purified and Escherichia coli expressed
RT enzymes.";
RL Eur. J. Biochem. 235:372-381(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Komuro A., Tobe T., Nakano Y., Yamaguchi T., Tomita M.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-117 FROM N.A.
RA Cordes M., Wollam C., Carter T.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 3-36; 48-74 AND 228-248.
RC TISSUE=Liver;
RX MEDLINE=93143333; PubMed=8424666;
RA Maines M.D., Trakshel G.M.;
RT "Purification and characterization of human biliverdin reductase.";
RL Arch. Biochem. Biophys. 300:320-326(1993).
RN [5]
RP SEQUENCE OF 3-22.
RC TISSUE=Liver;
RX MEDLINE=95014177; PubMed=7929092;
RA Yamaguchi T., Komoda Y., Nakajima H.;
RT "Biliverdin-IX alpha reductase and biliverdin-IX beta reductase from
RT human liver. Purification and characterization.";
RL J. Biol. Chem. 269:24343-24348(1994).
CC CC
CC -1- FUNCTION: CONVERTS BILIVERDIN TO BILIRUBIN.
CC -1- CATALYTIC ACTIVITY: Bilirubin + NAD(P) (+) = biliverdin + NAD(P)H.
CC -1- COFACTOR: BINDS ONE ZINC ION. HAS DUAL PH/COFACTOR (NADH, NADPH)
CC SPECIFICITY. USES NADH AT THE ACIDIC PH RANGE (6-6.7) AND NADPH AT
CC THE ALKALINE RANGE (8.5-8.7).
CC -1- PATHWAY: FINAL STEP IN HEME METABOLISM.
CC -1- SUBUNIT: MONOMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: LIVER.

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CC -1- SIMILARITY: TO E.COLI YHHX.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X93086; CAA63635.1; -.
DR EMBL; U34877; AAC35588.1; -.
DR EMBL; AC005189; AAC35526.1; -.
DR Genew; HGNC:1062; BLVRA.
DR MIM; 109750; -.
DR InterPro; IPR000583; GFO_IDH_MocA.
DR Pfam; PF01408; GFO_IDH_MocA; 1.
KW Oxidoreductase; NAD; NADP; Zinc.
FT PROPEP 1 2
FT CHAIN 3 296 BILIVERDIN REDUCTASE A.
FT DOMAIN 11 16 POLY-VAL.
FT METAL 280 280 ZINC (POTENTIAL).
FT METAL 281 281 ZINC (POTENTIAL).
FT METAL 292 292 ZINC (POTENTIAL).
FT METAL 293 293 ZINC (POTENTIAL).
FT CONFLICT 3 3 A -> T (IN REF. 2).
FT CONFLICT 154 155 SD -> AG (IN REF. 2).
FT CONFLICT 160 160 D -> E (IN REF. 2).
SQ SEQUENCE 296 AA; 33488 MW; 0DFD3B386F4DFC0A CRC64;

Query Match      66.7%; Score 32; DB 1; Length 296;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVEYPT 9
Db 95 LVEYPT 101

Search completed: April 22, 2003, 12:51:48
Job time : 5.5 secs

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GenCore version 5.1.4 ps_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:47:43 ; Search time 18 seconds
(without alignments)
103.024 Million cell updates/sec

Title: US-09-674-716b-7
Perfect score: 48
Sequence: 1 QQLVEYPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_page:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	77.1	278	10 Q8W454	Q8W454 arabidopsis
2	37	77.1	467	10 Q65550	Q65550 arabidopsis
3	36	75.0	84	8 Q9B313	Q9B313 neoceratodus
4	36	75.0	247	8 Q9MP34	Q9MP34 bothriomyrm
5	36	75.0	352	8 Q9XNV8	Q9XNV8 delomys dor
6	36	75.0	377	8 Q9XNXS	Q9XNXS scaptomyza
7	36	75.0	377	8 Q9XNV0	Q9XNV0 reithrodon
8	36	75.0	379	8 Q9TGL4	Q9TGL4 cervus elap
9	36	75.0	379	8 Q9TF64	Q9TF64 spermophilu
10	36	75.0	379	8 Q9TF12	Q9TF12 spermophilu
11	36	75.0	379	8 Q9TF11	Q9TF11 spermophilu
12	36	75.0	379	8 Q9TF08	Q9TF08 spermophilu
13	36	75.0	379	8 Q33887	Q33887 akodon toba
14	36	75.0	379	8 Q33940	Q33940 bolomys uri
15	36	75.0	379	8 Q94QC8	Q94QC8 cervus timo
16	36	75.0	380	8 Q9XNX7	Q9XNX7 oxymycterus

17	36	75.0	380	8 Q9XNX6	Q9XNX6 blarinomys
18	36	75.0	380	8 Q9XNX0	Q9XNX0 thomasmomys
19	36	75.0	380	8 Q9XNW9	Q9XNW9 thomasmomys
20	36	75.0	380	8 Q9XNW8	Q9XNW8 thomasmomys
21	36	75.0	380	8 Q9XNW7	Q9XNW7 thomasmomys
22	36	75.0	380	8 Q9XNW6	Q9XNW6 thomasmomys
23	36	75.0	380	8 Q9XNW3	Q9XNW3 rhipidomys
24	36	75.0	380	8 Q9XNV7	Q9XNV7 delomys sub
25	36	75.0	380	8 Q9TFX5	Q9TFX5 microtyzomy
26	36	75.0	380	8 Q35970	Q35970 thomasmomys
27	36	75.0	380	8 Q34853	Q34853 lenoxus api
28	36	75.0	380	8 Q9MNT7	Q9MNT7 andinomys e
29	36	75.0	380	8 Q9MNT5	Q9MNT5 andalgalomy
30	36	75.0	380	8 Q9MNT4	Q9MNT4 tapecomys p
31	36	75.0	380	8 Q9MNT3	Q9MNT3 tapecomys p
32	36	75.0	380	8 Q9MNT2	Q9MNT2 elignodonti
33	36	75.0	380	8 Q9MNT1	Q9MNT1 gramomys gri
34	36	75.0	380	8 Q9MNT0	Q9MNT0 gramomys dom
35	36	75.0	380	8 Q9MNS8	Q9MNS8 calomys cal
36	36	75.0	380	8 Q9MNS7	Q9MNS7 calomys lep
37	36	75.0	380	8 Q9T7L7	Q9T7L7 microtus ri
38	36	75.0	380	8 Q9MHF9	Q9MHF9 microtus lo
39	36	75.0	380	8 Q94WF7	Q94WF7 calomys mus
40	36	75.0	380	8 Q94V01	Q94V01 microtus oa
41	36	75.0	380	8 Q94U29	Q94U29 microtus gu
42	36	75.0	380	8 Q956Q2	Q956Q2 acomys igni
43	36	75.0	381	8 Q9TGS0	Q9TGS0 abrothrix o
44	36	75.0	381	8 Q9BIW5	Q9BIW5 abrothrix o
45	36	75.0	381	8 Q9BIW4	Q9BIW4 abrothrix s

ALIGNMENTS

RESULT 1

Q8W454 ID Q8W454 PRELIMINARY; PRT; 278 AA.
AC Q8W454; (TREMREL. 20, Created)
DT 01-MAR-2002 (TREMREL. 20, Last sequence update)
DT 01-MAR-2002 (TREMREL. 20, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Putative calmodulin-binding protein.
GN AT4G31000, F6118.90 OR AT4G31000.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RA Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Full Length cDNA Clones."
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY062856; AAL32934.1;
DR EMBL: AY074504; AAL69488.1;
SQ SEQUENCE 278 AA; 31406 MW; 398DCFB65C85A836 CRC64;

Query Match 77.1%; Score 37; DB 10; Length 278;

Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPPF 8
| : : : : :
Db 145 QHLIEYPPF 152

RESULT 2
O65550 PRELIMINARY; PRT; 467 AA.
AC O65550;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DE Putative calmodulin-binding protein.
GN P6118.90 OR A74G31000.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]

SEQUENCE FROM N.A.
RA Bevan M., Benes V., Rechmann S., Borkova D., Ansoerge W., Hoheisel J.,
RA Mewes H.W., Mayer K., Schueller C.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [2]

SEQUENCE FROM N.A.
RA Benes V., Rechmann S., Borkova D., Ansoerge W., Mewes H.W., Lemcke K.,
RA Mayer K.P.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]

SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL021198; CAA18193.1; -;
DR EMBL; AL161578; CAB79818.1; -;
SQ SEQUENCE 467 AA; 52831 MW; 4DB1FB318D553B3D CRC64;

Query Match 77.1%; Score 37; DB 10; Length 467;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPPF 8
| : : : : :
Db 334 QHLIEYPPF 341

RESULT 3
Q9B313 PRELIMINARY; PRT; 84 AA.
AC Q9B313;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome b (fragment).
GN CYTB.
OS Neoceratodus forsteri (Australian lungfish).
OC Chordata; Vertebrata; Euteleostomi;
OC Dipnoi; Ceratodontiformes; Ceratodontidae; Neoceratodus.
OX NCBI_TaxID=7892;
RN [1]

SEQUENCE FROM N.A.
RA Frentiu F., Ovenden J.R., Street R.;
RA "Australian lungfish (Neoceratodus forsteri) have low genetic
RT diversity at allozyme and mitochondrial loci: A conservation alert for
RT a living fossil?";
RL Conserv. Genet. 0:0-0(2001).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL

CC -1- COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF344663; AAK29031.1; -;
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON TER 1
SQ SEQUENCE 84 AA; 9673 MW; 1E7AFAD921592DAC CRC64;

Query Match 75.0%; Score 36; DB 8; Length 84;
Best Local Similarity 87.5%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QQLVEYPPF 9
| : : : : :
Db 27 QPVEYPPF 34

RESULT 4
Q9MP34 PRELIMINARY; PRT; 247 AA.
AC Q9MP34;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome b (fragment).
GN Cytb.
OS Bothriomyx meridionalis.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Formicidae; Dolichoderinae; Bothriomyx.
OX NCBI_TaxID=121499;
RN [1]_TaxID=121499;
RN SEQUENCE FROM N.A.
RC STRAIN=ACFC;
RA Chiotis M., Jermin L.S., Crozier R.H.;
RA "A molecular framework for the phylogeny of the ant subfamily
RT Dolichoderinae";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF146714; AAF66714.1; -;
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c1.
DR PROSITE; PS00193; CYTOCHROME_B_QQ; UNKNOWN 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON TER 1
SQ SEQUENCE 247 AA; 29263 MW; CC68F8BA0D065B1A CRC64;

Query Match 75.0%; Score 36; DB 8; Length 247;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QQLVEYPPF 9
| : : : : :
Db 201 QSLVEYPPF 208


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RESULT 5
Q9XNV8
ID Q9XNV8 PRELIMINARY; PRT; 352 AA.
AC Q9XNV8;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cytochrome B (Fragment).
GN CYTB.
OS Delonix dorsalis (striped Atlantic forest rat).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Delonix.
OX NCBI_TaxID=89119;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: Evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF108696; AAD45468.1; -.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN 1.
DR Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 352
SQ SEQUENCE 352 AA; 39631 MW; AA408DB627140D6C CRC64;

Query Match 75.0%; Score 36; DB 8; Length 352;
Best Local Similarity 87.5%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEPPT 9
DB 341 QVVEPPT 348

RESULT 6
Q9XNX5
ID Q9XNX5 PRELIMINARY; PRT; 377 AA.
AC Q9XNX5;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cytochrome B (Fragment).
GN CYTB.
OS Scaptomyces tumidus (swamp rat).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Scaptomyces.
OX NCBI_TaxID=89126;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: Evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A

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RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF108669; AAD45451.1; -.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN 1.
DR Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 377
SQ SEQUENCE 377 AA; 42392 MW; 692D67AE20B6F3BB CRC64;

Query Match 75.0%; Score 36; DB 8; Length 377;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEPPT 9
DB 337 QVVEPPT 344

RESULT 7
Q9XNV0
ID Q9XNV0 PRELIMINARY; PRT; 377 AA.
AC Q9XNV0;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cytochrome B (Fragment).
GN CYTB.
OS Reithrodon auritus (bunny rat).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Reithrodon.
OX NCBI_TaxID=56234;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
in South America: Evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF108694; AAD45476.1; -.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN 1.
DR Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 377
SQ SEQUENCE 377 AA; 42533 MW; 618DB37396EE6E97 CRC64;

Query Match 75.0%; Score 36; DB 8; Length 377;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEPPT 9

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Db 338 QPVEYPPT 345
| |||||
RESULT 8
Q9TGL4 PRELIMINARY; PRT; 379 AA.
AC Q9TGL4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Cervus elaphus (Red deer).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20229580; PubMed=10764539;
RA Kuwayama R, Ozawa T.
RT "Phylogenetic relationships among european red deer, wapiti, and sika
deer inferred from mitochondrial DNA sequences.";
RL Mol. Phylogenet. Evol. 15:115-123(2000).
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF157887; AAD50171.1; -
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c_1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN 1.
DR Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
SQ SEQUENCE 379 AA; 43024 MW; 1F115AE16850F5AA CRC64;

Query Match 75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPPT 9
Db 341 QPVEYPPT 348
| |||||
RESULT 10
Q9TF12 PRELIMINARY; PRT; 379 AA.
AC Q9TF12;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Spermophilus madrensis (Sierra Madre ground squirrel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Spermophilus.
OX NCBI_TaxID=99842;
RN [1]
RP SEQUENCE FROM N.A.
RA Harrison R.G., Sherman P.W., Yensen E., Hoffmann R.S.,
RT Bogdanowicz S.M.;
RL "A molecular phylogeny of ground squirrels and prairie dogs.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF157946; AAD50230.1; -
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c_1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN 1.
DR Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
SQ SEQUENCE 379 AA; 43067 MW; 7AD39152077DE39A CRC64;

Query Match 75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPPT 9
Db 341 QPVEYPPT 348
| |||||
RESULT 9
Q9TF64 PRELIMINARY; PRT; 379 AA.
AC Q9TF64;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Spermophilus lateralis trepidus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Spermophilus.
OX NCBI_TaxID=100390;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S32;

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Query Match      75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVVEYPT 9
Db 341 QVVEYPT 348

RESULT 11
Q9TF11 PRELIMINARY; PRT; 379 AA.
AC Q9TF11;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Spermophilus madrensis (Sierra Madre ground squirrel).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Spermophilus.
OX NCBI_TaxID=99842;
RN [1]
RP STRAIN=S98;
SQ SEQUENCE 379 AA; 43071 MW; B3D3852662B28B2B CRC64;

RA Harrison R.G., Sherman P.W., Yensen E., Hoffmann R.S.,
RA Bogdanowicz S.M.;
RT "A molecular phylogeny of ground squirrels and prairie dogs.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX) WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF157947; AAD50231.1; -.
DR InterPro; IPR000179; Cyt b_b6.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
SQ SEQUENCE 379 AA; 43071 MW; B3D3852662B28B2B CRC64;

Query Match      75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVVEYPT 9
Db 341 QVVEYPT 348

RESULT 12
Q9TF08 PRELIMINARY; PRT; 379 AA.
AC Q9TF08;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Spermophilus lateralis trepidus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Spermophilus.
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OX NCBI_TaxID=100390;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SEY1069;
RA Harrison R.G., Sherman P.W., Yensen E., Hoffmann R.S.,
RA Bogdanowicz S.M.;
RT "A molecular phylogeny of ground squirrels and prairie dogs.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX) WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF157950; AAD50234.1; -.
DR InterPro; IPR000179; Cyt b_b6.
DR Pfam; PF00032; cytochrome_b_C; 1.
DR Pfam; PF00033; cytochrome_b_N; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN_1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
SQ SEQUENCE 379 AA; 42994 MW; 767009AD223C18AD CRC64;

Query Match      75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QVVEYPT 9
Db 341 QVVEYPT 348

RESULT 13
Q33887 PRELIMINARY; PRT; 379 AA.
AC Q33887;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Akodon toba (Chaco grass mouse).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Akodon.
OX NCBI_TaxID=29101;
RN [1]
RP SEQUENCE OF 1-267 FROM N.A.
RC STRAIN=UMMZ CATALOG # 133965; TISSUE=LIVER;
RA Smith M.F., Patton J.L.;
RT "Diversification of South American murid rodents: Evidence from
RT mitochondrial DNA sequence data for the akodontine tribe.";
RL Biol. J. Linn. Soc. 50:149-177(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=UMMZ CATALOG # 133965; TISSUE=LIVER;
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
RT in South America: Evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=UMMZ CATALOG # 133965; TISSUE=LIVER;
RA Smith M.F.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX) WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
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CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; U03527; AAD12554.2; -.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME B_QO; UNKNOWN 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
SQ SEQUENCE 379 AA; 42689 MW; 8B946C25430PDCD0 CRC64;

Query Match 75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEPPT 9
Db 341 QPVEYPT 348
| | | | |

RESULT 14
Q33940 PRELIMINARY; PRT; 379 AA.
AC Q33940;
DT 01-NOV-1996 (TREMELREL. 01, Created)
DT 01-NOV-1999 (TREMELREL. 12, Last sequence update)
DT 01-DEC-2001 (TREMELREL. 19, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Bosomys urichi.
OG Eukaryota.
OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Bolomys.
OX NCBI_TaxID=100644;
RN [1]_TaxID=100644;
RP SEQUENCE OF 1-267 FROM N.A.
RC STRAIN-USNM CATALOG # 560661; TISSUE=LIVER;
RA Smith M.F., Patton J.L.;
RT "Diversification of South American murid rodents: Evidence from
RT mitochondrial DNA sequence data for the akodontine tribe.";
RL Biol. J. Linn. Soc. 50:149-177(1993).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-USNM CATALOG # 560661; TISSUE=LIVER;
RA Smith M.F., Patton J.L.;
RT "Phylogenetic relationships and the radiation of sigmodontine rodents
RT in South America: Evidence from cytochrome b.";
RL J. Mammal. Evol. 6:89-128(1999).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN-USNM CATALOG # 560661; TISSUE=LIVER;
RA Smith M.F.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; U03549; AAD12575.2; -.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
SQ SEQUENCE 379 AA; 42689 MW; 8B946C25430PDCD0 CRC64;

Query Match 75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEPPT 9
Db 341 QPVEYPT 348
| | | | |

RESULT 15
Q94QC8 PRELIMINARY; PRT; 379 AA.
AC Q94QC8;
DT 01-DEC-2001 (TREMELREL. 19, Created)
DT 01-DEC-2001 (TREMELREL. 19, Last sequence update)
DT 01-JUN-2002 (TREMELREL. 21, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Cervus timorensis macassanicus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=173988;
RN [1]_TaxID=173988;
RP SEQUENCE FROM N.A.
RC TISSUE=SPONGIOSA;
RA Lutz C.J., Kuehn R., Schroeder W., Rottmann O.;
RT "Phylogeny of Cervidae based on mitochondrial genes";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF423200; AAL17842.1; -.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; UNKNOWN 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
SQ SEQUENCE 379 AA; 42915 MW; F2337185154459B3 CRC64;

Query Match 75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEPPT 9
Db 341 QPVEYPT 348
| | | | |

Search completed: April 22, 2003, 12:53:49
Job time : 19 secs

DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
SQ SEQUENCE 379 AA; 42766 MW; 8B74E09004D8E663 CRC64;

Query Match 75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEPPT 9
Db 341 QPVEYPT 348
| | | | |

RESULT 15
Q94QC8 PRELIMINARY; PRT; 379 AA.
AC Q94QC8;
DT 01-DEC-2001 (TREMELREL. 19, Created)
DT 01-DEC-2001 (TREMELREL. 19, Last sequence update)
DT 01-JUN-2002 (TREMELREL. 21, Last annotation update)
DE Cytochrome b.
GN CYTB.
OS Cervus timorensis macassanicus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=173988;
RN [1]_TaxID=173988;
RP SEQUENCE FROM N.A.
RC TISSUE=SPONGIOSA;
RA Lutz C.J., Kuehn R., Schroeder W., Rottmann O.;
RT "Phylogeny of Cervidae based on mitochondrial genes";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -1- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -1- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; AF423200; AAL17842.1; -.
DR InterPro; IPR000179; Cyt_b_b6.
DR Pfam; PF00032; cytochrome_b_c1.
DR Pfam; PF00033; cytochrome_b_n; 1.
DR PROSITE; PS00192; CYTOCHROME_B_HEME; UNKNOWN 1.
DR PROSITE; PS00193; CYTOCHROME_B_QO; UNKNOWN 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
SQ SEQUENCE 379 AA; 42915 MW; F2337185154459B3 CRC64;

Query Match 75.0%; Score 36; DB 8; Length 379;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEPPT 9
Db 341 QPVEYPT 348
| | | | |

Search completed: April 22, 2003, 12:53:49
Job time : 19 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:45:19 ; Search time 22.8214 Seconds
(without alignments)
52.550 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SID82/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	48	100.0	9	21	AA132256
2	48	100.0	116	21	AA132262
3	48	100.0	145	21	AA132261
4	45	93.8	19	21	AA170804
5	45	93.8	122	21	AA170790
6	45	93.8	131	12	AA12232
7	45	93.8	132	12	AA12354
8	44	91.7	9	19	AA139823
9	44	91.7	113	19	AA139882
10	44	91.7	113	19	AA139804
					Light chain CDR L3
					Humanised anti-CD2
					Mouse anti-CD23 MA
					Murine anti-PAB-42
					Murine anti-PAB-42
					Mouse MAB 2E12 L c
					Light (kappa) chain
					Light chain CDR3 o
					Light chain of the
					Variable domain of

11	37	77.1	100	22	AA506969	Mouse germline kap
12	36	75.0	9	19	AAW39817	Light chain CDR3 o
13	36	75.0	113	19	AAW39801	Variable domain of
14	36	75.0	113	19	AAW39803	Variable domain of
15	36	75.0	241	18	AAW24063	Human WSX receptor
16	36	75.0	241	23	AAU09048	Insulin/insulin-li
17	36	75.0	251	23	ABP45299	Human ElyS binding
18	36	75.0	253	23	ABP44925	Human ElyS binding
19	36	75.0	274	19	AAW39899	Single chain Fv re
20	36	75.0	392	21	AAE10863	S11-VEGF2 construc
21	36	75.0	510	21	AAE10864	S11-VEGF2 constr
22	35	72.9	112	21	AAW39813	2G3 hybridoma VL d
23	35	72.9	126	20	AAW36951	Protein involved i
24	35	72.9	533	21	AAW27700	Arabidopsis thalia
25	35	72.9	536	21	AAW27699	Arabidopsis thalia
26	35	72.9	622	21	AAW27698	Arabidopsis thalia
27	34	70.8	9	21	AAW92171	Murine 13H10 light
28	34	70.8	113	21	AAW92164	Murine 13H10 light
29	34	70.8	146	18	AAW28154	Amino acid sequenc
30	34	70.8	585	23	ABP40069	Staphylococcus epi
31	34	70.8	604	22	AAW81648	S. epidermidis ope
32	33	68.8	9	14	AAW30450	C242:11 MAB kappa
33	33	68.8	82	22	ABW36950	Peptide #4456 enco
34	33	68.8	107	22	AAW33597	Human anti-Rh(D) c
35	33	68.8	108	14	AAW34019	BW 835 VK. Synthe
36	33	68.8	113	15	AAW59513	Sequence of the ma
37	33	68.8	113	21	AAW90819	260F9 hybridoma VL
38	33	68.8	133	14	AAW33954	gLI variable domai
39	33	68.8	133	14	AAW33951	CTM01 VL. Synthet
40	33	68.8	133	15	AAW59509	Sequence of the li
41	33	68.8	133	15	AAW59511	Sequence of the li
42	33	68.8	133	18	AAW29754	CDR-grafted humani
43	33	68.8	133	21	AAW56874	MAB CT-M-01 light
44	33	68.8	133	21	AAW56878	gLI variable domai
45	33	68.8	139	22	AAO00042	Human polypeptide

ALIGNMENTS

RESULT 1

AA132256

ID AA132256 standard; Peptide; 9 AA.

XX AA132256;

XX 15-FEB-2000 (first entry)

DT Light chain CDR L3 of mouse anti-CD23 MAB C11.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;

XX monoclinal antibody; chimeric antibody; humanised antibody;

XX complementarity determining region; CDR; autoimmune disease;

XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;

XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

XX urticaria; nephrotic syndrome; glomerulonephritis;

XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;

XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

XX graft-versus-host disease; COPD; bronchitis; diabetes;

XX B-cell malignancy; therapy.

XX Mus musculus.

OS WO958679-A1.

PN 18-NOV-1999.

PD 07-MAY-1999; 99WO-GB01434.

XX 09-MAY-1998; 98GB-0009839.

XX (GLAXO) GLAXO GROUP LTD.

PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 XX N-PSDB; AA234741.
 XX
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 XX diabetes, multiple sclerosis and psoriasis -
 XX
 XX Claim 1; Page 40; 81pp; English.
 XX
 XX This sequence represents complementarity determining region 3
 CC (CDR L3) of the light chain of murine anti-CD23 (FCERII) monoclonal
 CC antibody C11 (see also AAY32262). The invention provides altered
 CC antibodies, such as chimeric or humanised antibodies, which comprise
 CC sufficient of the amino acid sequences of C11 light and heavy chain
 CC CDRs (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies
 CC are used to block soluble CD23 formation for treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.
 XX
 XX Sequence 9 AA;

Query Match 100.0%; Score 48; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0;

Qy 1 QQLVEVPFT 9
 |||||
 Db 1 QQLVEVPFT 9

RESULT 2
 AAY32262
 ID AAY32262 standard; Protein; 116 AA.

XX AC AAY32262;

XX DT 15-FEB-2000 (first entry)

XX DE Humanised anti-CD23 Mab C11 light chain variable region.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse; human;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes;
 KW B-cell malignancy; therapy.

XX OS Homo sapiens.
 XX Synthetic.

XX FH Key Location/Qualifiers
 XX Region 1..23
 XX FT /note= "framework region 1"
 XX Region 24..39 /note= "CDR 1"
 XX FT /note= "CDR 1"
 XX Region 40..54
 XX FT /note= "framework region 2"
 XX Region 55..61 /note= "CDR 2"

FT Region 62..93
 FT /note= "framework region 3"
 FT Region 94..102
 FT /note= "CDR 3"
 FT Region 103..113
 FT /note= "framework region 4"
 XX W09958679-A1.
 XX 18-NOV-1999.
 XX 07-MAY-1999; 99WO-GB01434.
 XX 09-MAY-1998; 98GB-0009839.
 XX (GLAX) GLAXO GROUP LTD.
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 XX N-PSDB; AA234741.
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 XX diabetes, multiple sclerosis and psoriasis -
 XX Claim 9; Fig 3; 81pp; English.

XX This sequence represents the light chain variable region (VL) of
 CC humanised anti-CD23 (FCERII) monoclonal antibody C11, composed of
 CC a human framework (H5IGKVII) and the light chain complementarity
 CC determining regions (see AAY32254-56) of murine antibody C11. The
 CC DNA was constructed by splice overlap PCR. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies, which
 CC comprise sufficient of the amino acid sequences of the C11 light
 CC and heavy chain complementarity determining regions to render them
 CC capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble
 CC CD23 formation in human therapy, for the treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.

XX SQ Sequence 116 AA;

Query Match 100.0%; Score 48; DB 21; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.053;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEVPFT 9
 |||||
 Db 94 QQLVEVPFT 102

RESULT 3
 AAY32261
 ID AAY32261 standard; Protein; 145 AA.

XX AC AAY32261;

XX DT 15-FEB-2000 (first entry)

XX DE Mouse anti-CD23 Mab C11 light chain variable region.

XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Region 55..70
FT /note= "CDR L1"
FT Region 83..92
FT /note= "CDR L2"
FT Region 125..134
FT /note= "CDR L3"
XX
PN WO958679-A1.
XX
XX 18-NOV-1999.
XX
XX 07-MAY-1999; 99WO-GB01434.
XX
XX 09-MAY-1999; 98GB-0009839.
XX
XX (GLAXO) GLAXO GROUP LTD.
XX
XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
XX WPI; 2000-053101/04.
XX N-PSDB; AA234746.
XX
XX Cell receptor specific antibodies useful for treating e.g. arthritis,
XX diabetes, multiple sclerosis and psoriasis -
XX
XX Claim 8; Fig 2; 81pp; English.
XX
XX This sequence represents the light chain variable region (VL) of
XX murine anti-CD23 (FCBR1) monoclonal antibody C11. The invention
XX provides altered antibodies, such as chimeric or humanised
XX antibodies (see AAY32262 and AAY32263), which comprise sufficient of
XX the amino acid sequences of the C11 light and heavy chain
XX complementarity determining regions (see AAY32254-59) to render them
XX capable of binding to the CD23 type II molecule expressed on
XX haematopoietic cells. The antibodies are used to block soluble
XX CD23 formation in human therapy, for the treatment of arthritis,
XX lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
XX diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
XX syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
XX colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
XX asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
XX eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
XX (particularly chronic bronchitis) or diabetes (particularly type 1
XX diabetes), and B-cell malignancies (claimed). They are also useful
XX for studying interactions between CD23 and various ligands and
XX determining the binding agents.
XX
XX SQ Sequence 145 AA;

Query Match 100.0%; Score 48; DB 21; Length 145;
Best Local Similarity 100.0%; Pred. No. 0.067;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 125 QQLVEYPPT 133

RESULT 4
AAY70804
ID AAY70804 standard; peptide; 19 AA.
XX

AC AAY70804;
XX
XX 31-JUL-2000 (first entry)
DE
XX Murine anti-PAb-421 IDI-1 mAb light chain CDR based peptide IDI-1 L3.
XX
XX Murine; p53 protein; monoclonal antibody; mAb; PAb-421; IDI-1 L3;
KW light chain variable region; VL; complementarity determining region; CDR;
KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
KW DNA-binding domain; anti-idiotypic antibody.
XX
XX Mus sp.
XX
XX WO200023082-A1.
XX
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US24443.
XX
XX 19-OCT-1998; 98US-0104816.
XX
XX (YEDA) YEDA RES & DEV CO LTD.
XX
XX Cohen IR, Rotter V, Erez-Alon N, Herkel J;
XX WPI; 2000-339512/29.
XX
XX Treatment of systemic lupus erythematosus by down-regulating the
XX autoimmune response to the C-terminal DNA-binding domain of the p53
XX protein by an active compound comprising of antibodies to p53 or
XX fragments of p53 -
XX
XX Claim 78; Fig 10; 87pp; English.
XX
XX The patent discloses a method for the treatment of systemic lupus
XX erythematosus (SLE) by down-regulating the autoimmune response to the
XX C-terminal DNA-binding domain of p53 protein by an active compound.
XX The present sequence is a IDI-1 L3 peptide which comprises the
XX complementarity determining region (CDR) of the light chain of
XX IDI-1 monoclonal antibody (mAb). The IDI-1 mAb is an anti-idiotypic
XX antibody/Ab2 mAb specific for PAb-421 which is an Ab1 mAb specific
XX to the C-terminal DNA-binding domain of murine p53 protein.
XX The peptide corresponds to residues 92-110 of IDI-1 light chain
XX variable region. It is an example of the active compound useful in
XX the diagnosis, prevention and treatment of SLE in humans.
XX
XX SQ Sequence 19 AA;

Query Match 93.8%; Score 45; DB 21; Length 19;
Best Local Similarity 88.9%; Pred. No. 0.031;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 6 QQLVEYPPT 14

RESULT 5
AAY70790
ID AAY70790 standard; Protein; 122 AA.
XX
XX AAY70790;
XX
XX 31-JUL-2000 (first entry)
XX
XX Murine anti-PAb-421 IDI-1 mAb light chain variable region.
XX
XX Murine; p53 protein; PAb-421; monoclonal antibody; mAb; IDI-1;
KW anti-idiotypic antibody; DNA-binding domain;
KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
KW SLE; systemic lupus erythematosus; diagnosis; treatment; autoantigen;
KW light chain variable region; VL; complementarity determining region; CDR.

OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Region 27..42
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT 58..64
 FT /label= CDR
 FT /note= "Complementarity determining region"
 FT 97..105
 FT /label= CDR
 FT /note= "Complementarity determining region"
 XX WO200023082-A1.
 PN
 XX
 XX 27-APR-2000.
 XX
 XX 19-OCT-1999; 99WO-US24443.
 XX
 XX 19-OCT-1998; 98US-0104816.
 XX
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Cohen IR, Rotter V, Brez-Alon N, Herkel J;
 XX
 XX WPI; 2000-339512/29.
 XX
 XX Treatment of systemic lupus erythematosus by down-regulating the
 PT autoimmune response to the C-terminal DNA-binding domain of the p53
 PT protein by an active compound comprising of antibodies to p53 or
 PT fragments of p53 -
 XX
 XX Claim 78; Fig 9; 87pp; English.
 XX
 XX The patent discloses a method for the treatment of systemic lupus
 CC erythematosus (SLE) by down-regulating the autoimmune response to the
 CC C-terminal DNA-binding domain of p53 protein by an active compound.
 CC The present sequence is a light chain variable region of ID1-1 an
 CC anti-idiotypic antibody/Ab2 monoclonal antibody (mAb) specific for
 CC PAB-421 which is an Ab1 mAb specific to the C-terminal DNA-binding domain
 CC of murine p53 protein. The Ab1 and Ab2 mAbs and peptides based on
 CC complementarity determining regions of light and heavy chain variable
 CC regions of these antibodies, are examples of active compounds useful in
 CC the diagnosis, prevention and treatment of SLE in humans.
 XX
 XX Sequence 122 AA;
 SQ
 Query Match 93.8%; Score 45; DB 21; Length 122;
 Best Local Similarity 88.9%; Pred. No. 0.22;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 DB 97 QQLVEYPPT 105
 RESULT 6
 AAR12232
 ID AAR12232 standard; Protein; 131 AA.
 XX
 XX AAR12232;
 XX
 XX 19-AUG-1991 (first entry)
 DT
 XX Mouse Mab 2E12 L chain V region.
 DE
 XX HTV-1; chimera.
 XX
 XX Mus sp.
 OS
 XX WO9107494-A.
 PN
 XX

PD 30-MAY-1991.
 XX
 PF 13-NOV-1990; 90WO-US06627.
 XX*
 PR 13-NOV-1989; 89US-0433703.
 XX
 PA (XOMA-) XOMA CORP.
 XX
 PI Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
 XX
 XX WPI; 1991-178106/24.
 DR N-PSDB; AAQ12012.
 XX
 XX New chimeric mouse human antibodies - used in treatment, diagnosis
 PT and prophylaxis of HIV infections.
 PT
 XX Disclosure; Fig 1; 108pp; English.
 XX
 XX The mouse VL gene product may be used to produce chimeric mouse-
 CC human Abs against HIV-1 comprising human Ig constant regions and
 CC murine variable regions. These novel sequence are useful in
 CC treatment, diagnosis and prophylaxis of HIV infections, and may be
 CC produced by a bacterial, yeast or mammalian expression system.
 XX
 XX Sequence 131 AA;
 SQ
 Query Match 93.8%; Score 45; DB 12; Length 131;
 Best Local Similarity 88.9%; Pred. No. 0.24;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 DB 114 QQLVEYPPT 122
 RESULT 7
 AAR12354
 ID AAR12354 standard; Protein; 132 AA.
 XX
 XX AAR12354;
 XX
 XX 15-AUG-1991 (first entry)
 DT
 XX Light (kappa) chain variable region of murine 2E12
 DE immunoglobulin.
 DE
 XX Chimeric antibodies; immunoconjugates; HIV; AIDS.
 XX
 XX Mus musculus.
 OS
 XX WO9107493-A.
 PN
 XX 30-MAY-1991.
 PD
 XX
 XX 13-NOV-1990; 90WO-US06615.
 PF
 XX 13-NOV-1989; 89US-0433730.
 PR
 XX (XOMA-) XOMA CORP.
 PA
 XX (GREC) GREEN CROSS CORP.
 PA
 XX Better MD, Horwitz AH, Ghosh-Dastidar P, Robinson RR;
 PI
 XX WPI; 1991-178044/24.
 DR N-PSDB; AAQ12056.
 DR
 XX New chimeric mouse-human antibodies - used to detect, kill and
 PT remove HIV-1 antigen from sample
 PT
 XX Disclosure; fig 1; 107pp; English.
 XX
 XX This is the light (kappa)- chain variable (V) region of a mouse
 CC monoclonal antibody (Mab), 2E12, and is specific for an HIV-1
 CC

CC viral antigen. It is used in the construction of a chimeric Mab
 CC comprising heavy and light chains having murine V regions and human
 CC C regions. The chimeric Mabs are more effective than murine Mab
 CC 2E12 since they have an increased compatibility in humans. The
 CC heavy and light chain V-regions are joined by manipulating their
 CC respective joining (J) regions, to generate restriction enzyme
 CC recognition sites. The chimeric Mabs can be used as immuno-
 CC conjugates, in association with e.g. toxins for HIV treatment.
 CC They can also be used in diagnosis of HIV.
 CC See also AAQ12057-63.
 SQ Sequence 132 AA;

Query Match 93.8%; Score 45; DB 12; Length 132;
 Best Local Similarity 88.9%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 1;

QY 1 QQLVEYPFT 9
 |||||:
 Db 114 QQLVEYPFT 122

RESULT 8
 AAW39823
 ID AAW39823 standard; peptide; 9 AA.
 AC AAW39823;
 XX
 XX
 XX 16-JUN-1998 (first entry)
 XX

DE Light chain CDR3 of catalytic antibody 2A10.
 XX
 XX
 XX

KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 XX

OS Mus sp.
 XX
 XX WO9749800-A1.
 XX
 XX 31-DEC-1997.
 XX
 XX 25-JUN-1997; 97WO-US10965.
 XX
 XX 25-JUN-1996; 96US-0672345.
 XX
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 XX Landry DW;
 XX
 XX WPI; 1998-077166/07.
 XX
 XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX
 XX Claim 15; Page 82; 147pp; English.

XX AAW39821-23 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 2A10, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was
 CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 2A10 has a per minute Kcat
 CC of 0.011. The antibodies reduce the concentration of cocaine in a
 CC subject, and are used particularly for the treatment of an overdose. They
 CC are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved).
 XX
 XX Sequence 9 AA;

Query Match 91.7%; Score 44; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||:
 Db 1 QQFVEYPFT 9

RESULT 9
 AAW39882
 ID AAW39882 standard; Protein; 113 AA.
 XX
 XX AAW39882;
 AC AAW39882;
 XX

DT 16-JUN-1998 (first entry)
 XX
 XX Light chain of the catalytic antibody 2A10.
 XX

KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 XX

OS Mus sp.
 XX
 XX WO9749800-A1.
 XX
 XX 31-DEC-1997.
 XX
 XX 25-JUN-1997; 97WO-US10965.
 XX
 XX 25-JUN-1996; 96US-0672345.
 XX
 XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 XX Landry DW;
 XX
 XX WPI; 1998-077166/07.
 XX
 XX N-PSDB; AAV09789.
 XX

PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX
 XX Disclosure; Fig 21; 147pp; English.
 XX
 XX The present sequence represents the light chain of a catalytic antibody
 CC which is capable of degrading cocaine. A series of cocaine transition
 CC state analogues (TSAs) were prepared and used to immunise mice for
 CC production of hybridomas. Catalytic antibodies were identified by their
 CC capacity to release 3H-benzoic acid from 3H-phenyl cocaine. The
 CC antibodies reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved).
 XX
 XX Sequence 113 AA;

Query Match 91.7%; Score 44; DB 19; Length 113;
 Best Local Similarity 88.9%; Pred. No. 0.33;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||:
 Db 94 QQFVEYPFT 102

RESULT 10
 AAW39804
 ID AAW39804 standard; protein; 113 AA.

XX AC AAW39804;
 XX DT 16-JUN-1998 (first entry)
 XX DE Variable domain of the Kappa light chain of catalytic antibody 2A10.
 XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX OS Mus sp.
 XX PN WO9749800-A1.
 XX PD 31-DEC-1997.
 XX PF 25-JUN-1997; 97WO-US10965.
 XX PR 25-JUN-1996; 96US-0672345.
 XX PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX PI Landry DW;
 XX DR WPI; 1998-077166/07.
 XX PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX PS Claim 16; Pages 73-74; 147pp; English.
 XX CC AAW39801-05 represent the amino acid sequences of the variable domain
 CC of the Kappa light chain of catalytic antibodies which are able to
 CC degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release
 CC 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody (AAW39809
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state
 CC analogue. Antibody 2A10 has a per minute Kcat of 0.011. The antibodies
 CC reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can
 CC be achieved).
 XX SQ Sequence 113 AA;
 Query Match 91.7%; Score 44; DB 19; Length 113;
 Best Local Similarity 88.9%; Pred. No. 0.33; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QQLVEYPT 9
 Db 94 QQFVEYPT 102
 RESULT 11
 AAE06969
 ID AAE06969 standard; Protein; 100 AA.
 XX AC AAE06969;
 XX DT 16-OCT-2001 (first entry)
 XX DE Mouse germline kappa light chain variable (VK) region, 167/24.
 XX KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;

KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;
 KW multiple sclerosis; atherosclerosis; stenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VK; kappa light chain variable region.
 XX OS Mus sp.
 XX PN WO200157226-A1.
 XX PD 09-AUG-2001.
 XX PF 02-FEB-2001; 2001WO-US03537.
 XX PR 03-FEB-2000; 2000US-0497625.
 XX PA (MILL-) MILLENNIUM PHARM INC.
 XX PI Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 XX DR WPI; 2001-488888/53.
 XX PT Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT .
 XX PS Disclosure; Page 151; 183pp; English.
 XX CC The patent discloses a humanised antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanised antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherosclerosis and atherosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR-2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is mouse germline kappa light chain variable
 CC (VK) region, 167/24.
 XX SQ Sequence 100 AA;
 Query Match 77.1%; Score 37; DB 22; Length 100;
 Best Local Similarity 100.0%; Pred. No. 7.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QQLVEYPT 7
 Db 94 QQLVEYPT 100
 RESULT 12
 AAW39817
 ID AAW39817 standard; peptide; 9 AA.
 XX AC AAW39817;
 XX DT 16-JUN-1998 (first entry)
 XX

DE Light chain CDR3 of catalytic antibody 3B9.
 XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX Mus sp.
 OS WO9749800-A1.
 PN 31-DEC-1997.
 XX
 PD 25-JUN-1997; 97WO-US10965.
 XX
 PF 25-JUN-1996; 96US-0672345.
 XX
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PA Landry DW;
 XX
 PI WPI; 1998-077166/07.
 XX
 DR New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 PT
 XX Claim 11; Page 81; 147pp; English.
 PS AAW39815-17 represent the sequences of the light chain complementarity
 XX determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was
 CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 3B9 has a per minute Kcat
 CC of 0.11. The antibodies reduce the concentration of cocaine in a subject,
 CC and are used particularly for the treatment of an overdose. They are also
 CC used for treating addiction (by reducing the in vivo concentration that
 CC can be achieved).
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 75.0%; Score 36; DB 19; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 Db 1 QHFVDYPPT 9
 RESULT 13
 AAW39801
 ID AAW39801 standard; protein; 113 AA.
 XX
 AC AAW39801;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Variable domain of the Kappa light chain of catalytic antibody 3B9.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX WO9749800-A1.
 PN 31-DEC-1997.
 XX
 PD 25-JUN-1997; 97WO-US10965.
 XX
 PF 25-JUN-1996; 96US-0672345.
 XX
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PA Landry DW;
 XX
 PI WPI; 1998-077166/07.
 XX
 DR New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 PT
 XX Claim 11; Page 81; 147pp; English.
 PS AAW39815-17 represent the sequences of the light chain complementarity
 XX determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was
 CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 3B9 has a per minute Kcat
 CC of 0.11. The antibodies reduce the concentration of cocaine in a subject,
 CC and are used particularly for the treatment of an overdose. They are also
 CC used for treating addiction (by reducing the in vivo concentration that
 CC can be achieved).
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 75.0%; Score 36; DB 19; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 Db 1 QHFVDYPPT 9
 RESULT 13
 AAW39801
 ID AAW39801 standard; protein; 113 AA.
 XX
 AC AAW39801;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Variable domain of the Kappa light chain of catalytic antibody 3B9.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX WO9749800-A1.
 PN 31-DEC-1997.
 XX
 PD 25-JUN-1997; 97WO-US10965.
 XX
 PF 25-JUN-1996; 96US-0672345.
 XX
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PA Landry DW;
 XX
 PI WPI; 1998-077166/07.
 XX
 DR New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 PT
 XX Claim 11; Page 81; 147pp; English.
 PS AAW39815-17 represent the sequences of the light chain complementarity
 XX determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was
 CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 3B9 has a per minute Kcat
 CC of 0.11. The antibodies reduce the concentration of cocaine in a subject,
 CC and are used particularly for the treatment of an overdose. They are also
 CC used for treating addiction (by reducing the in vivo concentration that
 CC can be achieved).
 XX
 XX Sequence 9 AA;
 SQ
 Query Match 75.0%; Score 36; DB 19; Length 113;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 Db 94 QHFVDYPPT 102

PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US10965.
 XX
 PR 25-JUN-1996; 96US-0672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 XX Landry DW;
 PI WPI; 1998-077166/07.
 XX
 DR P-PSDB; AAV09791.
 XX
 PD New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 PT
 XX Claim 12; Pages 71-72; 147pp; English.
 PS AAW39801-05 represent the amino acid sequences of the variable domain
 XX of the kappa light chain of catalytic antibodies which are able to
 CC degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release
 CC 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state
 CC analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies
 CC reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can
 CC be achieved).
 XX
 XX Sequence 113 AA;
 SQ
 Query Match 75.0%; Score 36; DB 19; Length 113;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 Db 94 QHFVDYPPT 102
 RESULT 14
 AAW39803
 ID AAW39803 standard; protein; 113 AA.
 XX
 AC AAW39803;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Variable domain of the Kappa light chain of catalytic antibody 12H1.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX WO9749800-A1.
 PN 31-DEC-1997.
 XX
 PD 25-JUN-1997; 97WO-US10965.
 XX
 PF 25-JUN-1996; 96US-0672345.
 XX
 PR (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PA Landry DW;
 XX
 PI WPI; 1998-077166/07.
 XX
 DR P-PSDB; AAV09791.
 XX
 PD New catalytic antibodies able to decompose cocaine, single-chain
 XX analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 PT
 XX Claim 12; Pages 71-72; 147pp; English.
 PS AAW39801-05 represent the amino acid sequences of the variable domain
 XX of the kappa light chain of catalytic antibodies which are able to
 CC degrade cocaine. A series of cocaine transition state analogues (TSAs)
 CC were prepared and used to immunise mice for production of hybridomas.
 CC Catalytic antibodies were identified by their capacity to release
 CC 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody (AAW39806
 CC represents the heavy chain) was identified using TSA1, which is an
 CC immunogenic conjugate of a phosphate monoester transition state
 CC analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies
 CC reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used
 CC for treating addiction (by reducing the in vivo concentration that can
 CC be achieved).
 XX
 XX Sequence 113 AA;
 SQ
 Query Match 75.0%; Score 36; DB 19; Length 113;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 Db 94 QHFVDYPPT 102

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XX DR WPI; 1998-077166/07.
XX DR P-PSDB; AAV09802.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required
XX PT in far smaller doses than antibodies that antagonise cocaine by
XX PT simply binding
XX PS Claim 18; Page 73; 147pp; English.
XX CC AAW39801-05 represent the amino acid sequences of the variable domain
XX CC of the kappa light chain of catalytic antibodies which are able to
XX CC degrade cocaine. A series of cocaine transition state analogues (TSAs)
XX CC were prepared and used to immunise mice for production of hybridomas.
XX CC Catalytic antibodies were identified by their capacity to release
XX CC 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody (AAW39808
XX CC represents the heavy chain) was identified using TSAs, and has a per
XX CC minute Kcat of 0.016. The antibodies reduce the concentration of cocaine
XX CC in a subject, and are used particularly for the treatment of an
XX CC overdose. They are also used for treating addiction (by reducing the in
XX CC vivo concentration that can be achieved).
XX SQ Sequence 113 AA;
    Query Match 75.0%; Score 36; DB 19; Length 113;
    Best Local Similarity 66.7%; Pred. No. 13;
    Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QQLVEVPPT 9
Db 94 QHFDVPPT 102
    | | | | |
    | | | | |

RESULT 15
AAW24063
ID AAW24063 standard; Protein; 241 AA.
XX AC AAW24063;
XX DT 17-MAR-1998 (first entry)
XX DE Human WSX receptor agonist antibody clone #17.
XX KW Human; WSX receptor; clone #17; identification; purification;
XX KW ligand; activator; antibody; agonist; proliferation; obesity;
XX KW differentiation; anaemia; treatment; neoplasia; arteriosclerosis;
XX KW Type II diabetes; polycystic ovarian disease;
XX KW cardiovascular disease; osteoarthritis; dermatological disorder;
XX KW hypertension; insulin resistance; hypercholesterolaemia;
XX KW hypertriglyceridaemia; cancer; cholelithiasis.
XX OS Homo sapiens.
XX PN WO9725425-A1.
XX PD 17-JUL-1997.
XX PF 07-JAN-1997; 97WO-US00325.
XX PR 20-JUN-1996; 96US-0667197.
XX PR 08-JAN-1996; 96US-0585005.
XX PA (GETH ) GENENTECH INC.
XX PI Bennett B, Carter PJ, Chiang NY, Kim KJ, Matthews W;
XX PI Rodrigues ML;
XX DR WPI; 1997-372864/34.
XX WSX*receptor and related antibodies and ligands - used to develop
XX PT products for diagnosis and therapy, e.g. for improving
XX PT haematopoiesis or for treating tumours

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XX Example 14; Pages 122-123; 219pp; English.
XX CC The present sequence is an agonist antibody clone to the human WSX
XX CC receptor, which can be used to identify and purify ligands and
XX CC activators. An anti-WSX receptor antibody can be used as an agonist
XX CC to activate the WSX receptor, leading to enhanced proliferation or
XX CC differentiation of a cell expressing the WSX receptor. It can also
XX CC be used to decrease body weight and/or fat-depot weight and/or food
XX CC intake in an obese mammal. WSX receptor ligands can be used to
XX CC enhance proliferation or differentiation of lymphoid, myeloid or
XX CC erythroid blood cell lineages. This is useful when a mammal,
XX CC especially a human, is suffering from decreased blood cell levels,
XX CC i.e. anaemia, caused by chemotherapy, radiation therapy or bone
XX CC marrow transplantation therapy. It can also be used to repopulate
XX CC blood cells in a mammal. The products can also be used to treat,
XX CC e.g. neoplastic disorders, arteriosclerosis, Type II diabetes,
XX CC polycystic ovarian disease, cardiovascular diseases,
XX CC osteoarthritis, dermatological disorders, hypertension, insulin
XX CC resistance, hypercholesterolaemia, hypertriglyceridaemia, cancer
XX CC and cholelithiasis.
XX SQ Sequence 241 AA;
    Query Match 75.0%; Score 36; DB 18; Length 241;
    Best Local Similarity 66.7%; Pred. No. 30;
    Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 QQLVEVPPT 9
Db 223 QQLISYPLT 231
    | | | | |
    | | | | |

Search completed: April 22, 2003, 12:51:13
Job time : 23.8214 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:53:59 ; Search time 9.48214 Seconds
(without alignments)
76.055 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QOLVEYPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
 - 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
 - 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*
 - 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
 - 7: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
 - 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
 - 10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
 - 11: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
 - 12: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
 - 13: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*
 - 14: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	77.1	100	10	US-09-840-459-32
2	36	75.0	241	1	US-08-779-457-50
3	36	75.0	251	9	US-09-880-748-1310
4	36	75.0	253	9	US-09-880-748-936
5	33	68.8	82	10	US-09-864-761-47635
6	33	68.8	107	9	US-09-848-798-40
7	33	68.8	726	10	US-09-973-451-10
8	32	66.7	105	9	US-10-164-359-4
9	32	66.7	105	10	US-09-107-058-8
10	32	66.7	105	10	US-09-761-117-8
11	32	66.7	109	9	US-09-144-886-97
12	32	66.7	295	9	US-10-045-545-1
13	32	66.7	296	9	US-10-045-545-1
14	32	66.7	296	9	US-10-045-545-3
15	31	64.6	9	10	US-09-976-787-6
16	31	64.6	9	10	US-09-865-198-6
17	31	64.6	35	9	US-09-809-391-745
18	31	64.6	106	10	US-09-976-787-24
19	31	64.6	106	10	US-09-865-198-23

20	64.6	107	9	US-09-144-886-75	Sequence 75, Appl
21	64.6	108	10	US-09-976-787-8	Sequence 8, Appl
22	64.6	108	10	US-09-865-198-8	Sequence 8, Appl
23	64.6	112	10	US-09-764-877-2008	Sequence 2008, Ap
24	64.6	131	10	US-09-881-823-6	Sequence 6, Appl
25	64.6	169	10	US-09-815-242-5756	Sequence 5756, Ap
26	64.6	172	10	US-09-815-242-12613	Sequence 12613, A
27	64.6	172	10	US-09-815-242-12852	Sequence 12852, A
28	64.6	238	10	US-09-976-787-29	Sequence 28, Appl
29	64.6	238	10	US-09-865-198-28	Sequence 28, Appl
30	64.6	240	10	US-09-976-787-28	Sequence 28, Appl
31	64.6	240	10	US-09-865-198-27	Sequence 27, Appl
32	64.6	366	10	US-09-901-252-17	Sequence 17, Appl
33	64.6	380	10	US-09-098-079-25	Sequence 25, Appl
34	64.6	413	9	US-09-809-391-751	Sequence 751, App
35	64.6	734	9	US-09-738-626-5405	Sequence 5405, Ap
36	64.6	806	9	US-10-025-380-1117	Sequence 1117, Ap
37	64.6	806	10	US-10-025-380-1118	Sequence 1118, Ap
38	64.6	806	10	US-09-922-217-1117	Sequence 1117, Ap
39	64.6	806	10	US-09-922-217-1118	Sequence 1118, Ap
40	62.5	62	9	US-09-828-708-51	Sequence 51, Appl
41	62.5	62	9	US-09-309-196-116	Sequence 116, Appl
42	62.5	104	10	US-09-828-708-2	Sequence 2, Appl
43	62.5	168	10	US-09-764-864-1223	Sequence 1223, Ap
44	62.5	238	10	US-09-815-242-5463	Sequence 5463, Ap
45	62.5	242	10	US-09-815-242-12164	Sequence 12164, A

ALIGNMENTS

RESULT 1

US-09-840-459-32
Sequence 32, Application US/09840459
Patent No. US20020150576A1
GENERAL INFORMATION:
APPLICANT: Lakosa, Gregory J.
APPLICANT: Horvath, Christopher
APPLICANT: Newman, Walter
APPLICANT: Jones, S. Tarran
APPLICANT: O'Brien, Siobhan H.
APPLICANT: O'Keefe, Theresa
TITLE OF INVENTION: HUMANIZED ANTI-CCR2 ANTIBODIES AND METHODS OF USE THEREFOR
FILE REFERENCE: 1855.1052-012
CURRENT APPLICATION NUMBER: US/09/840,459
CURRENT FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: PCT/US01/03537
PRIOR FILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 09/497,625
PRIOR FILING DATE: 2000-02-03
PRIOR APPLICATION NUMBER: 09/359,193
PRIOR FILING DATE: 1999-07-22
PRIOR APPLICATION NUMBER: 09/121,781
PRIOR FILING DATE: 1998-07-23
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Fast-Seq for Windows Version 3.0
SEQ ID NO 32
LENGTH: 100
TYPE: PRT
ORGANISM: Mus musculus
US-09-840-459-32

Query Match 77.1%; Score 37; DB 10; Length 100;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOLVEYP 7

Db 94 QOLVEYP 100

RESULT 2

US-08-779-457-50
 ; Sequence 50, Application US/08779457
 ; Publication No. US2002019357A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Carter, Paul J.
 ; APPLICANT: Chang, Nancy Y.
 ; APPLICANT: Kyung, Jin Kim
 ; APPLICANT: Matthews, William
 ; APPLICANT: Rodriguez, Maria L.
 ; APPLICANT: Rodriguez, Maria L.
 ; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/779,457
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/667197
 ; FILING DATE: 06/20/96
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/585005
 ; FILING DATE: 01/08/96
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P0986P2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415/225-1994
 ; TELEFAX: 415/952-9881
 ; TELEX: 910/371-7168
 ; INFORMATION FOR SEQ ID NO: 50:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 241 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-779-457-50

Query Match 75.0%; Score 36; DB 1; Length 241;
 Best Local Similarity 66.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 |||: |||
 Db 223 QQLISYPLT 231

RESULT 3
 US-09-880-748-1310
 ; Sequence 1310, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1310
 ; LENGTH: 251
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-748-1310
 Query Match 75.0%; Score 36; DB 9; Length 251;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 |||: |||
 Db 232 QQLISYPLT 240
 RESULT 4
 US-09-880-748-936
 ; Sequence 936, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 936
 ; LENGTH: 253
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-880-748-936

Query Match 75.0%; Score 36; DB 9; Length 253;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QQLVEYPPT 9
 |||: |||
 Db 234 QQLISYPLT 242

RESULT 5
 US-09-864-761-47635
 ; Sequence 47635, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Acomica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312

;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 47635
;; LENGTH: 82
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL009031.1
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.1
;; OTHER INFORMATION: EST HUMAN HIT: AW612517.1, EVALUATE 7.00e-43
;; OTHER INFORMATION: SWISSPROT HIT: P54253, EVALUATE 1.00e-43
US-09-864-761-47635

Query Match 68.8%; Score 33; DB 10; Length 82;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVEYPP 8
Db 6 LVEYPP 11

RESULT 6
US-09-848-798-40
; Sequence 40, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RA(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/848,798
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
; PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224

;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 40
;; LENGTH: 107
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: anti-Rh(D) chain I09
US-09-848-798-40

Query Match 68.8%; Score 33; DB 9; Length 107;
Best Local Similarity 66.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPP 9
Db 88 QQLNSYPY 96

RESULT 7
US-09-973-451-10
; Sequence 10, Application US/09973451
; Patent No. US20020132328A1
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AM, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE
; TITLE OF INVENTION: (PARG) ENZYMES,
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/973,451
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/302,812
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,768
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 10
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
; FEATURE:
US-09-973-451-10

Query Match 68.8%; Score 33; DB 10; Length 726;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QQLVEYPP 7
Db 172 QELIEYP 178

RESULT 8
US-10-164-359-4
; Sequence 4, Application US/10164359
; Publication No. US20030012776A1
; GENERAL INFORMATION:
; APPLICANT: Chin, Knew-Voon
; TITLE OF INVENTION: Nucleic Acid and Protein Expressed Thereby and Their Involvement
; FILE OF INVENTION: Stress
; FILE REFERENCE: 601-1-108US
; CURRENT APPLICATION NUMBER: US/10/164,359
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: PCT/US00/33438
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 60/169,418
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4

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; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-359-4

Query Match          66.7%; Score 32; DB 9; Length 105;
Best Local Similarity 55.6%; Pred. No. 35;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 66 QQILEYAYT 74

RESULT 9
US-09-107-058-8
; Sequence 8, Application US/09107058
; Patent No. US20010010922A1
; GENERAL INFORMATION:
; APPLICANT: Dalla-Favera, Riccardo
; APPLICANT: Niu, Hui-Feng
; TITLE OF INVENTION: CLONING AND USES OF THE GENETIC
; LOCUS bcl-6
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/43771-A-PCT-US-Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-761-117-8
Query Match          66.7%; Score 32; DB 10; Length 105;
Best Local Similarity 55.6%; Pred. No. 35;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
Db 72 QQILEYAYT 80

RESULT 11
US-09-144-886-97
; Sequence 97, Application US/09144886
; Patent No. US20020155114A1
; GENERAL INFORMATION:
; APPLICANT: Marks, James D
; APPLICANT: Amerdorfer, Peter
; TITLE OF INVENTION: Therapeutic Monoclonal Antibodies That Neutralize
; Botulinum Neurotoxins
; FILE REFERENCE: 2500.117USO
; CURRENT APPLICATION NUMBER: US/09/144,886
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 97
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BoNT/A clone
; OTHER INFORMATION: 1F3 region VL epitope 4
US-09-144-886-97

Query Match          66.7%; Score 32; DB 9; Length 109;
Best Local Similarity 55.6%; Pred. No. 36;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 1 QQLVEYPFT 9
DB 90 QQYIGYPT 98

RESULT 12
US-10-045-545-4
; Sequence 4, Application US/10045545
; Publication No. US20030027124A1
; GENERAL INFORMATION:
; APPLICANT: Maines, Mahin D.
; TITLE OF INVENTION: METHODS OF MODIFYING CELL STRUCTURE AND REMODELING
; FILE REFERENCE: 176/60981
; CURRENT APPLICATION NUMBER: US/10/045,545
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/261,500
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-045-545-4

Query Match 66.7%; Score 32; DB 9; Length 295;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVEYPFT 9
DB 94 LVEYPMT 100

RESULT 13
US-10-045-545-1
; Sequence 1, Application US/10045545
; Publication No. US20030027124A1
; GENERAL INFORMATION:
; APPLICANT: Maines, Mahin D.
; TITLE OF INVENTION: METHODS OF MODIFYING CELL STRUCTURE AND REMODELING
; FILE REFERENCE: 176/60981
; CURRENT APPLICATION NUMBER: US/10/045,545
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/261,500
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-045-545-1

Query Match 66.7%; Score 32; DB 9; Length 296;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVEYPFT 9
DB 95 LVEYPMT 101

RESULT 14
US-10-045-545-3
; Sequence 3, Application US/10045545
; Publication No. US20030027124A1
; GENERAL INFORMATION:
; APPLICANT: Maines, Mahin D.
; TITLE OF INVENTION: METHODS OF MODIFYING CELL STRUCTURE AND REMODELING

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; FILE REFERENCE: 176/60981
; CURRENT APPLICATION NUMBER: US/10/045,545
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 60/261,500
; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 296
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-045-545-3

Query Match 66.7%; Score 32; DB 9; Length 296;
Best Local Similarity 85.7%; Pred. No. 98;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVEYPFT 9
DB 95 LVEYPMT 101

RESULT 15
US-09-976-787-6
; Sequence 6, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-6

Query Match 64.6%; Score 31; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.7e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 1 QQRSSYPFT 9

Search completed: April 22, 2003, 13:11:13
Job time : 10.4821 secs

```


GenCore version 5.1.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:48:24 ; Search time 4.91071 Seconds
(without alignments)
97.882 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	67	2 A84376	hypothetical prote
2	33	100.0	117	1 G2MSU1	Ig heavy chain V r
3	33	100.0	444	2 S09681	citrate transport
4	33	100.0	1043	2 F97302	hypothetical prote
5	30	90.9	85	2 T42185	conserved hypothet
6	30	90.9	298	2 AE1752	hypothetical prote
7	30	90.9	298	2 AH1728	Abid phage protein
8	30	90.9	315	2 H86836	carbamate kinase (
9	30	90.9	348	2 G69142	GDP-D-mannose dehy
10	30	90.9	358	2 H83554	hypothetical prote
11	30	90.9	375	2 E83163	hypothetical prote
12	30	90.9	417	2 T08724	hypothetical prote
13	30	90.9	448	2 E95249	PTS system, fic co
14	30	90.9	448	2 G98113	conserved hypothet
15	30	90.9	452	2 T00113	undecaprenyl-phosp
16	30	90.9	464	2 T28818	hypothetical prote
17	30	90.9	475	2 T46745	arginine/ornithine
18	30	90.9	476	2 D84505	probable membrane
19	30	90.9	480	2 S39978	scra protein - sta
20	30	90.9	480	2 D90038	PTS system, sucros
21	30	90.9	490	2 C86879	arginine/ornithine
22	30	90.9	518	1 G69804	multidrug-efflux t
23	30	90.9	535	2 S78598	D-ribulokinase (BC
24	30	90.9	583	2 C72544	probable glycol-tr
25	30	90.9	592	1 IKEBCA	colicin A - Citrob
26	30	90.9	592	2 T15600	hypothetical prote
27	30	90.9	608	2 JQ1462	phosphoenolpyruvat
28	30	90.9	667	1 VCLJGL	env polyprotein pr
29	30	90.9	847	2 JC4836	alpha-glucuronidas

ALIGNMENTS

RESULT 1

A84376

hypothetical protein Vng2253h [imported] - Halobacterium sp. NRC-1

C:Species: Halobacterium sp. NRC-1

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: A84376

R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1

A:Reference number: A84160; MUID:20504483; PMID:11016950

A:Accession: A84376

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-67 <STO>

A:Cross-references: GB:AB004437; NID:g10581666; PIDN:AG20373.1; GSPDB:GN00138

C:Genetics:

A:Gene: VNG2253H

Query Match 100.0%; Score 33; DB 2; Length 67;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5

Db 59 GYWS 63

RESULT 2

G2MSU1

Ig heavy chain V region (UPC10) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 23-Mar-2001

C:Accession: A02081

R:Auffray, C.; Slikov, J.L.; Ollo, R.; Rougeon, P.

Ann. Immunol. (Paris) 132D, 77-88, 1981

A:Title: Correlation between D region structure and antigen-binding specificity: evidence:
F;15-98/Domain: immunoglobulin homology <IMM>

A:Reference number: A02081; MUID:83021113; PMID:6181731

A:Accession: A02081

A:Molecule type: mRNA

A:Residues: 1-117 <AUF>

C:Comment: This chain was isolated from an Ig gamma-2a myeloma protein binding 2,6-leval

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotrimer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

F;22-96/Disulfide bonds: #status predicted

Query Match 100.0%; Score 33; DB 1; Length 117;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

A:Gene: lin2373

Query Match 90.9%; Score 30; DB 2; Length 298;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 Db 45 GYWLS 49

RESULT 8

H86836
 C:Species: Lactococcus lactis subsp. lactis (strain IL14)
 C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: H86836
 R:Boletín, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: H86836
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-315 <STO>
 A:Cross-references: GB:AE005176; PID:gl2724712; PIDN:AAK05794.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: arcC3
 C:Superfamily: carbamate kinase
 C:Keywords: phosphotransferase

Query Match 90.9%; Score 30; DB 2; Length 315;
 Best Local Similarity 80.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 Db 88 GYWMA 92

RESULT 9

G69142
 C:Species: Methanobacterium thermoautotrophicum (strain Delta H)
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
 C:Accession: G69142
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 Qi, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: G69142
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-348 <MTH>
 A:Cross-references: GB:AE000818; GB:AE000666; NID:g2621384; PIDN:AAB84839.1; PID:g262138
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH333
 C:Superfamily: GDP-D-mannose dehydratase

Query Match 90.9%; Score 30; DB 2; Length 348;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 Db 156 GYWMT 160

RESULT 10

H83554

hypothetical protein PA0736 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: H83554
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: H83554
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-358 <STO>
 A:Cross-references: GB:AE004508; GB:AE004091; NID:g9946611; PIDN:AAG04125.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA0736

Query Match 90.9%; Score 30; DB 2; Length 358;
 Best Local Similarity 80.0%; Pred. No. 2.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 Db 203 GYWLS 207

RESULT 11

E83163
 hypothetical protein PA3863 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C:Accession: E83163
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Br
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: E83163
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-375 <STO>
 A:Cross-references: GB:AE004803; GB:AE004091; NID:g9950035; PIDN:AAG07250.1; GSPDB:GN001
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA3863

Query Match 90.9%; Score 30; DB 2; Length 375;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |||||
 Db 19 GYWLS 23

RESULT 12

T08724
 hypothetical protein DKFP566D213.1 - human
 C:Species: Homo sapiens (man)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
 C:Accession: T08724
 R:Koehler, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
 submitted to the Protein Sequence Database, May 1999
 A:Reference number: Z18468
 A:Accession: T08724
 A:Molecule type: mRNA
 A:Residues: 1-417 <ROE>
 A:Cross-references: EMBL:AL050275
 A:Experimental source: fetal kidney; clone DKFP566D213

C:Genetics:

A:Note: DKF2p566D213.1

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 417;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 402 GYWLS 406

RESULT 13

B95249

PFS system, IIC component, probable [imported] - Streptococcus pneumoniae (strain TIGR4)

C:Species: Streptococcus pneumoniae

C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C:Accession: B95249

R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

on, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfle,

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: B95249

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-448 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK76187.1; PID:G14973641; GSPDB:GN00164; TIGR:SP4

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP2129

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 448;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 186 GYWLS 190

RESULT 14

G98113

conserved hypothetical protein spr1938 [imported] - Streptococcus pneumoniae (strain R6)

C:Species: Streptococcus pneumoniae

C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001

C:Accession: G98113

R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczyk, L.; Burgett, S.; DeHoff, B.S.; E

e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, F.; McAhren, S.; M

Y, P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A:Reference number: A97872; MUID:21429245; PMID:11544234

A:Accession: G98113

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-448 <KUR>

A:Cross-references: GB:AE007317; PIDN:AALO0740.1; PID:G15459636; GSPDB:GN00174

C:Genetics:

A:Gene: spr1938

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 448;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 186 GYWLS 190

RESULT 15

T00113

undecaprenyl-phosphate galactosephosphotransferase homolog - Actinobacillus actinomycete

C:Species: Actinobacillus actinomycetemcomitans

C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000

C:Accession: T00113

R:Nakano, Y.; Yoshida, Y.; Yamashita, Y.; Koga, T.

Biochim. Biophys. Acta 1442, 409-414, 1998

A:Title: A gene cluster for 6-deoxy-L-talan synthesis in Actinobacillus actinomycetemcom

A:Reference number: Z14111; MUID:99023768; PMID:9805002

A:Accession: T00113

A>Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-452 <NAK>

A:Cross-references: EMBL:AB010415; NID:G3132248; PIDN:BAA28142.1; PID:G3132265

A:Experimental source: strain NCTC 9710

C:Superfamily: xps2A protein

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 452;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5

Db 11 GYWLS 15

Search completed: April 22, 2003, 12:54:51

Job time : 6.91071 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:46:53 ; Search time 2.5 Seconds
(without alignments)
82.953 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYWS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	33	100.0	117	1 HV41_MOUSE	P01811 mus musculu
2	33	100.0	444	1 CITI_KLEPN	P16482 klebsiella
3	30	90.9	214	1 CAPA_KLULA	O74232 kluyveromy
4	30	90.9	292	1 AMPR_PROST	O69772 providencia
5	30	90.9	309	1 ARCC_ENTFC	P35836 enterococcu
6	30	90.9	475	1 ARCD_LACSK	O53092 lactobacill
7	30	90.9	478	1 ARCD_CLOPE	Q46170 clostridium
8	30	90.9	480	1 PTSE_STAXY	P51184 staphylococ
9	30	90.9	583	1 SYG_AERPE	Q95b58 aeropyrum p
10	30	90.9	592	1 CEA_CITPR	P04480 citrobacter
11	30	90.9	608	1 PPCR_NEOFR	P22130 neocallimas
12	30	90.9	667	1 ENV_GALV	P21415 gibbon ape
13	30	90.9	847	1 AGUA_TRIRE	Q99024 trichoderma
14	30	90.9	936	1 CAPP_RHOMR	Q59757 rhodothermu
15	30	90.9	1063	1 CZCA_ALCEU	P13511 alcaligenes
16	30	90.9	1063	1 CZCA_ALCSP	P94177 alcaligenes
17	30	90.9	1502	1 MRPE_RAT	O88269 rattus norv
18	30	90.9	1503	1 MRPE_HUMAN	O95255 homo sapien
19	29	87.9	252	1 PRIO_ATEPA	P51446 ateles pani
20	29	87.9	252	1 PRIO_RABIT	Q95211 oryctolagus
21	29	87.9	270	1 GPR1_YARLI	P41943 yarrowia li
22	29	87.9	271	1 YAD8_SCHPO	Q09834 schizosacch
23	29	87.9	287	1 LEPA_LEGPN	O68433 legionella
24	29	87.9	314	1 ARCC_LACSK	O53090 lactobacill
25	29	87.9	388	1 Y535_BUCAL	P57601 buchnera ap
26	29	87.9	395	1 ARP2_DROME	P45888 drosophila
27	29	87.9	482	1 ARCD_PSEAE	P18275 pseudomonas
28	29	87.9	494	1 AMY1_SACFI	P21567 saccharomyc
29	29	87.9	503	1 PR19_YEAST	P32523 saccharomyc
30	29	87.9	512	1 AMY1_DEBOC	P19269 debaryomyce
31	29	87.9	518	1 RTN_ECOLI	P76446 escherichia
32	29	87.9	533	1 GLPT_HUMAN	P57057 homo sapien
33	29	87.9	579	1 YGT6_YEAST	P53099 saccharomyc

34	29	87.9	587	1 PH84_YEAST	P25297 saccharomyc
35	29	87.9	598	1 CSTA_BACSU	P94532 bacillus su
36	29	87.9	615	1 SPPA_HAEIN	P45243 haemophilus
37	29	87.9	618	1 SPPA_ECOLI	P08395 escherichia
38	29	87.9	639	1 YII9_MYCTU	Q50614 mycobacteri
39	29	87.9	680	1 GAOA_DACDE	Q01745 daetylum d
40	29	87.9	774	1 YQV5_CAEEL	Q09554 caenorhabdi
41	29	87.9	776	1 VP4_ROT9D	Q06894 canine rota
42	29	87.9	776	1 VP4_ROT9F	Q07416 feline rota
43	29	87.9	776	1 VP4_ROT9Y	Q06895 human rotav
44	28	84.8	141	1 YEDD_SALTY	Q06399 salmonella
45	28	84.8	184	1 MUP3_MOUSE	P04939 mus musculu

ALIGNMENTS

RESULT 1
HV41_MOUSE STANDARD; PRT; 117 AA.
ID HV41_MOUSE
AC P01811;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig heavy chain V region UPC10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP MEDLINE=83021113; PubMed=6181731;
RX Auffray C., Sikorav J.L., Ollo R., Rougeon F.;
RA "Correlation between D region structure and antigen-binding
RT specificity: evidences from the comparison of closely related
RT immunoglobulin VH sequences.";
RL Ann. Immunol. (Paris) 132D:77-88 (1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOMA
CC PROTEIN BINDING 2,6-LEVAN.
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CC EMBL; M36631; AAA38078.1; -.
CC FIR; A02081; G2MSU1.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig_1.
CC SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13001 MW; B20A1074F8E99E7F CRC64;

Query Match 100.0%; Score 33; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
Db 31 GYWS 35
| | | | |

RESULT 2
CITI_KLEPN STANDARD; PRT; 444 AA.
ID CITI_KLEPN
AC P16482;
DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Citrate-proton symporter (Citrate transporter) (Citrate carrier
 protein)
 GN CITH OR CIT.
 OS Klebsiella pneumoniae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Klebsiella.
 RN NCBI_TaxID=573;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 13882;
 RX MEDLINE=90249385; PubMed=2186908;
 RA van der Rest M.E., Oosterhelt D., Konings W.N.;
 RT "DNA sequence of a citrate carrier of Klebsiella pneumoniae.";
 RL Eur. J. Biochem. 189:401-407(1990).
 CC -|- FUNCTION: UPTAKE OF CITRATE ACROSS THE BOUNDARY MEMBRANE WITH
 CC THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
 CC -|- PATHWAY: ALLOWS THE UTILIZATION OF CITRATE AS A SOLE SOURCE OF
 CC CARBON AND ENERGY.
 CC -|- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
 CC -|- SIMILARITY: TO CIT IN TN3411 AND PWR60 FOUND IN E.COLI AND TO
 CC CIT IN CITROBACTER AMALONITICUS.
 CC -|- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
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 CC EMBL; X51479; CAA35944.1; -;
 DR PIR; S09681; S09681.
 DR InterPro; IPR004736; Cit H symport.
 DR InterPro; IPR003662; Sub transporter.
 DR Pfam; PF00083; sugar tr; 1.
 DR TIGRfam; TIGR00883; 2A0106; 1.
 DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 2.
 DR PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
 DR Transprot; Transmembrane; Inner membrane; Citrate utilization;
 Symport.
 KW DOMAIN 1 41
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 62
 FT TRANSMEM 63 72
 FT DOMAIN 73 93
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 94 114
 FT DOMAIN 115 135
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 136 137
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 138 158
 FT DOMAIN 159 177
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 178 198
 FT DOMAIN 199 199
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 200 220
 FT DOMAIN 221 251
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 252 272
 FT DOMAIN 273 289
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 290 310
 FT DOMAIN 311 318
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 319 339
 FT DOMAIN 340 340
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 341 361
 FT DOMAIN 362 379
 FT CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 380 400
 FT DOMAIN 401 411
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 412 432
 FT DOMAIN 433 444
 FT CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 444 AA; 48142 MW; D431F732BEDA3EC2 CRC64;
 Query Match 100.0%; Score 33; DB 1; Length 444;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 DB 415 GYWS 419
 RESULT 3
 ID CAPA_KLULA STANDARD; PRT; 214 AA.
 AC O74232;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE F-actin capping protein alpha subunit (Fragment).
 GN CAP1.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Banfield D.K.;
 RT "DNA sequence of the SFT1 gene from Kluyveromyces lactis.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBB databases.
 CC -|- FUNCTION: F-ACTIN CAPPING PROTEINS BIND IN A CA(2+)-INDEPENDENT
 CC MANNER TO THE FAST GROWING ENDS OF ACTIN FILAMENTS (BARBED END)
 CC THEREBY BLOCKING THE EXCHANGE OF SUBUNITS AT THESE ENDS. UNLIKE
 CC OTHER CAPPING PROTEINS (SUCH AS GELSOLIN AND SEVERIN), THESE
 CC PROTEINS DO NOT SEVER ACTIN FILAMENTS (BY SIMILARITY).
 CC -|- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT (BY
 CC SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE F-ACTIN CAPPING PROTEIN ALPHA SUBUNIT
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; AF072674; AAC24885.1; -;
 DR InterPro; IPR002189; F-actin cap A.
 DR Pfam; PF01267; F-actin cap A; 1.
 DR PRINTS; PR00191; F-actin cap A.
 DR PRODOM; PD006960; F-actin cap A; 1.
 DR PROSITE; PS00748; F-actin capping A; 1.
 DR PROSITE; PS00749; F-actin capping A_2; 1.
 KW Actin-binding; Capping protein.
 FT NON_TER 1
 SQ SEQUENCE 214 AA; 24380 MW; 31851D6573630C02 CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 214;
 Best Local Similarity 80.0%; Pred. No. 60;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 DB 111 GYWS 115
 RESULT 4
 ID AMPR_PROST STANDARD; PRT; 292 AA.
 AC O69772;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Transcriptional activator protein ampr.
 GN AMPR.
 OS Providencia stuartii.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Providencia.
OX NCBI_TaxID=588;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VDG 96;
RA Koeck J.L., Basmaciogullari S., Parzy D., Barnaud G., Teyssou R.,
RA Buisson Y., Philippon A., Arlet G.J.;
RT "Cloning and sequencing of ampC and ampR genes from Providencia
RT stuartii";
RT Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RL FUNCTION: THIS PROTEIN IS A POSITIVE REGULATOR OF GENE EXPRESSION
CC OF BETA-LACTAMASE (AMPC).
CC
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC
CC -1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
CC REGULATORS.
CC
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CC
CC EMBL: Y17315; CAA76738.1; -;
DR InterPro; IPR000847; HTH_LysR.
DR InterPro; IPR005119; LysR_subst.
DR Pfam; PF00126; HTH 1; 1.
DR Pfam; PF03466; LysR_substrate; 1.
DR PRINTS; PR00039; HTHLYSR.
DR PROSITE; PS00044; HTH_LYSR_FAMILY; 1.
DR Transcription regulation; DNA-binding; Activator.
KW DNA_BIND 26 45 H-T-H MOTIF (POTENTIAL).
FT SEQUENCE 292 AA; 32741 MW; 9B2CEFF667E112F0 CRC64;
SQ

Query Match 90.9%; Score 30; DB 1; Length 292;
Best Local Similarity 80.0%; Pred. No. 82;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 264 GYWS 268
|||:|

RESULT 5
ARCC ENTFC STANDARD; PRT; 309 AA.
AC P35836; O54531;
DT 01-JUN-1994 (Rel. 29, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbamate kinase (EC 2.7.2.2).
GN ARCC.
OS Enterococcus faecium (Streptococcus faecium), and
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1352, 1351;
RN (1)
RP SEQUENCE FROM N.A.
RC SPECIES=E.faecium, and E.faecalis; STRAIN=D10, and ATCC 29212;
RA Marina A., Uriarte M., Barcelona B., Fresquet V., Cervera J.,
RA Rubio V.;
RT "Carbamate kinase from Enterococcus faecalis and Enterococcus faecium.
RT Cloning of the genes studies on the enzyme expressed in Escherichia
RT coli, sequences similarity with N-acetyl-L-glutamate kinase.";
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN (2)
RN SEQUENCE OF 1-32 AND 158-168, AND CHARACTERIZATION.
RC SPECIES=E.faecium; STRAIN=D10;
RX MEDLINE=94141928; PubMed=8308897;
RA Marina A., Bravo J., Fita I., Rubio V.;
RT "Crystallization, characterization and preliminary crystallographic
RT studies of carbamate kinase of Streptococcus faecium.";

RL J. Mol. Biol. 235:1345-1347(1994).
CC -1- CATALYTIC ACTIVITY: ATP + NH(3) = ADP + carbamoyl
CC phosphate.
CC -1- PATHWAY: Arginine degradation via arginine deiminase; third step.
CC -1- SUBUNIT: HOMODIMER (PREDOMINANTLY) AND HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE CARBAMATE KINASE FAMILY.
CC
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CC
CC EMBL: AJ223331; CAA11270.1; -;
DR EMBL; AJ223332; CAA11271.1; -;
DR PIR; S44002; S44002.
DR HSP; P95474; IR19.
DR InterPro; IPR001048; Aa_kinase.
DR InterPro; IPR003964; Bac_carb_kinase.
DR Pfam; PF00696; aak_kinase; 1.
DR TIGRFAMs; TIGR00746; arcC; 1.
KW Transferase; Kinase; Arginine metabolism.
FT INIT MET 0
FT CONFLICT 33 157 MISSING (IN REF. 2).
FT CONFLICT 168 168 I->D (IN REF. 2).
SQ SEQUENCE 309 AA; 32795 MW; 5014514A7FEEB290 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 309;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 86 GYWS 90
|||:|

RESULT 6
ARCD LACSK STANDARD; PRT; 475 AA.
ID ARCD_LACSK
AC O53092;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Arginine/ornithine antipporter.
GN ARCD.
OS Lactobacillus sakei.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1599;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=98361904; PubMed=9696763;
RA Zuniga M., Champomier-Verges M., Zagorec M., Perez-Martinez G.;
RT "Structural and functional analysis of the gene cluster encoding the
RT enzymes of the arginine deiminase pathway of Lactobacillus sake.";
RL J. Bacteriol. 180:4154-4159(1998).
CC -1- FUNCTION: CATALYZES AN ELECTRONUTRIENT EXCHANGE BETWEEN ARGININE
CC AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
CC ARGININE DEIMINASE PATHWAY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
CC PERMEASES.
CC
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CC

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CC EMBL; AJ001330; CAA04686.1; -.
DR InterPro; IPR002293; AA/rel_primease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
DR TIGRFAMs; TIGR00305; 2A0302; 1.
KW Transport; Antiport; Amino-acid transport; Transmembrane.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 42 62 POTENTIAL.
FT TRANSMEM 74 94 POTENTIAL.
FT TRANSMEM 101 121 POTENTIAL.
FT TRANSMEM 157 177 POTENTIAL.
FT TRANSMEM 205 225 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
FT TRANSMEM 283 303 POTENTIAL.
FT TRANSMEM 333 353 POTENTIAL.
FT TRANSMEM 361 381 POTENTIAL.
FT TRANSMEM 397 417 POTENTIAL.
FT TRANSMEM 451 471 POTENTIAL.
SQ SEQUENCE 475 AA; 51881 MW; 8B91A01F6A2203CC CRC64;

Query Match 90.9%; Score 30; DB 1; Length 475;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
   |||:|
Db 94 GYWS 98

RESULT 7
ID ARCD CLOPE STANDARD; PRT; 478 AA.
AC Q46170.
DT 15-DEC-1998 (Rel. 37, Created)
DE 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Arginine/ornithine antiporter.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=97199138; PubMed=9053381;
RA Ohtani K., Bando M., Swe T., Banu S., Oe M., Hayashi H., Shimizu T.;
RT "Collagenase gene (colA) is located in the 3'-flanking region of the
perfringolysin O (pfoA) locus in Clostridium perfringens.";
RL FEMS Microbiol. Lett. 146:155-159(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
CC -!- FUNCTION: CATALYZES AN ELECTRONEUTRAL EXCHANGE BETWEEN ARGININE
AND ORNITHINE TO ALLOW HIGH-EFFICIENCY ENERGY CONVERSION IN THE
ARGININE DIMINASE PATHWAY (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (potential).
CC -!- SIMILARITY: BELONGS TO THE ARCD/CADE/GERAB/LYSI FAMILY OF
PERMEASES.
-----
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DR EMBL; X97768; CAA66366.1; -.
DR EMBL; AP003185; BAB79876.1; -.
DR InterPro; IPR002293; AA/rel_primease1.
DR InterPro; IPR004841; Permease.
DR InterPro; IPR004754; R/O_antiport.
DR Pfam; PF00324; aa_permeases; 1.
DR TIGRFAMs; TIGR00905; 2A0302; 1.
KW Transport; Antiport; Amino-acid transport; Transmembrane;
Complete proteome.
FT TRANSMEM 11 31 POTENTIAL.
FT TRANSMEM 43 63 POTENTIAL.
FT TRANSMEM 83 103 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 130 150 POTENTIAL.
FT TRANSMEM 159 179 POTENTIAL.
FT TRANSMEM 203 223 POTENTIAL.
FT TRANSMEM 236 256 POTENTIAL.
FT TRANSMEM 284 304 POTENTIAL.
FT TRANSMEM 333 353 POTENTIAL.
FT TRANSMEM 359 379 POTENTIAL.
FT TRANSMEM 417 437 POTENTIAL.
FT TRANSMEM 456 476 POTENTIAL.
FT CONFLICT 83 83 MISSING (IN REF. 1).
FT CONFLICT 221 221 MISSING (IN REF. 1).
FT CONFLICT 352 352 A -> V (IN REF. 1).
FT CONFLICT 417 417 G -> E (IN REF. 1).
SQ SEQUENCE 478 AA; 51088 MW; A7BA24F7B53A344B CRC64;

Query Match 90.9%; Score 30; DB 1; Length 478;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
   |||:|
Db 96 GYWS 100

RESULT 8
ID PTSE STAXY STANDARD; PRT; 480 AA.
AC P51184;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE PTS system, sucrose-specific IIBC component (EIIBC-SCR) (Sucrose-
permease IIBC component) (Phosphotransferase enzyme II, BC component)
DE (EC 2.7.1.69) (EIIBC-SCR).
GN SCRA.
OS Staphylococcus xylosum.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1288;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 20267 / Isolate C2A;
RX MEDLINE=94049686; PubMed=8232209;
RA Wagner E., Goetz F., Brueckner R.;
RT "Cloning and characterization of the scrA gene encoding the sucrose-
specific Enzyme II of the phosphotransferase system from
Staphylococcus xylosum.";
RL Mol. Gen. Genet. 241:33-41(1993).
CC -!- FUNCTION: THIS IS A COMPONENT OF THE PHOSPHOENOLPYRUVATE-DEPENDENT
SUGAR PHOSPHOTRANSFERASE SYSTEM (PTS), A MAJOR CARBOHYDRATE ACTIVE
-TRANSPORT SYSTEM. THE IICD DOMAINS CONTAIN THE SUGAR BINDING SITE
AND THE TRANSMEMBRANE CHANNEL; THE IIA DOMAIN CONTAINS THE PRIMARY
CC PHOSPHORYLATION SITE (THE DONOR IS PHOSPHO-HPR); IIA TRANSFERS ITS
CC PHOSPHORYL GROUP TO THE IIB DOMAIN WHICH FINALLY TRANSFERS IT TO
THE SUGAR.
CC -!- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein
histidine + sugar phosphate.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
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CC CC -1- SIMILARITY: CONTAINS 1 PTS EIIB DOMAIN.
CC CC -1- SIMILARITY: CONTAINS 1 PTS EIIC DOMAIN.
CC CC
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CC CC
CC EMBL; K69800; CAA49461.1.; -.
CC InterPro; IPR001996; PTS_EIIB.
CC InterPro; IPR003352; PTS_EIIC.
CC Pfam; PF00367; PTS_EIIB; 1.
CC Pfam; PF02378; PTS_EIIC; 1.
CC Pfam; PF001476; PTS_EIIB; 1.
CC TIGRFAMs; TIGR00826; EIIBC; 1.
CC PROSITE; PS01035; PTS_EIIB_CYS; 1.
CC Phosphotransferase system; Sugar transport; Transferase;
CC Transmembrane; Inner membrane; Phosphorylation.
CC DOMAIN 1 ? EIIB DOMAIN.
CC DOMAIN ? 480 EIIC DOMAIN.
CC MOD_RES 26 26 PHOSPHORYLATION (BY SIMILARITY).
CC MOD_RES 325 325 PHOSPHORYLATION (BY SIMILARITY).
CC SEQUENCE 480 AA; 51326 MW; AB4E1D9785D84E47 CRC64;
CC
CC Query Match 90.9%; Score 30; DB 1; Length 480;
CC Best Local Similarity 80.0%; Pred. No. 1.3e+02;
CC Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 GYWS 5
CC |||||
CC Ddb 290 GYWS 294
CC
CC RESULT 9
CC SYG_AERPE
CC ID SYG_AERPE STANDARD; PRT; 583 AA.
CC AC Q9YBF8;
CC DT 16-OCT-2001 (Rel. 40, Created)
CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE GLYCyl-CRNA synthetase (EC 6.1.1.14) (Glycine-tRNA ligase) (GlyRS) .
CC GN GLYS OR APE1639
CC OS Aeropyrum pernix.
CC OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
CC OC Desulfurococaceae; Aeropyrum.
CC NCBI_TaxID=56636;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=K1;
CC RX MEDLINE=99310339; PubMed=10382966;
CC RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,
CC RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
CC RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
CC RA Takamizawa M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
CC RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
CC RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
CC RT "Complete genome sequence of an aerobic hyper-thermophilic
CC crenarchaeon, Aeropyrum pernix K1."
CC RL DNA Res. 6:83-101(1999).
CC CC -1- CATALYTIC ACTIVITY: ATP + glycine + tRNA(Gly) = AMP + diphosphate
CC CC + GLYCyl-tRNA(Gly).
CC CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC CC
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DR EMBL; X01008; AAA25503.1; -.
DR EMBL; M37402; AAA72879.1; -.
DR PIR; A03504; IKEBCA.
DR PDB; 1COL; 15-JUL-93.
DR InterPro; IPR000293; Channel_colicin.
DR Pfam; PF01024; Colicin; 1.
DR PRINTS; PR00280; Channel_colicin.
DR ProDom; PD002657; Channel_colicin; 1.
DR PROSITE; PS00276; CHANNEL_COLICIN; 1.
KW Antibiotic; Bacteriocin; Plasmid; Transmembrane; 3D-structure.
FT TRANSMEM 528 548
FT TRANSMEM 555 575
FT TRANSMEM 396 418
FT HELIX 420 434
FT HELIX 435 435
FT TURN 437 438
FT TURN 444 455
FT HELIX 456 456
FT TURN 458 460
FT HELIX 464 475
FT TURN 476 476
FT HELIX 479 489
FT HELIX 491 493
FT TURN 496 497
FT HELIX 498 515
FT HELIX 519 530
FT TURN 531 532
FT HELIX 535 552
FT HELIX 557 575
FT TURN 577 577
FT HELIX 578 586
FT TURN 587 588
SQ SEQUENCE 592 AA; 62992 MW; B80FA1F52A8CFC5D CRC64;

Query Match 90.9%; Score 30; DB 1; Length 592;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
DB 136 GYWLS 140
|||||

RESULT 11
PFCK_NEOFR STANDARD; PRT; 608 AA.
AC P22130;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoenolpyruvate carboxykinase [GTP] (EC 4.1.1.32)
DE (Phosphoenolpyruvate carboxylase) (PEPCK).
OS Neocallimastix frontalis (Rumen fungus).
OC Eukaryota; Fungi; Chytridiomycota; Neocallimasticales;
OC Neocallimastixaceae; Neocallimastix.
OX NCBI_TaxID=4757;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92184115; PubMed=1339359;
RA Raymond P., Geourjon C., Roub B., Durand R., Fevre M.;
RT "Sequence of the phosphoenolpyruvate carboxykinase-encoding cDNA from
RT the rumen anaerobic fungus Neocallimastix frontalis: comparison of
RT the amino acid sequence with animals and yeast.";
RL Gene 110:57-63 (1992).
CC -1- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
CC + CO(2).
CC -1- PATHWAY: Rate-limiting gluconeogenic enzyme.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP]
CC FAMILY.
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DR EMBL; M59372; AAA33553.1; -.
DR PIR; JQ1462; JQ1462.
DR InterPro; IPR000364; PEP_carboxykin.
DR Pfam; PF00821; PEPCK; 1.
DR ProDom; PD004738; PEP_carboxykin; 1.
DR PROSITE; PS00505; PEPCK_GTP; 1.
KW Gluconeogenesis; Lyase; Decarboxylase; GTP-binding.
FT NP_BIND 217 224
FT ACT_SITE 269 269
FT POTENTIAL.
SQ SEQUENCE 608 AA; 66904 MW; C4D2B249A92B7D26 CRC64;

Query Match 90.9%; Score 30; DB 1; Length 608;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
DB 478 GYWLS 482
|||||

RESULT 12
ENV_GALV STANDARD; PRT; 667 AA.
AC P21415;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ENV polyprotein precursor [Contains: Knob protein GP70; Spike protein
DE P15E].
DE P15E].
GN ENV.
OS Gibbon ape leukemia virus.
OC Viruses; Retroviridae; Retroviridae; Gammaretrovirus.
OX NCBI_TaxID=11840;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90051069; PubMed=2683360;
RA Delassus S., Sonigo P., Wain-Hobson S.;
RT "Genetic organization of gibbon ape leukemia virus.";
RL Virology 173:205-213 (1989).
CC
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-----
DR EMBL; M26927; AAA46811.1; -.
DR PIR; C32595; VCLJGL.
DR HSP; P03385; LMOP.
DR InterPro; IPR002050; Env_polyprotein.
DR Pfam; PF00429; ENV_polyprotein; 1.
KW Coat protein; Glycoprotein; Polyprotein; Transmembrane; Signal.
FT SIGNAL 1 42
FT CHAIN 43 489
FT CHAIN 490 667
FT TRANSMEM 492 508
FT TRANSMEM 637 653
FT CARBOHYD 301 301
FT CARBOHYD 344 344
FT CARBOHYD 415 415
FT CARBOHYD 421 421
FT CARBOHYD 433 433
FT CARBOHYD 453 453

```

SQ SEQUENCE 667 AA; 73729 MW; 5FPB32F00D8631BE CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 667;
 Best Local Similarity 80.0%; Pred. No. 1.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 |||:
 Db 180 GYWS 184

RESULT 13
 AGUA TRIRE STANDARD; PRT; 847 AA.
 AC Q99024;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Alpha-glucuronidase precursor (EC 3.2.1.139) (Alpha-glucosiduronase) (GLXI).
 DE Trichoderma reesei (Hypocrea jecorina).
 OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Hypocreales; Hypocreaceae; Hypocrea.
 ON NCBI_TaxID=51453;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=QM9414 / SUB C-30;
 RX MEDLINE=96257277; PubMed=8654984;
 RA Margolles-Clark E., Saloheimo M., Siika-Aho M., Penttilae M.;
 RT "The alpha-glucuronidase-encoding gene of Trichoderma reesei.";
 RL Gene 172:171-172(1996).
 CC -!- FUNCTION: RELEASES 4-O-METHYLGLUCURONIC ACID FROM XYLAN.
 CC -!- CATALYTIC ACTIVITY: An alpha-D-glucuronoside + H(2)O = an alcohol + D-glucuronate.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO FAMILY 67 OF GLYCOSYL HYDROLASES.
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 CC EMBL; Z68706; CAA92949.1; -
 DR InterPro; IPR005154; Glyco_hydro_67.
 DR Pfam; PF03648; Glyco_hydro_67; 1.
 KW Xylan degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 847 ALPHA-GLUCURONIDASE.
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 321 321 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 586 586 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 692 692 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 740 740 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 767 767 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 847 AA; 93424 MW; 214AAE487382FDB4 CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 847;
 Best Local Similarity 80.0%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 |||:
 Db 119 GYWS 123

RESULT 14
 CAPP RHOMR STANDARD; PRT; 936 AA.

AC O59757;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoenolpyruvate carboxylase (EC 4.1.1.31) (PEPCASE) (PEPC).
 GN PPC OR PEPC.
 OS Rhodothermus marinus (Rhodothermus obamensis).
 OC Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales;
 OC Crenotrichaceae; Rhodothermus.
 ON NCBI_TaxID=29549;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OKD7;
 RX MEDLINE=97420683; PubMed=9276668;
 RA Takai K., Sako Y., Uchida A., Ishida Y.;
 RT "Extremely thermostable phosphoenolpyruvate carboxylase from an extreme thermophile, Rhodothermus obamensis.";
 RL J. Biochem. 122:32-40(1997).
 CC -!- FUNCTION: TO FORM OXALOACETATE, A FOUR-CARBON DICARBOXYLIC ACID SOURCE FOR THE TRICARBOXYLIC ACID CYCLE. THE OPTIMUM TEMPERATURE FOR ACTIVITY IS 75 DEGREES CELSIUS. THE ENZYME EXHIBITS A PH OPTIMUM OF 8.0.
 CC -!- CATALYTIC ACTIVITY: Phosphate + oxaloacetate = H(2)O + phosphoenolpyruvate + CO(2).
 CC -!- COFACTOR: ABSOLUTE REQUIREMENT FOR DIVALENT CATIONS.
 CC -!- PATHWAY: Tricarboxylic acid cycle.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- SIMILARITY: BELONGS TO THE PEPCASE FAMILY.
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 CC EMBL; X99379; CAA67760.1; -
 DR HSP; P00864; 1FY.
 DR InterPro; IPR001449; PEPCase.
 DR Pfam; PF00311; PEPCase; 1.
 DR PRINTS; PR00150; PEPCARBLASE.
 DR PROSITE; PS00393; PEPCASE 2; 1.
 DR PROSITE; PS00781; PEPCASE 1; 1.
 KW Lyase; Carbon dioxide fixation; Tricarboxylic acid cycle.
 FT ACT_SITE 155 155 BY SIMILARITY.
 FT ACT_SITE 595 595 BY SIMILARITY.
 SQ SEQUENCE 936 AA; 107886 MW; C9AA94C3F26C345A CRC64;
 Query Match 90.9%; Score 30; DB 1; Length 936;
 Best Local Similarity 80.0%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
 |||:
 Db 598 GYWS 602

RESULT 15
 CZCA ALCEU STANDARD; PRT; 1063 AA.
 ID CZCA ALCEU
 AC P13511; P94142;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cobalt-zinc-cadmium resistance protein czca (Cation efflux system protein czca).
 GN CZCA.
 OS Alkaligenes eutrophus (Ralstonia eutropha).
 OG Plasmid pMOL30.
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 ON NCBI_TaxID=510;

```

RN SEQUENCE FROM N.A.
RP STRAIN=CH34;
RX MEDLINE=90017477; PubMed=2678100;
RA Nies D.H., Nies A., Chu L., Silver S.;
RT "Expression and nucleotide sequence of a plasmid-determined divalent
RL cation efflux system from Alcaligenes eutrophus.";
RN Proc. Natl. Acad. Sci. U.S.A. 86:7351-7355(1989).
[2]
RP REVISIONS TO 918 AND 959-960.
RC STRAIN=CH34;
RA van der Lelie D., Schwuchow T., Wuerztz S., Schwidetzky U.,
RA Baeyens W., Scheel P.O., Nies D.H.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: HAS A LOW CATION TRANSPORT ACTIVITY FOR CO(2+), IT IS
CC ESSENTIAL FOR THE EXPRESSION OF COBALT, ZINC, AND CADMIUM
CC RESISTANCE. CZCA AND CZCB TOGETHER WOULD ACT IN ZN(2+) EFFLUX
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (CZCABC).
CC -!- INDUCTION: BY CADMIUM, COPPER AND ZINC.
CC -!- SIMILARITY: BELONGS TO THE ACRB/ACRD/ACRF FAMILY.
CC -----
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CC -----
DR EMBL; X98451; CAA67084.1; -
DR FIR; A33830; A33830.
DR InterPro; IPR001036; Acrflvin_res.
DR InterPro; IPR004763; CzCA.
DR Pfam; PF00873; ACR_tran; 1.
DR TIGRFAMs; TIGR00914; 2A0601; 1.
KW Plasmid; Transport; Zinc; Cobalt; Cadmium resistance; Transmembrane.
FT TRANSMEM 14 29 POTENTIAL.
FT TRANSMEM 350 370 POTENTIAL.
FT TRANSMEM 452 472 POTENTIAL.
FT TRANSMEM 487 507 POTENTIAL.
FT TRANSMEM 534 554 POTENTIAL.
FT TRANSMEM 883 903 POTENTIAL.
FT TRANSMEM 906 926 POTENTIAL.
FT TRANSMEM 937 957 POTENTIAL.
FT TRANSMEM 982 1004 POTENTIAL.
FT TRANSMEM 1013 1033 POTENTIAL.
SQ SEQUENCE 1063 AA; 115668 MW; 1E95B7923996AEBB CRC64;

Query Match 90.9%; Score 30; DB 1; Length 1063;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYVMS 5
Db 862 GYVMT 866

```

Search completed: April 22, 2003, 12:51:50
 Job time : 4.5 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:47:43 ; Search time 10 Seconds:
(without alignments)
103.024 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	67	Q9HN48	Q9HN48 halobacteri
2	33	100.0	377	Q9IA87	Q9IA87 campylobom
3	33	100.0	377	Q9IAH6	Q9IAH6 boulengerom
4	33	100.0	377	Q9IAH4	Q9IAH4 brienyomyrus
5	33	100.0	377	Q9IAH3	Q9IAH3 brienyomyrus
6	33	100.0	377	Q9IAH2	Q9IAH2 brienyomyrus
7	33	100.0	377	Q9IAH1	Q9IAH1 brienyomyrus
8	33	100.0	377	Q9IAH0	Q9IAH0 campylobom
9	33	100.0	377	Q9IAH9	Q9IAH9 campylobom
10	33	100.0	377	Q9IAG7	Q9IAG7 genyomyrus
11	33	100.0	377	Q9IAG6	Q9IAG6 gnathonemus
12	33	100.0	377	Q9IAG4	Q9IAG4 hippopotamy
13	33	100.0	377	Q9IAG3	Q9IAG3 hippopotamy
14	33	100.0	377	Q9IAG2	Q9IAG2 hippopotamy
15	33	100.0	377	Q9IAG1	Q9IAG1 hyperopisus
16	33	100.0	377	Q9IAF9	Q9IAF9 ivindomyrus

17	33	100.0	377	13	Q9IAF8	Q9IAF8 marcusenius
18	33	100.0	377	13	Q9IAE7	Q9IAE7 marcusenius
19	33	100.0	377	13	Q9IAF6	Q9IAF6 marcusenius
20	33	100.0	377	13	Q9IAF5	Q9IAF5 marcusenius
21	33	100.0	377	13	Q9IAF4	Q9IAF4 marcusenius
22	33	100.0	377	13	Q9IAF0	Q9IAF0 mormyrus ov
23	33	100.0	377	13	Q9IAE9	Q9IAE9 mormyrus ru
24	33	100.0	377	13	Q9IAE6	Q9IAE6 paramormyro
25	33	100.0	377	13	Q9IAE1	Q9IAE1 pollimyrus
26	33	100.0	377	13	Q9IAE0	Q9IAE0 pollimyrus
27	33	100.0	377	13	Q9IAD9	Q9IAD9 stomatorhin
28	33	100.0	377	13	Q9IAD8	Q9IAD8 stomatorhin
29	33	100.0	377	13	Q9IAD7	Q9IAD7 stomatorhin
30	33	100.0	377	13	Q9IAD6	Q9IAD6 stomatorhin
31	33	100.0	377	13	Q9IAD5	Q9IAD5 stomatorhin
32	33	100.0	721	10	Q9FRN4	Q9FRN4 oryza sativ
33	33	100.0	1028	5	Q8SXA6	Q8SXA6 drosophila
34	33	100.0	1043	16	Q97E41	Q97E41 clostridium
35	33	100.0	1254	5	Q9VF51	Q9VF51 drosophila
36	30	90.9	77	2	Q9SAW3	Q9SAW3 escherichia
37	30	90.9	79	2	Q9WTF7	Q9WTF7 escherichia
38	30	90.9	79	16	Q9JMR3	Q9JMR3 escherichia
39	30	90.9	86	2	Q9ZGR9	Q9ZGR9 escherichia
40	30	90.9	175	10	Q8RKS1	Q8RKS1 arabidopsis
41	30	90.9	253	2	Q32816	Q32816 lactococcus
42	30	90.9	272	8	Q9G7X3	Q9G7X3 phylotrypes
43	30	90.9	285	17	Q8U3V4	Q8U3V4 pyrococcus
44	30	90.9	298	16	Q925X5	Q925X5 listeria in
45	30	90.9	314	4	Q9BTL6	Q9BTL6 homo sapien

ALIGNMENTS

RESULT 1

Q9HN48	PRELIMINARY;	PRT;	67 AA.
ID	Q9HN48		
AC	Q9HN48		
DT	01-MAR-2001 (TRENBLrel. 16, Created)		
DT	01-MAR-2001 (TRENBLrel. 16, Last sequence update)		
DT	01-JUN-2001 (TRENBLrel. 17, Last annotation update)		
DE	Vng2253h.		
GN	VNG2253H.		
OS	Halobacterium sp. (strain NRC-1).		
OC	Archaea; Euryarchaeota; Halobacteria; Halobacteriales;		
OC	Halobacteriaceae; Halobacterium.		
OX	NCBI_TaxID=64091;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20504483; PubMed=11016950;		
RA	Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,		
RA	Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,		
RA	Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,		
RA	Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,		
RA	Maddock G.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,		
RA	Iseebarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,		
RA	Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,		
RA	Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;		
RL	"Genome sequence of Halobacterium species NRC-1.;"		
DR	EMBL; A005110; U.S.A. 97:12176-12181(2000).		
KW	Complete proteome.		
SQ	SEQUENCE 67 AA; 6601 MW; A6BAF23FCBB8B648 CRC64;		

Query Match 100.0%; Score 33; DB 17; Length 67;

Best Local Similarity 100.0%; Pred. No. 41;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYMS 5

Db 59 GYMS 63

```
RESULT 2
Q91867
ID Q91867 PRELIMINARY; PRT; 377 AA.
AC Q91867;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Campylobacterium tamandua.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Campylomormyrus.
OX NCBI_TaxID=91719;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidae;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201625; AAF43336.1; -.
DR EMBL; AF201624; AAF43335.1; -.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41387 MW; D52A9E361A56AB43 CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 368 GYWS 372

RESULT 3
Q91A86
ID Q91A86 PRELIMINARY; PRT; 377 AA.
AC Q91A86;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Boulengeromyrus knoepffleri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Boulengeromyrus.
OX NCBI_TaxID=91717;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidae;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201616; AAF43327.1; -.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41428 MW; B60EDB613EA0FDBE CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 368 GYWS 372
```

```
RESULT 4
Q91AH4
ID Q91AH4 PRELIMINARY; PRT; 377 AA.
AC Q91AH4;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Brienomyrus hopkinsi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Brienomyrus.
OX NCBI_TaxID=112141;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidae;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201618; AAF43329.1; -.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41403 MW; 0A4599C6604C8123 CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 368 GYWS 372

RESULT 5
Q91AH3
ID Q91AH3 PRELIMINARY; PRT; 377 AA.
AC Q91AH3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Brienomyrus longicaudatus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Brienomyrus.
OX NCBI_TaxID=112142;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidae;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201619; AAF43330.1; -.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1
FT NON_TER 377
SQ SEQUENCE 377 AA; 41403 MW; 0A4599C6604C8123 CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 368 GYWS 372

RESULT 6
```



```
Q9IAH2
ID Q9IAH2 PRELIMINARY; PRT; 377 AA.
AC Q9IAH2;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Brienomyrus niger.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Brienomyrus.
OX NCBI_TaxID=42637;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201620; AAF43331.1; -.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1 377
FT NON_TER 377 377
SQ SEQUENCE 377 AA; 41522 MW; 2E93DC79A8B6EC4A CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 368 GYWS 372

RESULT 7
Q9IAH1
ID Q9IAH1 PRELIMINARY; PRT; 377 AA.
AC Q9IAH1;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Brienomyrus sp. CU79740.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Brienomyrus.
OX NCBI_TaxID=112278;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201621; AAF43332.1; -.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1 377
FT NON_TER 377 377
SQ SEQUENCE 377 AA; 41475 MW; 735853EEA67408FE CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 368 GYWS 372

RESULT 8
Q9IAH0
ID Q9IAH0 PRELIMINARY; PRT; 377 AA.
AC Q9IAH0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Campylomormyrus numenius.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Campylomormyrus.
OX NCBI_TaxID=112143;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201622; AAF43333.1; -.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1 377
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SQ SEQUENCE 377 AA; 41360 MW; C0E574061A4C986A CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 368 GYWS 372

RESULT 9
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ID Q9IAG9 PRELIMINARY; PRT; 377 AA.
AC Q9IAG9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Recombination-activating protein 2 (Fragment).
OS Campylomormyrus sp. JPS1-2000.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
OC Osteoglossiformes; Mormyridae; Campylomormyrus.
OX NCBI_TaxID=112279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20115608; PubMed=10648209;
RA Sullivan J.P., Lavoue S., Hopkins C.D.;
RT "Molecular systematics of the African electric fishes (Mormyroidea;
RT Teleostei) and a model for the evolution of their electric organs.";
RL J. Exp. Biol. 203:665-683(2000).
DR EMBL; AF201623; AAF43334.1; -.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON_TER 1 377
FT NON_TER 377 377
SQ SEQUENCE 377 AA; 41357 MW; DDA7ED06162C799A CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
DB 368 GYWS 372

RESULT 10
Q9IAG7
ID Q9IAG7 PRELIMINARY; PRT; 377 AA.
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AC Q91AG7;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Genomyrus donnyi.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Genomyrus.
 OX NCBI_TaxID=89589;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201627; AAF43338.1; -.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1
 FT NON_TER 377
 SQ SEQUENCE 377 AA; 41287 MW; F43A9AFC686C0F67 CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYVMS 5
 Db 368 GYVMS 372
 RESULT 11
 Q91AG6
 ID Q91AG6 PRELIMINARY; PRT; 377 AA.
 AC Q91AG6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Gnathonemus petersii.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Gnathonemus.
 OX NCBI_TaxID=42645;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201628; AAF43339.1; -.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
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 FT NON_TER 377
 SQ SEQUENCE 377 AA; 41372 MW; 2406A9E13FE299F CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYVMS 5
 Db 368 GYVMS 372
 RESULT 12
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 ID Q91AG4 PRELIMINARY; PRT; 377 AA.
 AC Q91AG4;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Hippopotamyrus discorhynchus (Zambezi parrotfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Hippopotamyrus.
 OX NCBI_TaxID=112147;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201630; AAF43341.1; -.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
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 SQ SEQUENCE 377 AA; 41293 MW; 9F7C51AF898736C4 CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYVMS 5
 Db 368 GYVMS 372
 RESULT 13
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 ID Q91AG3 PRELIMINARY; PRT; 377 AA.
 AC Q91AG3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Hippopotamyrus pictus.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Hippopotamyrus.
 OX NCBI_TaxID=112148;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the African electric fishes (Mormyroidea: Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683(2000).
 DR EMBL; AF201631; AAF43342.1; -.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1
 FT NON_TER 377
 SQ SEQUENCE 377 AA; 41491 MW; 1BE26037590CA937 CRC64;
 Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYVMS 5
 Db 368 GYVMS 372
 RESULT 14
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 ID Q91AG2 PRELIMINARY; PRT; 377 AA.
 AC Q91AG2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Hippopotamyrus wilverthi.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Hippopotamyrus.
 OX NCBI_TaxID=112149;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the African electric fishes (Mormyroidea;
 RT Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683 (2000).
 DR EMBL; AF201632; AAF43343.1; -.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1
 FT NON_TER 377 377
 SQ SEQUENCE 377 AA; 41285 MW; C62A314A621D3AEE CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
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 Db 368 GYWMS 372

RESULT 15

Q9IAG1
 ID Q9IAG1 PRELIMINARY; PRT; 377 AA.
 AC Q9IAG1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Recombination-activating protein 2 (Fragment).
 OS Hyperopisus bebe.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteoglossomorpha;
 OC Osteoglossiformes; Mormyridae; Hyperopisus.
 OX NCBI_TaxID=91725;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20115608; PubMed=10648209;
 RA Sullivan J.P., Lavoue S., Hopkins C.D.;
 RT "Molecular systematics of the African electric fishes (Mormyroidea;
 RT Teleostei) and a model for the evolution of their electric organs.";
 RL J. Exp. Biol. 203:665-683 (2000).
 DR EMBL; AF201633; AAF43344.1; -.
 DR InterPro; IPR004321; RAG2.
 DR Pfam; PF03089; RAG2; 1.
 FT NON_TER 1
 FT NON_TER 377 377
 SQ SEQUENCE 377 AA; 41324 MW; C35A2BBE34EF6FC CRC64;

Query Match 100.0%; Score 33; DB 13; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWMS 5
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 Db 368 GYWMS 372

Search completed: April 22, 2003, 12:53:50
 Job time : 11 secs

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:45:19 ; Search time 12.6786 seconds
(without alignments)
52.550 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33

Sequence: 1 GYVMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	5	21	Light chain CDR H1
2	33	100.0	137	21	Mouse anti-CD23 MA
3	33	100.0	444	21	Humanised anti-CD2
4	33	100.0	1254	22	Drosophila melanog
5	30	90.9	40	22	Novel human diagno
6	30	90.9	43	17	V39, monoclonal an
7	30	90.9	64	20	Human secreted pro
8	30	90.9	181	20	Chlamydia pneumoni
9	30	90.9	210	22	Novel signal trans
10	30	90.9	242	21	Rat HT glycoprotei

11	30	90.9	242	22	AA556053	Skin cell protein,
12	30	90.9	242	23	ABB72253	Rat protein isolat
13	30	90.9	242	23	ABB72250	Rat protein isolat
14	30	90.9	242	23	ABB72301	Staphylococcus epi
15	30	90.9	243	23	ABP39269	Enterococcus faeca
16	30	90.9	310	22	AAU35317	GALV retrovirus su
17	30	90.9	310	22	AA119867	Lactococcus lactis
18	30	90.9	315	23	ABB55045	Arabidopsis thalia
19	30	90.9	359	21	AA131982	Activating polyep
20	30	90.9	374	22	AA119870	Arabidopsis thalia
21	30	90.9	379	21	AA131981	Human secreted pro
22	30	90.9	392	21	AA138394	Amino acid sequenc
23	30	90.9	420	20	AA113362	EGF-like homologue
24	30	90.9	420	20	AA105281	Human PRO214 prote
25	30	90.9	420	21	AA124396	Human PRO214 amino
26	30	90.9	420	21	AA188569	Human polypeptide
27	30	90.9	420	22	AA139899	Human PRO214 polyp
28	30	90.9	420	22	AA112316	PRO214. Homo sapi
29	30	90.9	420	22	AA168594	Human PRO214 prote
30	30	90.9	420	22	AA180230	Human TANGO 206 po
31	30	90.9	420	22	AA148106	Mouse TANGO 206 po
32	30	90.9	420	22	AA148110	Human TANGO 206 va
33	30	90.9	420	22	AA148133	Human TANGO 206 va
34	30	90.9	420	22	AA148134	Human TANGO 206 va
35	30	90.9	420	22	AA148135	Human TANGO 206 va
36	30	90.9	420	22	AA148136	Mouse TANGO 206 va
37	30	90.9	420	22	AA148137	Mouse TANGO 206 va
38	30	90.9	420	22	AA148138	Mouse TANGO 206 va
39	30	90.9	420	22	AA127228	Human EXMAD-6 SQ
40	30	90.9	420	23	AB195431	Human angiogenesis
41	30	90.9	420	23	AB184825	Human PRO214 prote
42	30	90.9	420	23	AA183652	Human PRO protein,
43	30	90.9	448	21	AA137919	Streptococcus pneu
44	30	90.9	449	21	AA181542	Streptococcus pneu
45	30	90.9	451	23	AB125569	Streptococcus poly

ALIGNMENTS

RESULT 1

AA132257

ID AA132257 standard; Peptide; 5 AA.

XX AA132257;

AC AA132257;

XX

DT 15-FEB-2000 (first entry)

XX

DE Light chain CDR H1 of mouse anti-CD23 MAb C11.

XX

KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;

KW monoclonal antibody; chimeric antibody; humanised antibody;

KW complementarity determining region; CDR; autoimmune disease;

KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;

KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

KW urticaria; nephrotic syndrome; glomerulonephritis;

KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;

KW Sjogren's syndrome; allergy; rhinitis; eczema; insulinitis;

KW graft-versus-host disease; COPD; bronchitis; diabetes;

KW B-cell malignancy; therapy.

XX

OS Mus musculus.

XX

PN WO9958679-A1.

XX

PD 18-NOV-1999.

XX

PF 07-MAY-1999; 99WO-GB01434.

XX

PR 09-MAY-1998; 98GB-0009839.

XX

PA (GLAX) GLAXO GROUP LTD.

XX

FH Key Location/Qualifiers
 FT Region 1..30
 FT /note= "framework region 1"
 FT Region 31..35
 FT /note= "CDR 1"
 FT Region 36..49
 FT /note= "framework region 2"
 FT Region 50..68
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 FT Region 69..100
 FT /note= "framework region 3"
 FT Region 101..103
 FT /note= "CDR 3"
 FT Region 104..111
 FT /note= "framework region 4"
 FT Region 112..444
 FT /note= "constant region"
 XX
 PN WO9958679-A1.
 XX
 PD 18-NOV-1999.
 XX
 PP 07-MAY-1999; 99WO-GB01434.
 XX
 PR 09-MAY-1998; 98GB-0009839.
 XX
 PA (GLAX) GLAXO GROUP LTD.
 XX
 PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX
 DR WPI: 2000-053101/04.
 DR N-PSDB; AAZ34748.
 XX
 FT Cell receptor specific antibodies useful for treating e.g. arthritis,
 FT diabetes, multiple sclerosis and psoriasis -
 PS Claim 9; Fig 4; 81pp; English.
 XX
 CC This amino acid sequence represents the heavy chain of humanised
 CC anti-CD23 (FCER1) monoclonal antibody C11, composed of a human
 CC framework (HSGKRVII) and the heavy chain complementarity
 CC determining regions (see AY32257-59) of murine antibody C11. The
 CC DNA was constructed by splice overlap PCR. The invention provides
 CC altered antibodies, such as chimeric or humanised antibodies, which
 CC comprise sufficient of the amino acid sequences of the C11 light
 CC and heavy chain complementarity determining regions to render them
 CC capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble
 CC CD23 formation in human therapy, for the treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.
 XX
 SQ Sequence 444 AA;
 Query Match 100.0%; Score 33; DB 21; Length 444;
 Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 DB 31 GYWS 35
 RESULT 4
 ABB62006

ID ABB62006 standard; Protein; 1254 AA.
 AC ABB62006;
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 12810.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KM pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09231.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 FI
 DR WPI: 2001-656860/75.
 DR N-PSDB; ABL06109.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 12810; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 1254 AA;
 Query Match 100.0%; Score 33; DB 22; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWS 5
 DB 1139 GYWS 1143
 RESULT 5
 ABB07533
 ID ABB07533 standard; Protein; 40 AA.
 XX
 AC ABB07533;
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #7524.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.

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PN WO200175067-A2.
XX
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS71720.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID No 37892; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAG0010-AAG3037 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX SQ Sequence 40 AA;
XX
XX Query Match 90.9%; Score 30; DB 22; Length 40;
XX Best Local Similarity 80.0%; Pred. No. 71;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GYWS 5
XX |||||
XX Db 33 GYWS 37
XX
XX RESULT 6
XX AAR35472
XX ID AAR95472 standard; peptide; 43 AA.
XX
XX AAR95472;
XX
XX 05-NOV-1996 (first entry)
XX
XX V39, monoclonal antibody SM-3 derived antigen binding peptide.
XX
XX Abtide; prostate specific mucin antigen; human prostate cancer; LNCAp;
XX diagnostic; detection; imaging; tumour; phage; peptide library; breast;
XX polymorphic; epithelial.
XX
XX Synthetic.
XX
XX WO9609411-A1.
XX

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XX 28-MAR-1996.
XX
XX 20-SEP-1995; 95WO-US11934.
XX
XX 07-JUN-1995; 95US-0488161.
XX
XX 21-SEP-1994; 94US-0310192.
XX
XX (CYTO-) CYTOGEN CORP.
XX
XX Alvarez VL;
XX
XX WPI; 1996-188471/19.
XX
XX New isolated peptide(s) with specific binding activities - obtd. by
XX screening random peptide libraries, for use in diagnostic and
XX therapeutic compns.
XX
XX Claim 38; Page 75; 106pp; English.
XX
XX AAR95459-R95509 are antigen binding peptides ("abrides") derived from
XX the monoclonal antibody SM-3 which recognises a specific polymorphic
XX epithelial mucin tumour antigen found on human breast cancer cells.
XX The abrides are identified from random peptide libraries using
XX specific ligand binding. Abrides mimic the binding specificity of
XX large molecules such as antibodies and receptors but have a much
XX smaller size allowing their production at a lower cost and reducing
XX the extent of their immunogenicity aiding in vivo delivery. The
XX abrides are useful for the diagnosis, detection, imaging and
XX treatment of disease, e.g. tumours, prostate cancer and breast
XX cancer.
XX
XX SQ Sequence 43 AA;
XX
XX Query Match 90.9%; Score 30; DB 17; Length 43;
XX Best Local Similarity 80.0%; Pred. No. 77;
XX Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GYWS 5
XX |||||
XX Db 6 GYWS 10
XX
XX RESULT 7
XX AAY07813
XX ID AAY07813 standard; Protein; 64 AA.
XX
XX AAY07813;
XX
XX 06-JUL-1999 (first entry)
XX
XX Human secreted protein fragment encoded from gene 70.
XX
XX Human; secreted protein; prevention; treatment; protein therapy;
XX gene therapy; diagnosis; cancer; tumour; neurodegenerative disorder;
XX developmental abnormality; foetal deficiency; blood disorder; lymphoma;
XX leukemia; immune system disorder; autoimmune disease; hepatic disease;
XX renal disease; inflammation; allergy; asthma; sepsis; diabetes; AIDS;
XX Alzheimer's disease; cognitive disorder; schizophrenia; osteoporosis;
XX arthritis; psoriasis; digestive; endocrine; infection.
XX
XX Homo sapiens.
XX
XX WO9909155-A1.
XX
XX 25-FEB-1999.
XX
XX 18-AUG-1998; 98WO-US17044.
XX
XX 16-JUN-1998; 98US-0092956.
XX
XX 15-JUL-1998; 98US-0092956.
XX
XX 19-AUG-1997; 97US-0056368.
XX
XX 19-AUG-1997; 97US-0056368.
XX

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PR 19-AUG-1997; 97US-0056535.
PR 19-AUG-1997; 97US-0056555.
PR 19-AUG-1997; 97US-0056556.
PR 19-AUG-1997; 97US-0056628.
PR 19-AUG-1997; 97US-0056629.
PR 19-AUG-1997; 97US-0056726.
PR 19-AUG-1997; 97US-0056728.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Brewer LA, Duan R, Ebner R, Endress GA, Feng P;
PI Florence C, Florence KA, Komatsoulis GA, Lafleur DW;
PI Moore PA, Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR;
PI Young PE;
XX
XX WPI; 1999-190160/16.
DR N-PSDB; AAX37438.
XX
XX New isolated human genes and the secreted polypeptides they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1b; Page 264; 280pp; English.
PS
XX This invention describes novel isolated human secreted proteins and
CC their encoding nucleic acid sequences. The products of the invention
CC are useful for preventing, treating or ameliorating medical conditions
CC e.g. by protein or gene therapy. Also pathological conditions can be
CC diagnosed by determining the presence or amount of expression of
CC the new polypeptides in a sample or by determining the presence or
CC absence of mutations in the new polynucleotides. Specific uses are
CC described for each of the 70 polynucleotides, based on which tissues
CC they are most highly expressed in, and include developing products for
CC the diagnosis or treatment of cancer, tumours, neurodegenerative
CC disorders, developmental abnormalities and foetal deficiencies, blood
CC disorders, leukemias, diseases of the immune system, autoimmune
CC diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC asthma, sepsis, diabetes, Alzheimer's and cognitive disorders,
CC schizophrenia, osteoporosis, arthritis, psoriasis, digestive/endocrine
CC disorders, infections and AIDS. The human secreted proteins of the
CC invention are represented in AAX07744-Y07850 and the encoding nucleic
CC acids are represented in AAX37369-X37441.
XX
SQ Sequence 64 AA;
Query Match 90.9%; Score 30; DB 20; Length 64;
Best Local Similarity 80.0%; Pred. No. 1.2e+02; Mismatches 0; Gaps 0;
Matches 4; Conservative 1; Indels 0;

QY 1 GYVMS 5
Db 45 GYVLS 49
|||:|
|||:|

RESULT 8
AAX35482
ID AAY35482 standard; Protein; 181 AA.
XX
XX AAY35482;
AC
XX
XX 13-SEP-1999 (first entry)
DT
XX
XX Chlamydia pneumoniae transmembrane protein sequence.
DE
XX
XX Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;
KW vaccine; neutralising epitope.
XX
XX Chlamydia pneumoniae.
OS
XX
XX WO927105-A2.
PN
XX
XX 03-JUN-1999.
PD

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XX 20-NOV-1998; 98WO-IB01890.
PF
XX 04-NOV-1998; 98US-0107078.
PR 21-NOV-1997; 97FR-0014673.
XX
XX (GEST ) GENSET.
PA
XX Griffais R;
PI
XX WPI; 1999-357842/30.
DR
XX Genome sequence of Chlamydia pneumoniae
PT
XX Page 1244; Disclosure; 1912pp; English.
PS
XX AAY34584-V35879 represent the proteins encoded by all the open reading
CC frames in the complete genome (see AAX9190) of Chlamydia pneumoniae.
CC C. pneumoniae causes respiratory disease such as pneumonia and
CC bronchitis and is thought to be a contributing factor in heart
CC disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584-V35879) can be used in
CC immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotide sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae.
XX
XX Sequence 181 AA;
SQ
Query Match 90.9%; Score 30; DB 20; Length 181;
Best Local Similarity 80.0%; Pred. No. 3.3e+02; Mismatches 0; Gaps 0;
Matches 4; Conservative 1; Indels 0;

QY 1 GYVMS 5
Db 48 GYVLS 52
|||:|
|||:|

RESULT 9
AAU17327
ID AAU17327 standard; Protein; 210 AA.
XX
XX AAU17327;
AC
XX
XX 07-NOV-2001 (first entry)
DT
XX
XX Novel signal transduction pathway protein, Seq ID 892.
DE
XX
XX Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour;
KW antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer;
KW immune system disorder; rheumatoid arthritis; inflammatory condition;
KW organ transplant rejection; infection; hepatitis C; blood disorder;
KW sickle cell anaemia; hyperproliferative disorder; Gaucher's disease;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW chromosomal abnormality; Down syndrome; ischaemia; renal disorder;
KW cardiovascular; respiratory; wound healing; endocrine; Addison's disease;
KW reproductive system; gastrointestinal; liver disorder; AIDS;
KW acquired immune deficiency syndrome.
XX
XX Homo sapiens.
OS
XX
XX WO200154733-A1.
PN
XX
XX 02-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01312.
PF
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR

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PR 17-MAR-2000; 2000US-0190076.
 PR 18-APR-2000; 2000US-0198123.
 PR 19-MAY-2000; 2000US-0205515.
 PR 07-JUN-2000; 2000US-0209467.
 PR 28-JUN-2000; 2000US-0214886.
 PR 30-JUN-2000; 2000US-0215135.
 PR 07-JUL-2000; 2000US-0216647.
 PR 07-JUL-2000; 2000US-0218880.
 PR 11-JUL-2000; 2000US-0217487.
 PR 11-JUL-2000; 2000US-0217496.
 PR 14-JUL-2000; 2000US-0218290.
 PR 26-JUL-2000; 2000US-0220963.
 PR 26-JUL-2000; 2000US-0220964.
 PR 14-AUG-2000; 2000US-0224518.
 PR 14-AUG-2000; 2000US-0224519.
 PR 14-AUG-2000; 2000US-0225213.
 PR 14-AUG-2000; 2000US-0225214.
 PR 14-AUG-2000; 2000US-0225266.
 PR 14-AUG-2000; 2000US-0225267.
 PR 14-AUG-2000; 2000US-0225268.
 PR 14-AUG-2000; 2000US-0225270.
 PR 14-AUG-2000; 2000US-0225447.
 PR 14-AUG-2000; 2000US-0225757.
 PR 14-AUG-2000; 2000US-0225758.
 PR 14-AUG-2000; 2000US-0225759.
 PR 18-AUG-2000; 2000US-0226279.
 PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 23-AUG-2000; 2000US-0227182.
 PR 30-AUG-2000; 2000US-0227009.
 PR 01-SEP-2000; 2000US-0228287.
 PR 01-SEP-2000; 2000US-0228287.
 PR 01-SEP-2000; 2000US-0228343.
 PR 01-SEP-2000; 2000US-0228344.
 PR 01-SEP-2000; 2000US-0228345.
 PR 05-SEP-2000; 2000US-0228509.
 PR 06-SEP-2000; 2000US-0228513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 08-SEP-2000; 2000US-0232081.
 PR 12-SEP-2000; 2000US-0231968.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234597.
 PR 25-SEP-2000; 2000US-0234598.
 PR 26-SEP-2000; 2000US-0235484.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.

PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.
 PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249264.
 PR 17-NOV-2000; 2000US-0249285.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PR (HUMA-) HUMAN GENOME SCI INC.
 PR Rosen CA, Barash SC, Ruben SM;
 PR WPI; 2001-465460/50.
 PR N-PSDB; AAS27244.
 PR Novel polypeptides useful for diagnosing, treating, preventing and/or
 PT prognosing disorders related to the proteins, including cancers, immune
 PT disorders and neuronal disorders -
 PR Claim 1; SEQ ID No 892; 880pp; English.
 PR The invention relates to novel isolated polypeptides (I), and
 CC

polynucleotides (II). (I), (II) and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthritis), inflammatory conditions, organ transplant rejections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (sickle cell anaemia), myeloproliferative disorders, primary haematopoietic disorders, hyperproliferative disorders (e.g. Gaucher's disease and cancer), neurodegenerative disorders (e.g. Alzheimer's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), ischaemic injury (e.g. stroke), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders, in wound healing, epithelial cell proliferation, endocrine disorders (e.g. Addison's disease), reproductive system disorders, gastrointestinal disorder (inflammatory disorders), liver disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAU17059-AAU17683 represent novel signal transduction pathway protein, amino acid sequences of the invention.

Query Match	90.9%;	Score 30;	DB 22;	Length 210;
Best Local Similarity	80.0%;	Pred. No. 3.9e+02;		
Matches	4;	Conservative	1;	Mismatches 0;
			Indels	0;
			Gaps	0;

Qy	1	GYWMS	5
		:	
Db	68	GYWLS	72

RESULT 10
AAV76114
ID AAV76114 standard: Protein: 242 AA.

AA
AC
AAAY76114;

27-MAR-2000 (first entry)

XX
DE Rat HT glycoprotein homologue, SEO ID NO:393.

Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast;
 embryonic skin cell; keratinocyte stem cell; transit amplifying cell;
 secreted; transmembrane; inflammation; cancer; neurological disease;
 angiogenesis; tumour vascularisation; growth disorder;
 developmental disorder; skin wound; hair follicle disorder;
 anti-inflammatory; cytostatic; neuroprotective; vulvury.

XX OS Rattus sp.

XX
PN
W09955865-A1-XX
PD
04-NOV-1999.XX
DE 29-APP-1999.

XX
DE
DE
20-222-1000-
98115-0069726

PR 09-NOV-1998; 98US-0188930.

PA (GENE-) GENESIS RES & DEV CO

PI Strachan L, Sleeman M, Watson JD,

AA
DR WPI; 2000-072177/06.

DR N-PSDB; AA261822.
XX

PT Novel polynucleotides useful for the treatment of various conditions including wounds and cancer -

XX
 00
 01-10 4. Page 000. English

XX
The following information was derived from rat

dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences AAY75942-Y76123 represent polypeptides encoded by cDNA sequences derived from several mouse, rat or human skin cell types. Sequences AAY75942-Y75947, AAY76020-Y76031, AAY76094-Y76104 and AAY76119 are proteins with an N-terminal signal sequence, indicating that they are secreted. Sequences AAY75986-Y75989, AAY76061-Y76071, AAY76106-Y76109 and AAY76121-Y76122 are proteins with one or more putative transmembrane domains.

AA	Sequence	242 AA;
SO		

Query Match 90.9%; Score 30; DB 21; Length 242;
Best Local Similarity 80.0%; Pred. No. 4.4e+02;
Matches 4: Conservative 1; Mismatches 0; Indels

QY 1 GYWS 5
|||:
Db 224 GYWS 228

RESULT 11
AAB56053
ID AAB56053 standard: Protein: 242 AA.

AA
AC AAB56053;

XX DT 08-MAR-2003 (first entry)

XX DE skin cell protein. SFO TD NO: 393.

XX Rat; skin cell; cytostatic; antiinflammatory; anti-HIV;
KW neotropic; neuroprotective; vulnary; immunomodulatory; vaccine;
KW keratinocyte growth stimulation; cancer; angiogenesis inhibition;
KW inflammation; neurological disease.

AA Rattus sp.

XX
PN
WQ200069884-A2.XX
PD
23-NOV-2000XX
15 MAY 2000

XX 00000 0312202

XX

XXXXXX

XX
17
"PROV. CO, SHERIFFS OFFICE"
"17-11-1964"

DR N-PSDB; AAC99755.

XX New isolated polynucleotide used in the identification of genetic
PT disorders and encoding polypeptides used for treating inflammatory
PT disease, cancer and neurological diseases -
PT

XX
P9= Claim 4: Page 297-298; 352pp; English.

The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV-1) to leukocytes, and treating inflammatory disease, cancer and

CC neurological diseases. The polynucleotide can be used as a marker, in
 CC the identification of genetic disorders, and for the design of
 CC oligonucleotides for examining expression patterns.

XX SQ Sequence 242 AA;

Query Match 90.9%; Score 30; DB 22; Length 242;
 Best Local Similarity 80.0%; Pred. NO. 4.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVMS 5
 |||:|
 Db 224 GYVLS 228

RESULT 12

ABB72253
 ID ABB72253 standard; Protein; 242 AA.

XX AC ABB72253;

XX DT 04-APR-2002 (first entry)

XX DE Rat protein isolated from skin cells SEQ ID NO: 393.

XX KW Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
 KW developmental defect; inflammatory disease; dermatological; vulnary;
 KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.

XX OS Rattus sp.

XX PN WO200190357-A1.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-NZ00099.

XX PR 24-MAY-2000; 2000US-206650P.

XX PR 25-JUL-2000; 2000US-221232P.

XX PA (GENE-) GENESIS RES & DEV CORP LTD.

XX PI Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
 XX WPI; 2002-122020/16.

XX PT New polynucleotides and polypeptides encoded by the polynucleotides
 PT isolated from skin cells, useful for treating skin wounds, cancers,
 PT growth and developmental defects, inflammatory diseases, or for
 PT modulating immune responses -

XX PS Example 2; Page 246-247; 466pp; English.

XX CC The present invention provides the protein and coding sequences of cDNAs
 CC isolated from human, murine and rat skin cell libraries. The sequences
 CC can be used in the development of therapeutic agents useful in the
 CC treatment of skin diseases, including skin wounds, cancer, growth
 CC defects, developmental defects and inflammatory diseases. The proteins
 CC have important roles in the induction of hair growth, cell proliferation
 CC and cell-cell interaction, in maintaining tissue integrity, in wound
 CC healing and in modulating immune responses. The present sequence is a
 CC polypeptide of the invention.

XX SQ Sequence 242 AA;

Query Match 90.9%; Score 30; DB 23; Length 242;
 Best Local Similarity 80.0%; Pred. NO. 4.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVMS 5
 |||:|
 Db 224 GYVLS 228

RESULT 13

ABB72290
 ID ABB72290 standard; Protein; 242 AA.

XX AC ABB72290;

XX DT 04-APR-2002 (first entry)

XX DE Rat protein isolated from skin cells SEQ ID NO: 502.

XX KW Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
 KW developmental defect; inflammatory disease; dermatological; vulnary;
 KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.

XX OS Rattus sp.

XX PN WO200190357-A1.

XX PD 29-NOV-2001.

XX PF 24-MAY-2001; 2001WO-NZ00099.

XX PR 24-MAY-2000; 2000US-206650P.

XX PR 25-JUL-2000; 2000US-221232P.

XX PA (GENE-) GENESIS RES & DEV CORP LTD.

XX PI Watson JD, Strachan L, Sleeman M, Onrust R, Murison JG, Kumble KD;
 XX WPI; 2002-122020/16.

XX PT New polynucleotides and polypeptides encoded by the polynucleotides
 PT isolated from skin cells, useful for treating skin wounds, cancers,
 PT growth and developmental defects, inflammatory diseases, or for
 PT modulating immune responses -

XX PS Claim 4; Page 308; 466pp; English.

XX CC The present invention provides the protein and coding sequences of cDNAs
 CC isolated from human, murine and rat skin cell libraries. The sequences
 CC can be used in the development of therapeutic agents useful in the
 CC treatment of skin diseases, including skin wounds, cancer, growth
 CC defects, developmental defects and inflammatory diseases. The proteins
 CC have important roles in the induction of hair growth, cell proliferation
 CC and cell-cell interaction, in maintaining tissue integrity, in wound
 CC healing and in modulating immune responses. The present sequence is a
 CC polypeptide of the invention.

XX SQ Sequence 242 AA;

Query Match 90.9%; Score 30; DB 23; Length 242;

Best Local Similarity 80.0%; Pred. NO. 4.4e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVMS 5

|||:|
 Db 224 GYVLS 228

RESULT 14

ABB72301
 ID ABB72301 standard; Protein; 242 AA.

XX AC ABB72301;

XX DT 04-APR-2002 (first entry)

XX DE Rat protein isolated from skin cells SEQ ID NO: 625.

XX KW Human; rat; mouse; skin cell; skin wound; cancer; growth defect;
 KW developmental defect; inflammatory disease; dermatological; vulnary;
 KW immunomodulator; anti-inflammatory; cytostatic; neuroprotective.

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	30	90.9	64	9	US-10-144-929-162	Sequence 162, App
2	30	90.9	210	9	US-09-764-868-892	Sequence 892, App
3	30	90.9	242	9	US-09-866-050A-393	Sequence 393, App
4	30	90.9	242	9	US-09-866-050A-502	Sequence 502, App
5	30	90.9	242	9	US-09-866-050A-625	Sequence 625, App
6	30	90.9	310	10	US-09-815-242-10910	Sequence 10910, A
7	30	90.9	392	9	US-10-050-704-180	Sequence 180, App
8	30	90.9	392	9	US-10-144-929-156	Sequence 156, App
9	30	90.9	420	9	US-09-905-231A-109	Sequence 109, App
10	30	90.9	420	9	US-09-902-853A-109	Sequence 109, App
11	30	90.9	420	9	US-09-907-824-109	Sequence 109, App
12	30	90.9	420	9	US-09-907-841-109	Sequence 109, App
13	30	90.9	420	9	US-09-904-011-109	Sequence 109, App
14	30	90.9	420	9	US-10-028-072-290	Sequence 290, App
15	30	90.9	420	9	US-09-906-742-109	Sequence 109, App
16	30	90.9	420	9	US-10-121-049-290	Sequence 290, App
17	30	90.9	420	9	US-10-123-904-290	Sequence 290, App
18	30	90.9	420	9	US-10-140-470-290	Sequence 290, App
19	30	90.9	420	9	US-09-796-753-84	Sequence 84, Appl

RESULT 2
US-09-764-868-892
; Sequence 892, Application US/09764868
; Patent No. US2002016871A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

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; FILE REFERENCE: PT332
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 892
; LENGTH: 210
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-868-892
```

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Query Match          90.9%; Score 30; DB 9; Length 210;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GYWMS 5
    |||:|
Db 68 GYWLS 72
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RESULT 3

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US-09-866-050A-393
; Sequence 393, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866.050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 393
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Rat
US-09-866-050A-393
```

```
Query Match          90.9%; Score 30; DB 9; Length 242;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 GYWMS 5
    |||:|
Db 224 GYWLS 228
```

RESULT 4

```
US-09-866-050A-502
; Sequence 502, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866.050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502
```

```
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Rat
US-09-866-050A-502
```

```
Query Match          90.9%; Score 30; DB 9; Length 242;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GYWMS 5
    |||:|
Db 224 GYWLS 228
```

RESULT 5

```
US-09-866-050A-625
; Sequence 625, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866.050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 625
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Rat
US-09-866-050A-625
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```
Query Match          90.9%; Score 30; DB 9; Length 242;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GYWMS 5
    |||:|
Db 224 GYWLS 228
```

RESULT 6

```
US-09-815-242-10910
; Sequence 10910, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
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RESULT 8
US-10-144-929-156
; Sequence 156, Application US/10144929
; Publication No. US20030069405A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 70 Human Secreted Proteins
; FILE REFERENCE: P2014P1
; CURRENT APPLICATION NUMBER: US/10/144,929
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: US/09/251,329

```

, GENERAL INFORMATION:
, APPLICANT: Genentech, Inc.
, APPLICANT: Ashkenazi, Avi
, APPLICANT: Botstein, David
, APPLICANT: Desnoyers, Luc
, APPLICANT: Eaton, Dan L.
, APPLICANT: Ferrara, Napoleone
, APPLICANT: Filvaroff, Ellen
, APPLICANT: Fong, Sherman
, APPLICANT: Gao, Wei-Qiang
, APPLICANT: Gerber, Hanspeter
, APPLICANT: Gershtein, Mary E.
, APPLICANT: Goddard, A.
, APPLICANT: Godowski, Paul J.
, APPLICANT: Grimaldi, Christopher J.
, APPLICANT: Gurney, Austin L.
, APPLICANT: Hillan, Kenneth, J.
, APPLICANT: Kljavin, Ivar J.
, APPLICANT: Mather, Jennie P.
, APPLICANT: Pan, James
, APPLICANT: Paoni, Nicholas F.
, APPLICANT: Roy, Margaret Ann
, APPLICANT: Stewart, Timothy A.
, APPLICANT: Tumas, Daniel
, APPLICANT: Williams, P. Mickey
, APPLICANT: Wood, William, I.
, TITLE OF INVENTION: Secreted and Transmitted
, TITLE OF INVENTION: Acids Encoding
, FILE REFERENCE: 10466-14
, CURRENT APPLICATION NUMBER: US/09/090909
, CURRENT FILING DATE: 2003-07-12
, PRIOR APPLICATION NUMBER: PCT/US00/000000
, PRIOR FILING DATE: 2000-02-22
, PRIOR APPLICATION NUMBER: US 60/143
, PRIOR FILING DATE: 1999-07-07
, PRIOR APPLICATION NUMBER: US 60/145
, PRIOR FILING DATE: 1999-07-26
, PRIOR APPLICATION NUMBER: US 60/146
, PRIOR FILING DATE: 1999-07-28
, PRIOR APPLICATION NUMBER: PCT/US99/000000
, PRIOR FILING DATE: 1999-09-08
, PRIOR APPLICATION NUMBER: PCT/US99/000000
, PRIOR FILING DATE: 1999-09-13
, PRIOR APPLICATION NUMBER: PCT/US99/000000
, PRIOR FILING DATE: 1999-09-15

```

```

; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 109
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-291A-109

```

```

Query Match          90.9%; Score 30; DB 9; Length 420;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GYWS 5
    |||||
Db 402 GYWS 406

```

```

RESULT 10
US-09-902-853-109
; Sequence 109, Application US/09902853
; Publication No. US20020192859A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tunas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18

```

```

; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 109
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-902-853-109

```

```

Query Match          90.9%; Score 30; DB 9; Length 420;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 GYWS 5
    |||||
Db 402 GYWS 406

```

```

RESULT 11
US-09-907-824-109
; Sequence 109, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.

```

```

; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 109
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-907-824-109

```

```

Query Match          90.9%; Score 30; DB 9; Length 420;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GYWS 5
      |||||
Db      402 GYWS 406

```

```

RESULT 12
US-09-907-841-109
; Sequence 109, Application US/09907841
; Publication No. US20020198366A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone

```

```

; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 109
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-841-109

```

```

Query Match          90.9%; Score 30; DB 9; Length 420;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1 GYWS 5
      |||||
Db      402 GYWS 406

```

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RESULT 13
US-09-904-011-109
; Sequence 109, Application US/09904011
; Publication No. US20030003530A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen

```

```

; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904,011
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
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; PRIOR FILING DATE: 1999-07-28
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; PRIOR FILING DATE: 1999-09-08
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; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 109
; LENGTH: 420
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-904-011-109

Query Match          90.9%; Score 30; DB 9; Length 420;
Best Local Similarity 80.0%; Pred No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 GYWS 5
Db      402 GYWS 406

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RESULT 14
US-10-028-072-290
; Sequence 290, Application US/10028072
; Publication No. US20030004311A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang
; TITLE OF INVENTION:
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/028,072
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
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; PRIOR APPLICATION NUMBER: 60/063329
; PRIOR FILING DATE: 1997-10-27
; PRIOR APPLICATION NUMBER: 60/063550
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063561

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; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063704
 ; PRIOR FILING DATE: 1997-10-29
 ; PRIOR APPLICATION NUMBER: 60/063733
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 ; PRIOR APPLICATION NUMBER: 60/079294
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 ; PRIOR APPLICATION NUMBER: 60/079728
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; PRIOR APPLICATION NUMBER: 60/084627
 ; PRIOR FILING DATE: 1998-05-07
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 ; PRIOR FILING DATE: 1998-05-07
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 ; PRIOR FILING DATE: 1998-06-24
 ; PRIOR APPLICATION NUMBER: 60/090863
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: 60/091360
 ; PRIOR FILING DATE: 1998-07-01
 ; PRIOR APPLICATION NUMBER: 60/091519
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07

Query Match 90.9%; Score 30; DB 9; Length 420;
 Best Local Similarity 80.0%; Pred. No. 3.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
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 Db 402:GYWS 406

RESULT 15
 US-09-906-742-109
 ; Sequence 109, Application US/09906742
 ; Publication No. US20030023054A1
 ; GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherwan
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
ACIDS
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,742
PRIOR FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
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PRIOR FILING DATE: 1999-09-15
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PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 109
LENGTH: 420
TYPE: PRT
ORGANISM: Homo Sapien
US-09-906-742-109

Query Match 90.9%; Score 30; DB 9; Length 420;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0;
Gaps 0;

QY 1 GYWMS 5
|||:
Db 402 GYWLS 406

Search completed: April 22, 2003, 13:11:14
Job time : 6.26786 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:48:49 ; Search time 4.375 Seconds
(without alignments)
33.626 Million cell updates/sec

Title: US-09-674-716B-9
Perfect score: 33
Sequence: 1 GYMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	30	90.9	43	US-09-273-685-39	Sequence 39, Appl
3	30	90.9	43	PCT-US95-11934-39	Sequence 39, Appl
4	30	90.9	243	US-09-134-001C-4114	Sequence 4114, Ap
5	30	90.9	667	US-09-315-127-5	Sequence 5, Appl
6	30	90.9	667	US-09-315-127-6	Sequence 6, Appl
7	29	87.9	5	US-08-480-434-22	Sequence 22, Appl
8	29	87.9	5	US-08-480-434-31	Sequence 31, Appl
9	29	87.9	5	US-08-053-451B-22	Sequence 22, Appl
10	29	87.9	5	US-08-053-451B-31	Sequence 31, Appl
11	29	87.9	14	US-08-204-656B-11	Sequence 11, Appl
12	29	87.9	14	US-08-470-702-11	Sequence 11, Appl
13	29	87.9	14	US-08-467-831-11	Sequence 11, Appl
14	29	87.9	20	US-08-053-451B-114	Sequence 114, App
15	29	87.9	119	US-08-053-451B-125	Sequence 125, App
16	29	87.9	121	US-08-480-434-29	Sequence 29, Appl
17	29	87.9	121	US-08-053-451B-29	Sequence 29, Appl
18	29	87.9	126	US-08-480-434-18	Sequence 18, Appl
19	29	87.9	126	US-08-480-434-19	Sequence 19, Appl
20	29	87.9	126	US-08-053-451B-18	Sequence 18, Appl
21	29	87.9	126	US-08-053-451B-19	Sequence 19, Appl
22	29	87.9	679	US-09-257-536-2	Sequence 2, Appl
23	29	87.9	679	US-09-512-230-2	Sequence 2, Appl
24	28	84.8	274	US-09-570-367C-19	Sequence 19, Appl
25	28	84.8	482	US-09-134-001C-4309	Sequence 4309, Ap
26	27	81.8	5	US-08-244-626-12	Sequence 12, Appl
27	27	81.8	5	US-08-480-434-32	Sequence 32, Appl

28	27	81.8	5	2	US-08-318-157B-23	Sequence 23, Appl
29	27	81.8	5	2	US-08-053-451B-32	Sequence 32, Appl
30	27	81.8	24	4	US-08-525-539A-19	Sequence 19, Appl
31	27	81.8	98	1	US-07-942-245-37	Sequence 37, Appl
32	27	81.8	99	1	US-08-244-626-10	Sequence 10, Appl
33	27	81.8	109	1	US-07-942-245-17	Sequence 17, Appl
34	27	81.8	115	4	US-09-376-330-20	Sequence 20, Appl
35	27	81.8	116	3	US-08-483-749A-18	Sequence 18, Appl
36	27	81.8	117	1	US-07-958-140-3	Sequence 3, Appl
37	27	81.8	117	3	US-08-545-809A-95	Sequence 95, Appl
38	27	81.8	117	5	PCT-US93-09166-3	Sequence 3, Appl
39	27	81.8	119	2	US-08-318-157B-2	Sequence 2, Appl
40	27	81.8	119	2	US-08-318-157B-8	Sequence 8, Appl
41	27	81.8	119	2	US-08-318-157B-9	Sequence 9, Appl
42	27	81.8	119	2	US-08-318-157B-10	Sequence 10, Appl
43	27	81.8	119	2	US-08-318-157B-11	Sequence 11, Appl
44	27	81.8	119	2	US-08-318-157B-12	Sequence 12, Appl
45	27	81.8	119	2	US-08-318-157B-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-08-488-161-39
; Sequence 39, Application US/08488161
; Patent No. 5885577
; *GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Abtides) From
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,161
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Marrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-176
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-161-39

Query Match 90.9%; Score 30; DB 2; Length 43;
Best Local Similarity 80.0%; Pred. No. 45;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GYMS 5
DB 6 GYMLS 10

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; Sequence 39, Application US/09273685
; Patent No. 6015561
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; TITLE OF INVENTION: Antigen Binding Peptides (Aptides) From
; Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/273,685
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/488,161
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-176
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-273-685-39
Query Match 90.9%; Score 30; DB 3; Length 43;
Best Local Similarity 80.0%; Pred. No. 45;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
Db 6 GYWLS 10

RESULT 3
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; Sequence 39, Application PC/TUS9511934
; GENERAL INFORMATION:
; APPLICANT: Cycogen Corporation
; TITLE OF INVENTION: Antigen Binding Peptides (Aptides) From
; Peptide Libraries
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/11934
; FILING DATE: 20-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-196-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-11934-39
Query Match 90.9%; Score 30; DB 5; Length 43;
Best Local Similarity 80.0%; Pred. No. 45;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
Db 6 GYWLS 10

RESULT 4
US-09-134-001C-4114
; Sequence 4114, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4114
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4114
Query Match 90.9%; Score 30; DB 4; Length 243;
Best Local Similarity 80.0%; Pred. No. 2,3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
Db 52 GYWLS 56

RESULT 5
US-09-315-127-5
; Sequence 5, Application US/09315127
; Patent No. 6448390
; GENERAL INFORMATION:
; APPLICANT: The University of Tennessee, c/o Richard Cox
; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
; Liposome Vectors and Use in Gene and Drug Therapy
; FILE REFERENCE: 44137-5023, U. of Tennessee
; CURRENT APPLICATION NUMBER: US/09/315,127
```


; CURRENT FILING DATE: 1999-05-20
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 5
 ; LENGTH: 667
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 US-09-315-127-5

Query Match 90.9%; Score 30; DB 4; Length 667;
 Best Local Similarity 80.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
 Db 180 GYWS 184

RESULT 6

US-09-315-127-6
 ; Sequence 6, Application US/09315127
 ; Patent No. 6448390
 ; GENERAL INFORMATION:
 ; APPLICANT: The University of Tennessee, c/o Richard Cox
 ; TITLE OF INVENTION: Stable Envelope Proteins for Retroviral, Viral and
 ; FILE REFERENCE: 44137-5023, U. of Tennessee
 ; CURRENT APPLICATION NUMBER: US/09/315,127
 ; CURRENT FILING DATE: 1999-05-20
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 6
 ; LENGTH: 667
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: SEQ ID NO. 4,
 ; OTHER INFORMATION: envelope protein produced by retroviral vector of
 ; OTHER INFORMATION: seq. id no. 3
 US-09-315-127-6

Query Match 90.9%; Score 30; DB 4; Length 667;
 Best Local Similarity 80.0%; Pred. No. 5.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
 Db 180 GYWS 184

RESULT 7

US-08-480-434-22
 ; Sequence 22, Application US/08480434
 ; Patent No. 5811248
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles C. Dittow, et al.
 ; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
 ; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,434

; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Albert P. Halluin
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 7606-053
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 854-3660
 ; TELEFAX: (415) 854-3694
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: N
 ; ANTI-SENSE: N
 US-08-480-434-22

Query Match 87.9%; Score 29; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 2e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5
 Db 1 GYWS 5

RESULT 8

US-08-480-434-31
 ; Sequence 31, Application US/08480434
 ; Patent No. 5811248
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles C. Dittow, et al.
 ; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
 ; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,434
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Albert P. Halluin
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 7606-053
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 854-3660
 ; TELEFAX: (415) 854-3694
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 31:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: N
 ; ANTI-SENSE: N
 US-08-480-434-31

Query Match 87.9%; Score 29; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 2e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |:|:|
 Db 1 GFWS 5

RESULT 9

US-08-053-451B-22
 ; Sequence 22, Application US/08053451B
 ; Patent No. 5955584

GENERAL INFORMATION:
 ; APPLICANT: Chen, Francis W.

APPLICANT: Ditlow, Charles C.
 ; APPLICANT: Calenoff, Emanuel

TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC

TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF

NUMBER OF SEQUENCES: 176

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053.451B

FILING DATE: 26-APR-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.

REGISTRATION NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 7606-033-999

TELEPHONE: 415-854-3660

TELEFAX: 415-854-3694

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

LENGTH: 5 amino acids

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA

HYPOTHETICAL: N

ANTI-SENSE: N

US-08-053-451B-22

Query Match 87.9%; Score 29; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 2e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |:|:|
 Db 1 GFWS 5

RESULT 10

US-08-053-451B-31

; Sequence 31, Application US/08053451B

; Patent No. 5955584

GENERAL INFORMATION:

APPLICANT: Chen, Francis W.

APPLICANT: Calenoff, Emanuel

TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
 TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053.451B

FILING DATE: 26-APR-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.

REGISTRATION NUMBER: 25,227

REFERENCE/DOCKET NUMBER: 7606-033-999

TELEPHONE: 415-854-3660

TELEFAX: 415-854-3694

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

TYPE: amino acid

LENGTH: 5 amino acids

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA

HYPOTHETICAL: N

ANTI-SENSE: N

US-08-053-451B-31

Query Match 87.9%; Score 29; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 2e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWMS 5
 |:|:|
 Db 1 GFWS 5

RESULT 11

US-08-204-656B-11

; Sequence 11, Application US/08204656B

; Patent No. 5538882

GENERAL INFORMATION:

APPLICANT: Matsui, Ikuro

APPLICANT: Ishikawa, Kazuhiko

APPLICANT: Miyairi, Sachio

APPLICANT: Honda, Koichi

TITLE OF INVENTION: Variant-Type Carbohydrate Hydrolase,

TITLE OF INVENTION: Variant Gene Of The Enzyme And Method For Producing

TITLE OF INVENTION: Oligosaccharide Using The Enzyme

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Birch, Stewart, Kolasch & Birch, LLP

STREET: 8110 Gatehouse Road, Suite 500 East

CITY: Falls Church

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22042

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/204,656B
FILING DATE: 02-MAR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-204-656B-11

Query Match 87.9%; Score 29; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWM 4
|||||
DB 10 GYWM 13

RESULT 12

US-08-470-702-11
Sequence 11, Application US/08470702
Patent No. 5631149
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,702
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-470-702-11

Query Match 87.9%; Score 29; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWM 4
|||||
DB 10 GYWM 13

RESULT 13

US-08-467-831-11
Sequence 11, Application US/08467831
Patent No. 5635378
GENERAL INFORMATION:
APPLICANT: MATSUI, IKUO
APPLICANT: ISHIKAWA, KAZUHIKO
APPLICANT: MIYAIRI, SACHIO
APPLICANT: HONDA, KOICHI
TITLE OF INVENTION: VARIANT-TYPE CARBOHYDRATE HYDROLASE,
TITLE OF INVENTION: VARIANT GENE OF THE ENZYME AND METHOD FOR PRODUCING
TITLE OF INVENTION: OLIGOSACCHARIDE USING THE ENZYME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
STREET: 8110 Gatehouse Road, Suite 500 East
CITY: Falls Church
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22042
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,831
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/204,656
FILING DATE: 02-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: WEINER, MARC S.
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 234-252P
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-467-831-11

Query Match

87.9%; Score 29; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 23;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWM 4
|:|:|
Db 10 GYWM 13

RESULT 14

US-08-053-451B-114
; Sequence 114, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-053-451B-114

Query Match 87.9%; Score 29; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 33;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWM 5
|:|:|
Db 10 GYWM 14

RESULT 15

US-08-053-451B-125
; Sequence 125, Application US/08053451B
; Patent No. 5955584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-053-451B-125

Query Match 87.9%; Score 29; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWM 5
|:|:|
Db 31 GYWM 35

Search completed: April 22, 2003, 12:55:42
Job time : 5.375 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	98	100.0	101	2	S26460	Ig heavy chain V r
2	98	100.0	115	2	S38714	Ig heavy chain V r
3	93	94.9	106	2	S24521	Ig heavy chain V r
4	93	94.9	115	1	AVMS06	Ig heavy chain V r
5	91	92.9	113	1	AVMSAB	Ig heavy chain V r
6	91	92.9	113	1	AVMS61	Ig heavy chain V r
7	91	92.9	113	1	AVMS09	Ig heavy chain V r
8	91	92.9	113	1	AVMSB7	Ig heavy chain V r
9	91	92.9	115	1	AVMS82	Ig heavy chain V r
10	89	90.8	115	2	A25803	Ig heavy chain V r
11	86	87.8	113	1	AVMS57	Ig heavy chain V r
12	85	86.7	113	1	HVMSAM	Ig heavy chain V r
13	75.5	77.0	111	1	HVMSAM	Ig heavy chain V r
14	73	74.5	139	2	PC1213	Ig heavy chain pre
15	68	69.4	64	2	I77394	Ig heavy chain V r
16	68	69.4	121	2	S09958	Ig heavy chain V r
17	67	68.4	100	2	S26462	Ig heavy chain V r
18	67	68.4	110	2	PH1091	Ig heavy chain V r
19	67	68.4	110	2	PH1092	Ig heavy chain pre
20	67	68.4	119	2	A27630	Ig heavy chain V r
21	67	68.4	121	2	A41940	Ig heavy chain pre
22	67	68.4	141	2	I32513	Ig heavy chain pre
23	66	67.3	125	2	S67945	Ig heavy chain pre
24	65	66.3	139	2	G29380	Ig heavy chain BrE
25	64	65.3	110	2	PH1093	Ig heavy chain pre
26	63	64.3	220	2	S68211	Ig heavy chain V r
27	63	64.3	444	2	PC4436	monoclonal antibody
28	61	62.2	119	2	PH1293	Ig heavy chain pre
29	61	62.2	137	2	S42467	Ig heavy chain V r

Qy 1 EIRKSDNYATHYAESVKG 19
|||
Db 49 EIRKSDNYATHYAESVKG 67

```
RESULT 3
S24521
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S24521
R:Kaartinen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24490
A:Accession: S24521
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-106 <KAA>
A:Cross-references: EMBL:X66664; NID:G51247; PIDN:CAA47226.1; PID:G51248
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-106/Domain: immunoglobulin homology <IMM>

Query Match 94.9%; Score 93; DB 2; Length 106;
Best Local Similarity 94.7%; Pred. NO. 7.5e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 56 EIRLKSNNYATHYAESVKG 74

RESULT 4
AVMS06
Ig heavy chain V-III region (J606) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: C92811; A02072
R:Johnson, N.; Sliankard, J.; Paul, L.; Hood, L.
J. Immunol. 128, 302-307, 1982
A:Title: The complete V domain amino acid sequences of two myeloma inulin-binding proteins.
A:Reference number: A92811; MUID:82099361; PMID:6798111
A:Accession: C92811
A:Molecule type: protein
A:Residues: 1-115 <JOH>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. NO. 8.2e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 5
AVNSAE
Ig heavy chain V-III region (A4) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 24-Apr-1984 #sequence_revision 30-Jun-1993 #text_change 31-Mar-1997
C:Accession: A93818; A02072
R:Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A:Reference number: A93818; MUID:78158406; PMID:417344
A:Accession: A93818
A:Molecule type: protein
A:Residues: 1-113 <VRA>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. NO. 1.7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 6
AVMS61
Ig heavy chain V-III region (U61) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: B93818; A02072
R:Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A:Reference number: A93818; MUID:78158406; PMID:417344
A:Accession: B93818
A:Molecule type: protein
A:Residues: 1-113 <VRA>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. NO. 1.7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 7
AVMS09
Ig heavy chain V-III region (E109) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: C93818; A02072
R:Vrana, M.; Rudikoff, S.; Potter, M.
Proc. Natl. Acad. Sci. U.S.A. 75, 1957-1961, 1978
A:Title: Sequence variation among heavy chains from inulin-binding myeloma proteins.
A:Reference number: A93818; MUID:78158406; PMID:417344
A:Accession: C93818
A:Molecule type: protein
A:Residues: 1-113 <VRA>
C:Comment: This chain was isolated from a myeloma protein that binds inulin.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-100/Domain: immunoglobulin homology <IMM>
F:22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. NO. 1.7e-07;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
|||||:|||||
Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 8
AVMSB7
Ig heavy chain V-III region (ABE-47N) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996
C:Accession: A90400; A02072
```

R;Vrana, M.; Rudikoff, S.; Potter, M.

Biochemistry 16, 1170-1175, 1977

A;Title: Heavy-chain variable-region sequence from an inulin-binding myeloma protein.

A;Reference number: A90400; MUID:77134726; PMID:402936

A;Accession: A90400

A;Molecule type: protein

A;Residues: 1-113 <VRA>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 113;

Best Local Similarity 94.7%; Pred. No. 1.7e-07;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

||||| |||||||

Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 9

AVMS82

Ig heavy chain V-III region (W3082) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996

C;Accession: D92811; A02072

R;Johnson, N.; Slankard, J.; Paul, L.; Hood, L.

J. Immunol. 128, 302-307, 1982

A;Title: The complete V domain amino acid sequences of two myeloma inulin-binding proteins

A;Reference number: A92811; MUID:82099361; PMID:679811

A;Accession: D92811

A;Molecule type: protein

A;Residues: 1-115 <JOH>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 92.9%; Score 91; DB 1; Length 115;

Best Local Similarity 94.7%; Pred. No. 1.7e-07;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

||||| |||||||

Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 10

A25803

Ig heavy chain V region (281.3) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 16-Aug-1996

C;Accession: A25803

R;Herbat, H.; Grutter, T.; Aebersold, R.; Braun, D.G.

Biol. Chem. Hoppe-Seyler 367, 843-851, 1986

A;Title: The complete amino-acid sequence of the variable domain of a monoclonal anti-sc

A;Reference number: A25803; MUID:87076047; PMID:3539142

A;Accession: A25803

A;Molecule type: protein

A;Residues: 1-115 <HER>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

Query Match 90.8%; Score 89; DB 2; Length 115;

Best Local Similarity 89.5%; Pred. No. 3.6e-07;

Matches 17; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

||||| |||||||

Db 50 QIRLASDNYATHYAESVKG 68

RESULT 11

AVMS57

Ig heavy chain V-III region (T957) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Aug-1996

C;Accession: A92810; A02072

R;Rudikoff, S.; Potter, M.

J. Immunol. 127, 191-194, 1981

A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a n

A;Reference number: A92810; MUID:81216632; PMID:6787122

A;Accession: A92810

A;Molecule type: protein

A;Residues: 1-113 <RUD>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 87.8%; Score 86; DB 1; Length 113;

Best Local Similarity 89.5%; Pred. No. 1.1e-06;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

||||| |||||||

Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 12

HVMSAM

Ig heavy chain V region (AMPC1) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Aug-1982 #sequence_revision 18-Aug-1982 #text_change 31-Mar-1997

C;Accession: A02073

R;Rudikoff, S.; Potter, M.

J. Immunol. 127, 191-194, 1981

A;Title: Immunoglobulin heavy chains from anti-inulin myeloma proteins: evidence for a n

A;Reference number: A92810; MUID:81216632; PMID:6787122

A;Accession: A02073

A;Molecule type: protein

A;Residues: 1-113 <RUD>

C;Comment: This chain was isolated from a myeloma protein that binds inulin.

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-100/Domain: immunoglobulin homology <IMM>

F;22-98/Disulfide bonds: #status predicted

Query Match 86.7%; Score 85; DB 1; Length 113;

Best Local Similarity 89.5%; Pred. No. 1.6e-06;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19

||||| |||||||

Db 50 EIRLKSNNYATHYAESVKG 68

RESULT 13

MMMS76

Ig heavy chain V-III region (HPC76) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1980 #sequence_revision 30-Sep-1980 #text_change 31-Mar-1997

C;Accession: A02074

R;Bernard, O.; Gough, N.M.

Proc. Natl. Acad. Sci. U.S.A. 77, 3630-3634, 1980

A;Title: Nucleotide sequence of immunoglobulin heavy chain joining segments between tran

A;Reference number: A02074; MUID:81013937; PMID:6251474

A;Accession: A02074

A;Molecule type: mRNA

A;Residues: 1-111 <BER>

A;Note: the sequence was also determined from the differentiated gene

Search completed: April 22, 2003, 12:54:51
Job time : 18.6607 secs

OM protein - protein search, using sw model

Result No.	Score	Query		ID	Description
		Match	Length		
1	93	94.9	115	1 HV32 MOUSE	P01801 mus musculu
2	91	92.9	113	1 HV27 MOUSE	P01796 mus musculu
3	91	92.9	113	1 HV28 MOUSE	P01797 mus musculu
4	91	92.9	113	1 HV29 MOUSE	P01798 mus musculu
5	91	92.9	113	1 HV30 MOUSE	P01799 mus musculu
6	91	92.9	115	1 HV33 MOUSE	P01802 mus musculu
7	86	87.8	111	1 HV31 MOUSE	P01800 mus musculu
8	85	86.7	113	1 HV34 MOUSE	P01803 mus musculu
9	75.5	77.0	111	1 HV35 MOUSE	P01804 mus musculu
10	57	58.2	142	1 HV01 RAT	P01805 rattus norv
11	48	49.0	122	1 HV10 MOUSE	P01790 mus musculu
12	48	49.0	123	1 HV18 MOUSE	P01787 mus musculu
13	48	49.0	123	1 HV19 MOUSE	P01788 mus musculu
14	48	49.0	123	1 HV22 MOUSE	P01791 mus musculu
15	48	49.0	123	1 HV25 MOUSE	P01794 mus musculu
16	46	46.9	122	1 HV20 MOUSE	P01789 mus musculu
17	46	46.9	144	1 HV26 MOUSE	P01795 mus musculu
18	45	45.9	485	1 HUNB CLOAL	Q96785 clognita alb
19	44	44.9	123	1 HV23 MOUSE	P01792 mus musculu
20	42	42.9	250	1 V186 MYCGE	P47432 mycoplasma
21	42	42.9	595	1 VPI_EPCPH	P19192 bacterioph
22	42	42.9	822	1 BBPA_PSEAE	Q07806 pseudomonas
23	41.5	42.3	117	1 HV17 MOUSE	P01786 mus musculu
24	41	41.8	123	1 HV24 MOUSE	P01793 mus musculu
25	41	41.8	126	1 HV3K HUMAN	P01772 homo sapien
26	41	41.8	318	1 RLPA_TREPA	Q83958 treponema p
27	41	41.8	385	1 HUNB_BOMMO	O18326 bombyx mori
28	41	41.8	664	1 DHSB_HUMAN	P31040 homo sapien
29	41	41.8	665	1 DHSB_BOVIN	P31039 bos taurus
30	41	41.8	705	1 CATE_RHIME	P31039 bos taurus
31	41	41.8	868	1 N180 YEAST	P33440 saccharomy
32	40.5	41.3	627	1 GLGB_BACSU	P39118 bacillus su
33	40	40.8	116	1 HV05 CARAU	P19181 carassius a

```

RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RL proteins.";
RC Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
DR PIR; A93818; AVMSAB.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DISULFID 22 98
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C121C598285 CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 2.9e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 3
HV28_MOUSE
ID HV28_MOUSE STANDARD; PRT; 113 AA.
AC P01797;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region U61.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RL proteins.";
RC Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
DR PIR; B93818; AVMS61.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DISULFID 22 98
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12671 MW; 76634C121C598285 CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 2.9e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 4
HV29_MOUSE
ID HV29_MOUSE STANDARD; PRT; 113 AA.
AC P01798;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

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DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region E109.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=78158406; PubMed=417344;
RA Vrana M., Rudikoff S., Potter M.;
RT "Sequence variation among heavy chains from inulin-binding myeloma
RL proteins.";
RC Proc. Natl. Acad. Sci. U.S.A. 75:1957-1961 (1978).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
DR PIR; C93818; AVMS09.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DISULFID 22 98
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12647 MW; EE50F2F20EDB129B CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 2.9e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
DB 50 EIRLKSHNYATHYAESVKG 68

RESULT 5
HV30_MOUSE
ID HV30_MOUSE STANDARD; PRT; 113 AA.
AC P01799;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region ABE-47N.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=77134726; PubMed=402936;
RA Vrana M., Rudikoff S., Potter M.;
RT "Heavy-chain variable-region sequence from an inulin-binding myeloma
RL protein.";
RC Biochemistry 16:1170-1175 (1977).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS INULIN.
DR PIR; A90400; AVMSB7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DISULFID 22 98
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12675 MW; 76658C16C779845E CRC64;

Query Match 92.9%; Score 91; DB 1; Length 113;
Best Local Similarity 94.7%; Pred. No. 2.9e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19

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Db 50 EIRLKSHNYATHYAESVKG 68
RESULT 6
HV33 MOUSE
ID HV33_MOUSE STANDARD; PRT; 115 AA.
AC P01802;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region W3082.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82099361; PubMed=6798111;
RA Johnson N., Siankard J., Paul L., Hood L.;
RT "The complete V domain amino acid sequences of two myeloma inulin-
binding proteins."
RL J. Immunol. 128:302-307(1982).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
DR PIR; D92811; AVMS82.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12887 MW; 9B4517648C121C5A CRC64;

Query Match 92.9%; Score 91; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 2.9e-08;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
Db 50 EIRLKSHNYATHYAESVKG 68

RESULT 7
HV31 MOUSE
ID HV31_MOUSE STANDARD; PRT; 113 AA.
AC P01800;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region T957.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81216632; PubMed=6787122;
RA Rudikoff S., Potter M.;
RT "Immunoglobulin heavy chains from anti-inulin myeloma proteins:
evidence for a new heavy chain joining segment."
RL J. Immunol. 127:191-194(1981).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
BINDS INULIN.
DR PIR; A92810; AVMS57.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT DISULFID 22 98
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12691 MW; 7A6D906AAA966E9E CRC64;

Query Match 86.7%; Score 85; DB 1; Length 113;
Best Local Similarity 89.5%; Pred. No. 2.9e-07;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EIRLKSDNYATHYAESVKG 19
Db 50 EIRLKSHNYATHYAESVKG 68

RESULT 9
HV35 MOUSE
ID HV35_MOUSE STANDARD; PRT; 111 AA.
AC P01804;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region HPC76 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81013937; PubMed=6251474;
RA Bernard O., Gough N.M.;
RT "Nucleotide sequence of immunoglobulin heavy chain joining segments
between translocated VH and mu constant regions genes."
RL Proc. Natl. Acad. Sci. U.S.A. 77:3630-3634(1980).
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE FIRST 197 RESIDUES OF THE C

```

CC REGION WAS ALSO DETERMINED & DIFFERS IN ONLY 3 POSITIONS FROM THE
 CC CORRESPONDING PORTION OF THE MOUSE MOPC 104E MU CHAIN.

DR PIR; A02074; MHM576.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT NON_TER 1 111
 FT NON_TER 111 111
 SQ SEQUENCE 111 AA; 12304 MW; 0BDE98EC7348056A CRC64;

Query Match 77.0%; Score 75.5; DB 1; Length 111;
 Best Local Similarity 89.5%; Pred. No. 1.1e-05;
 Matches 17; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 EIRLKSNDNYATHYAESVKG 19
 ||||| ||||| ||||| |||||
 DB 45 EIRLKS-GYATHYAESVKG 62

RESULT 10
 HV01_RAT
 ID HV01_RAT STANDARD; PRT; 142 AA.
 AC P01805;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region IR2 precursor.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83064537; PubMed=6292865;
 RA Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
 RT "Structure and evolution of the heavy chain from rat immunoglobulin
 RT E";
 RL Nucleic Acids Res. 10:6041-6049(1982).
 CC -I- MISCELLANEOUS: THE MRNA WAS ISOLATED FROM AN IGH-SECRETING
 CC IMMUNOCYTOMA THAT ARISES SPONTANEOUSLY IN LOU/C/WSL RATS.

DR PIR; A02075; EVTR2.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 142 IG HEAVY CHAIN V REGION IR2.
 FT NON_TER 142 142
 SQ SEQUENCE 142 AA; 16024 MW; DE29B6CFE745DF3B CRC64;

Query Match 58.2%; Score 57; DB 1; Length 142;
 Best Local Similarity 52.6%; Pred. No. 0.016;
 Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIRLKSNDNYATHYAESVKG 19
 ||||| :||| :||| :|||
 DB 69 EIRKANNVAVYKSLKG 87

RESULT 11
 HV21_MOUSE
 ID HV21_MOUSE STANDARD; PRT; 122 AA.
 AC P01790;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region MS11.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81054880; PubMed=6776528;
 RA Robinson E.A., Appella E.;
 RA "Complete amino acid sequence of a mouse immunoglobulin alpha chain
 RT (MOPC 511).";
 RT Proc. Natl. Acad. Sci. U.S.A. 77:4909-4913(1980).
 CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
 CC BINDS PHOSPHORYLCHOLINE.

DR PIR; A02070; AVMTS.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR003006; Ig MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 KW Immunoglobulin V region.
 FT NON_TER 122 122
 SQ SEQUENCE 122 AA; 13652 MW; 9F4837731EA50207 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 122;
 Best Local Similarity 52.9%; Pred. No. 0.43;
 Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19
 |:::| |:::|
 DB 52 RNKANDYTEYSASVKG 68

RESULT 12
 HV18_MOUSE
 ID HV18_MOUSE STANDARD; PRT; 123 AA.
 AC P01787;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE (TEPC 15).
 RX MEDLINE=76222762; PubMed=819932;
 RA Rudikoff S., Potter M.;
 RA "Size differences among immunoglobulin heavy chains from
 RT phosphorylcholine-binding proteins";
 RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
 RN [2]
 RP SEQUENCE FROM N.A. (H107).
 RX MEDLINE=80199926; PubMed=6769593;
 RA Early P., Huang H., Davis M., Calame K., Hood L.;
 RA "An immunoglobulin heavy chain variable region gene is generated from
 RT three segments of DNA: VH, D and JH";
 RL Cell 19:981-992(1980).
 RN [3]
 RP SEQUENCE (S107).
 RX MEDLINE=76110488; PubMed=813561;
 RA Rudikoff S., Barstad P., Potter M., Hood L.;
 RA Unpublished results, cited by:
 RL Hood L., Campbell J.H., Egin S.C.R.;
 RL Annu. Rev. Genet. 9:305-353(1975).
 RN [4]
 RP SEQUENCE (HPCM1; HPCM2 AND HPCM3).
 RX MEDLINE=81197602; PubMed=7231520;
 RA Gearhart P.J., Johnson N.D., Douglas R., Hood L.;
 RA "IgG antibodies to phosphorylcholine exhibit more diversity than
 RT their IgM counterparts";
 RL Nature 291:29-34(1981).
 CC -I- MISCELLANEOUS: ALL THOSE SEQUENCE APPEARS TO BE IDENTICAL.
 CC -I- MISCELLANEOUS: THESE CHAINS WERE ISOLATED FROM MYELOMA AND

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CC HYBRIDOMA PROTEINS THAT BIND PHOSPHORYLCHOLINE.
DR PIR; A02070; AVMS75.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13777 MW; 9D58086DE12F7000 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 123;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19
DB 52 RNKANDYTTTEYSASVKG 68

RESULT 13
HV19 MOUSE
ID HV19 MOUSE STANDARD; PRT; 123 AA.
AC P01788;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA Barstad P.;
RL Thesis (1975), California Institute of Technology / Pasadena, U.S.A.
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A02070; AVMS75.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13805 MW; 9D581401912F7000 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 123;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19
DB 52 RNKANDYTTTEYSASVKG 68

RESULT 14
HV22 MOUSE
ID HV22 MOUSE STANDARD; PRT; 123 AA.
AC P01791;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region HPCM6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J.; Johnson N.D.; Douglas R.; Hood L.;

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RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A02070; AVMS75.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13895 MW; 81361892ECBF7000 CRC64;

Query Match 49.0%; Score 48; DB 1; Length 123;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19
DB 52 RNKANDYTTTEYSASVKG 68

RESULT 15
HV25 MOUSE
ID HV25 MOUSE STANDARD; PRT; 123 AA.
AC P01794;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region HPCG14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=81197602; PubMed=7231520;
RA Gearhart P.J.; Johnson N.D.; Douglas R.; Hood L.;
RT "IgG antibodies to phosphorylcholine exhibit more diversity than
RT their IgM counterparts.";
RL Nature 291:29-34(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT
CC BINDS PHOSPHORYLCHOLINE.
DR PIR; A02070; AVMS75.
DR HSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT NON_TER 123 123
SQ SEQUENCE 123 AA; 13807 MW; A7584FB098B7785D CRC64;

Query Match 49.0%; Score 48; DB 1; Length 123;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19
DB 52 RNKANDYTTTEYSASVKG 68

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Search completed: April 22, 2003, 12:51:51
Job time : 10.5 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:47:43 ; Search time 38 seconds
(without alignments)
103.024 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRKSDNYATHYAEVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rhodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	69.4	64	11 Q61750	Q61750 mus musculus
2	51	52.0	469	11 Q8R3V9	Q8R3V9 mus musculus
3	51	52.0	480	11 Q91XE1	Q91XE1 mus musculus
4	49	50.0	361	2 Q9RBZ2	Q9RBZ2 pseudomonas
5	47	48.0	357	2 Q9RBZ3	Q9RBZ3 pseudomonas
6	46	46.9	2910	10 Q9FND5	Q9FND5 arabidopsis
7	45	45.9	121	4 Q9UL71	Q9UL71 homo sapien
8	45	45.9	422	5 Q8WR61	Q8WR61 lymantria d
9	45	45.9	450	16 Q8U6S1	Q8U6S1 agrobacteri
10	44	44.9	362	2 Q45962	Q45962 clostridium
11	43	43.9	182	17 Q35037	Q35037 archaeoglob
12	43	43.9	290	17 Q8TZK5	Q8TZK5 pyrococcus
13	43	43.9	310	16 Q99ZF6	Q99ZF6 streptococc
14	43	43.9	474	16 P73837	P73837 synecocyst
15	43	43.9	476	16 Q8YCK5	Q8YCK5 brucella me
16	43	43.9	485	16 Q8YT50	Q8YT50 anabaena sp

17	43	43.9	534	5 Q9XUT8	Q9XUT8 caenorhabdi
18	42.5	43.4	405	2 Q93NC6	Q93NC6 myxococcus
19	42.5	43.4	766	4 P82987	P82987 homo sapien
20	42	42.9	124	12 Q9PZ19	Q9PZ19 xestia c-ni
21	42	42.9	369	16 Q98BT5	Q98BT5 rhizobium l
22	42	42.9	416	5 Q96360	Q96360 hyphantria
23	42	42.9	553	16 Q34751	Q34751 bacillus su
24	42	42.9	679	17 Q59078	Q59078 pyrococcus
25	42	42.9	749	10 Q94F83	Q94F83 oryza sativ
26	42	42.9	1074	5 Q97289	Q97289 plasmodium
27	42	42.9	1261	2 Q69247	Q69247 bacillus li
28	42	42.9	1288	2 Q66071	Q66071 bacillus li
29	42	42.9	1394	5 Q960N9	Q960N9 drosophila
30	42	42.9	1485	5 Q9VJ80	Q9VJ80 drosophila
31	41.5	42.3	751	11 P70535	P70535 rattus norv
32	41	41.8	131	4 Q9UL88	Q9UL88 homo sapien
33	41	41.8	145	5 Q9VA95	Q9VA95 drosophila
34	41	41.8	299	16 Q99UF7	Q99UF7 staphylococ
35	41	41.8	381	11 Q9EQL9	Q9EQL9 rattus norv
36	41	41.8	403	16 Q8YX13	Q8YX13 anabaena sp
37	41	41.8	483	3 Q94206	Q94206 claviopsis p
38	41	41.8	532	11 Q92124	Q92124 mus musculu
39	41	41.8	646	16 Q53670	Q53670 mycobacteri
40	41	41.8	656	11 Q920L2	Q920L2 rattus norv
41	41	41.8	661	11 Q921P5	Q921P5 mus musculu
42	41	41.8	663	16 Q9PI96	Q9PI96 campylobact
43	41	41.8	667	17 Q8UOR3	Q8UOR3 pyrococcus
44	41	41.8	724	12 Q9J8C9	Q9J8C9 spodoptera
45	41	41.8	762	16 Q97KV6	Q97KV6 clostridium

ALIGNMENTS

RESULT 1

Q61750	Q61750	PRELIMINARY;	PRT;	64 AA.
AC	Q61750;			
DT	01-NOV-1996 (Tremblrel. 01, Created)			
DT	01-NOV-1996 (Tremblrel. 01, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	JH-Cdelta locus (Fragment).			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C;			
RX	MEDLINE=92017847; PubMed=1922069;			
RA	Owens J.D.Jr. , Finkelman F.D., Mountz J.D., Mushinski J.F.;			
RT	"Nonhomologous recombination at sites within the mouse JH-Cdelta locus			
RT	accompanies Cmu deletion and switch to immunoglobulin D secretion.";			
RL	Mol. Cell. Biol. 11:5660-5670(1991).			
DR	EMBL; M64568; AAA39341.1; .			
DR	HSSP; P01789; IMCP.			
DR	InterPro; IPR003600; IG_like.			
DR	SMART; SM00410; IG_like; 1.			
FT	NON TER 1			
SQ	SEQUENCE 64 AA; 7594 MW; FE83625079AC2F28 CRC64;			

Query Match 69.4%; Score 68; DB 11; Length 64;
Best Local Similarity 72.2%; Pred. No. 0.00061;
Matches 13; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IRLKSDNYATHYAEVKG 19
Db 9 ITVKSNDYGYAEVKG 26

RESULT 2

Q8R3V9 Q8R3V9 PRELIMINARY; PRT; 469 AA.

RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. II.
 RT Sequence features of the regions of 1,044,062 bp covered by thirteen
 RT physically assigned P1 clones.";
 RL DNA Res. 4:291-300 (1997).
 DR EMBL; AB006702; BAB11602.1; -.
 DR EMBL; AB017062; BAB11602.1; JOINED.
 SQ SEQUENCE 2910 AA; 325351 MW; A847EC3FE1427DF7 CRC64;
 Query Match 46.9%; Score 46; DB 10; Length 2910;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 4 LKSDNYATHYAESVK 18
 DB 297 LKEDNHQEEYAESVE 311
 || ||: |||||:
 || ||: |||||:

RESULT 7
 Q9UL71 PRELIMINARY; PRT; 121 AA.
 ID Q9UL71
 AC Q9UL71
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Myosin-reactive immunoglobulin heavy chain variable region
 DE (fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98271139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 RT fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192 (1998).
 DR EMBL; AF035043; AAD56279.1; -.
 DR HSSP; P01772; 2FBA.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 121 121
 FT NON_TER 121 121
 SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 45.9%; Score 45; DB 4; Length 121;
 Best Local Similarity 50.0%; Pred. No. 8.7;
 Matches 8; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 4 LKSDNYATHYAESVK 19
 DB 51 ISGDBGSTYADSVKG 66
 : ||: |||||:
 : ||: |||||:

RESULT 8
 Q8WR61 PRELIMINARY; PRT; 422 AA.
 ID Q8WR61
 AC Q8WR61
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hemolin.
 OS Lymantria dispar (Gypsy moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Noctuoidea; Lymantriidae; Lymantria.
 OX NCBI_TaxID=13123;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Denlinger D.L., Lee K.-Y., Horodyski F.M., Valaitis A.P.;
 RT "Molecular characterization of the insect immune protein hemolin and
 RT the high induction during embryonic diapause in the gypsy moth,
 RT Lymantria dispar.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF453868; AAL49765.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00408; IGC2; 3.
 SQ SEQUENCE 422 AA; 47234 MW; 0DC52EC4BF142617 CRC64;

Query Match 45.9%; Score 45; DB 5; Length 422;
 Best Local Similarity 53.3%; Pred. No. 37;
 Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAE 15
 DB 42 EVRFKADNYSTALLE 56
 ||: |||||:
 ||: |||||:

RESULT 9
 Q8U651 PRELIMINARY; PRT; 450 AA.
 ID Q8U651
 AC Q8U651
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Nitroliotriacetate monooxygenase, component A.
 GN ATU0084 OR AGR_PTI_161.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OG Plasmid pTiC58.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Neeter E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58";
 RL Science 294:2317-2323 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmieu K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Planagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT Agrobacterium tumefaciens C58";
 RL Science 294:2323-2328 (2001).
 DR EMBL; AE009427; AAL46320.1; -.
 DR EMBL; AE007935; AAK31044.1; -.
 KW Monooxygenase; Plasmid; Complete proteome.
 SQ SEQUENCE 450 AA; 50163 MW; D3ADB8261D68C026 CRC64;

Query Match 45.9%; Score 45; DB 16; Length 450;
 Best Local Similarity 58.3%; Pred. No. 40;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 DNYATHYAESVK 18
 DB 57 DNYGQHFDATVK 68

RESULT 10
 ID Q45962 PRELIMINARY; PRT; 362 AA.
 AC Q45962;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE RepB.
 GN REPB.
 OS Clostridium butyricum.
 OG Plasmid pCB101.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1492;
 RN [1]_TaxID=1492;
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCIB 7423;
 RA Brehm J.K., Penneck A., Young M., Oultram J.D., Minton N.P.;
 RT "Physical characterisation of the replication origin of the cryptic
 RT plasmid pCB101 isolated from Clostridium butyricum NCIB 7423."
 RL Plasmid 0:0-0(0).
 DR EMBL; X62684; CAA44562.1; -
 DR InterPro; IPR000989; Rep.
 DR Pfam; PF01446; Rep; 1.
 KW Plasmid.
 SQ SEQUENCE 362 AA; 43052 MW; FC8A02436E259A49 CRC64;

Query Match 44.9%; Score 44; DB 2; Length 362;
 Best Local Similarity 53.8%; Pred. No. 45;
 Matches 7; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 ERLKSDNYATHY 13
 DB 170 EVTFKNDNYHPHY 182

RESULT 11
 ID Q35037 PRELIMINARY; PRT; 182 AA.
 AC Q35037;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ISA1083-2, putative transposase.
 GN AF1352 AND AF2139.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
 RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii H.O., Woese C.R.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Weiss R.A.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeson Archaeoglobus fulgidus.";

RL Nature 390:364-370(1997).
 DR EMBL; AB001010; AAB89893.1; -
 DR EMBL; AB000956; AAB89112.1; -
 DR TIGR; AF1352; -
 DR TIGR; AF2139; -
 DR InterPro; IPR001584; Rve.
 DR Pfam; PF00665; Rve; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 182 AA; 20733 MW; 860E5DBDE445CDE7 CRC64;

Query Match 43.9%; Score 43; DB 17; Length 182;
 Best Local Similarity 58.3%; Pred. No. 30;
 Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 DNYATHYAESVK 18
 DB 91 DNFKTHAKVK 102

RESULT 12
 ID Q87ZK5 PRELIMINARY; PRT; 290 AA.
 AC Q87ZK5;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein PF1986.
 GN PF1986.
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VCI / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome."
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB010292; AAL82110.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 290 AA; 34518 MW; 7697BA58D6794B7E CRC64;

Query Match 43.9%; Score 43; DB 17; Length 290;
 Best Local Similarity 61.5%; Pred. No. 51;
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 LKSDNYATHYAES 16
 DB 34 LKEWYAAHYVDS 46

RESULT 13
 ID Q99ZF6 PRELIMINARY; PRT; 310 AA.
 AC Q99ZF6;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative macrolide-efflux protein.
 GN MREA OR SPV1250.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:45:19 ; Search time 48.1786 Seconds
(without alignments)
52.550 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98
Sequence: 1 EIRLKSNDYATHYAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq 101002:*

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- 3: /SID22/gcgdata/geneseq/genesecp-emb1/AA1982.DAT:*
- 4: /SID22/gcgdata/geneseq/genesecp-emb1/AA1983.DAT:*
- 5: /SID22/gcgdata/geneseq/genesecp-emb1/AA1984.DAT:*
- 6: /SID22/gcgdata/geneseq/genesecp-emb1/AA1985.DAT:*
- 7: /SID22/gcgdata/geneseq/genesecp-emb1/AA1986.DAT:*
- 8: /SID22/gcgdata/geneseq/genesecp-emb1/AA1987.DAT:*
- 9: /SID22/gcgdata/geneseq/genesecp-emb1/AA1988.DAT:*
- 10: /SID22/gcgdata/geneseq/genesecp-emb1/AA1989.DAT:*
- 11: /SID22/gcgdata/geneseq/genesecp-emb1/AA1990.DAT:*
- 12: /SID22/gcgdata/geneseq/genesecp-emb1/AA1991.DAT:*
- 13: /SID22/gcgdata/geneseq/genesecp-emb1/AA1992.DAT:*
- 14: /SID22/gcgdata/geneseq/genesecp-emb1/AA1993.DAT:*
- 15: /SID22/gcgdata/geneseq/genesecp-emb1/AA1994.DAT:*
- 16: /SID22/gcgdata/geneseq/genesecp-emb1/AA1995.DAT:*
- 17: /SID22/gcgdata/geneseq/genesecp-emb1/AA1996.DAT:*
- 18: /SID22/gcgdata/geneseq/genesecp-emb1/AA1997.DAT:*
- 19: /SID22/gcgdata/geneseq/genesecp-emb1/AA1998.DAT:*
- 20: /SID22/gcgdata/geneseq/genesecp-emb1/AA1999.DAT:*
- 21: /SID22/gcgdata/geneseq/genesecp-emb1/AA2000.DAT:*
- 22: /SID22/gcgdata/geneseq/genesecp-emb1/AA2001.DAT:*
- 23: /SID22/gcgdata/geneseq/genesecp-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	19	21	AA1980.DAT:*
2	98	100.0	137	21	AA1981.DAT:*
3	98	100.0	286	22	AA1982.DAT:*
4	98	100.0	444	21	AA1983.DAT:*
5	95	96.9	100	22	AA1984.DAT:*
6	95	96.9	299	22	AA1985.DAT:*
7	93	94.9	115	14	AA1986.DAT:*
8	93	94.9	116	20	AA1987.DAT:*
9	93	94.9	119	19	AA1988.DAT:*
10	93	94.9	120	18	AA1989.DAT:*

11	93	94.9	122	21	AA1990.DAT:*
12	93	94.9	142	18	AA1991.DAT:*
13	93	94.9	142	20	AA1992.DAT:*
14	93	94.9	143	11	AA1993.DAT:*
15	93	94.9	255	23	AA1994.DAT:*
16	93	94.9	256	23	AA1995.DAT:*
17	93	94.9	503	23	AA1996.DAT:*
18	93	94.9	570	20	AA1997.DAT:*
19	91	92.9	19	22	AA1998.DAT:*
20	91	92.9	151	22	AA1999.DAT:*
21	91	92.9	151	23	AA2000.DAT:*
22	88	89.8	160	16	AA2001.DAT:*
23	88	89.8	554	16	AA2002.DAT:*
24	85	86.7	114	13	AA2003.DAT:*
25	85	86.7	114	13	AA2004.DAT:*
26	85	86.7	114	21	AA2005.DAT:*
27	80.5	82.1	119	18	AA2006.DAT:*
28	80	81.6	17	21	AA2007.DAT:*
29	74	75.5	16	20	AA2008.DAT:*
30	74	75.5	100	22	AA2009.DAT:*
31	74	75.5	119	18	AA2010.DAT:*
32	74	75.5	119	19	AA2011.DAT:*
33	74	75.5	119	22	AA2012.DAT:*
34	74	75.5	119	22	AA2013.DAT:*
35	74	75.5	119	22	AA2014.DAT:*
36	74	75.5	119	22	AA2015.DAT:*
37	74	75.5	119	23	AA2016.DAT:*
38	73	74.5	134	12	AA2017.DAT:*
39	73	74.5	134	12	AA2018.DAT:*
40	73	74.5	139	14	AA2019.DAT:*
41	72	73.5	119	17	AA2020.DAT:*
42	72	73.5	253	16	AA2021.DAT:*
43	71	72.4	119	19	AA2022.DAT:*
44	70	71.4	19	21	AA2023.DAT:*
45	70	71.4	125	21	AA2024.DAT:*

ALIGNMENTS

RESULT 1
AA1980.DAT:*

ID AA1980.DAT:*

AC AA1980.DAT:*

DT 15-FEB-2000 (first entry)

DE Light chain CDR H2 of mouse anti-CD23 MAb C11.

XX CD23; FCER1; IGE receptor; monoclonal antibody; C11; mouse; monoclonal antibody; chimeric antibody; humanised antibody; complementarity determining region; CDR; autoimmune disease; inflammation; arthritis; lupus erythematosus; multiple sclerosis; urticaria; nephrotic syndrome; diabetes; uveitis; dermatitis; psoriasis; inflammatory bowel disease; ulcerative colitis; Crohn's disease; Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis; graft-versus-host disease; COPD; bronchitis; diabetes; B-cell malignancy; therapy.

OS Mus musculus.

XX WO9958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB01434.

XX 09-MAY-1998; 98GB-0009839.

XX (GLAX) GLAXO GROUP LTD.

PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 DR N-PSDB; AA234743.
 XX
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis -
 XX Claim 1; Page 40; 81pp; English.
 XX
 XX This sequence represents complementarity determining region 2
 CC (CDR H2) of the heavy chain of murine anti-CD23 (FCERII) monoclonal
 CC antibody C11 (see also AA32263). The invention provides altered
 CC antibodies, such as chimeric or humanised antibodies, which comprise
 CC sufficient of the amino acid sequences of C11 light and heavy chain
 CC CDRs (see AA32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies
 CC are used to block soluble CD23 formation for treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.
 XX Sequence 19 AA;
 XX
 XX Query Match 100.0%; Score 98; DB 21; Length 19;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKSNDNYATHAESVKG 19
 DB 1 EIRLKSNDNYATHAESVKG 19
 XX
 XX RESULT 2
 XX AA32260
 XX ID AA32260 standard; Protein; 137 AA.
 XX
 XX AC AA32260;
 XX
 XX DT 15-FEB-2000 (first entry)
 XX
 XX DE Mouse anti-CD23 MAb C11 heavy chain variable region.
 XX
 XX CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes;
 KW B-cell malignancy; therapy.
 XX
 XX OS Mus musculus.
 XX
 XX Key Location/Qualifiers
 FH Region 59..63
 FT /note= "CDR H1"
 FT Region 78..96
 FT /note= "CDR H2"
 FT Region 129..131
 FT /note= "CDR H3"
 XX
 XX W0958679-A1.

PD 18-NOV-1999.
 XX
 XX 07-MAY-1999; 99WO-GB01434.
 DR N-PSDB; AA234745.
 XX
 XX 09-MAY-1998; 98GB-0009839.
 PR (GLAX) GLAXO GROUP LTD.
 XX
 XX Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 PI WPI; 2000-053101/04.
 XX N-PSDB; AA234745.
 DR
 XX Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis -
 XX Claim 8; Fig 1; 81pp; English.
 XX
 XX This sequence represents the heavy chain variable region (VH) of
 CC murine anti-CD23 (FCERII) monoclonal antibody C11. The invention
 CC provides altered antibodies, such as chimeric or humanised
 CC antibodies (see AA32262 and AA32263), which comprise sufficient of
 CC the amino acid sequences of the C11 light and heavy chain
 CC complementarity determining regions (see AA32254-59) to render them
 CC capable of binding to the CD23 type II molecule expressed on
 CC haematopoietic cells. The antibodies are used to block soluble
 CC CD23 formation in human therapy, for the treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.
 XX Sequence 137 AA;
 XX
 XX Query Match 100.0%; Score 98; DB 21; Length 137;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-08;
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKSNDNYATHAESVKG 19
 DB 78 EIRLKSNDNYATHAESVKG 96
 XX
 XX RESULT 3
 XX AAB50426
 XX ID AAB50426 standard; Protein; 286 AA.
 XX
 XX AC AAB50426;
 XX
 XX DT 13-MAR-2001 (first entry)
 XX
 XX DE Antibody 33F12 catalytic fragment.
 XX
 XX KW Antibody 33F12; ketone compound; antitumour; cytotoxic;
 KW targeted drug delivery.
 XX
 XX OS Unidentified.
 XX
 XX PN WO200071556-A1.
 XX
 XX PD 30-NOV-2000.
 XX
 XX PF 24-MAY-2000; 2000WO-US14366.
 XX
 XX PR 25-MAY-1999; 99US-0318661.
 XX (SCRI) SCRIPPS RES INST.
 XX PA

XX PI Barbas CF, Shabat D, Rader C, List B, Lerner RA;
 XX DR WPI; 2001-061339/07.
 XX DR N-PSDB; AAC90472.
 XX PT New ketone compounds containing active agents useful as carriers for
 XX PT e.g. antitumor agents, antibiotics or fluorescent molecules -
 XX PS Disclosure; Fig 10; 45pp; English.
 XX CC The present sequence may be used in the activation of new ketone prodrug
 XX CC compounds containing active agents. The ketone derivatives are useful as
 XX CC carriers for antitumor agents such as cytotoxic agents, where the
 XX CC antitumor agent is a microtubule stabilising agent such as paclitaxel,
 XX CC epothilone or its therapeutically active analogue or an anthracycline
 XX CC antibiotic such as doxorubicin or its therapeutically active analogue.
 XX CC The ketone derivatives are useful for targeted drug delivery.
 XX CC The inactive molecules in the ketone compounds are converted to
 XX CC active molecules by retro-Michael reaction. The antibody has
 XX CC bifunctional activity and specifically immunoreacts with cell surface
 XX CC antigen of a target cell. The active ingredients can be mixed
 XX CC effectively with excipients as per desired amount along with the
 XX CC buffering agent to enhance the effectiveness and activity of the
 XX CC compound.
 XX SQ Sequence 286 AA;
 Query Match 100.0%; Score 98; DB 22; Length 286;
 Best Local Similarity 100.0%; Pred. No. 3.4e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRKSDNVATHYAESVKG 19
 DB 203 EIRKSDNVATHYAESVKG 221
 RESULT 4
 AA32263
 ID AAY32263 standard; Protein; 444 AA.
 XX AC AAY32263;
 XX DT 15-FEB-2000 (first entry)
 XX DE Humanised anti-CD23 Mab C11 heavy chain.
 XX KW CD23; FCERII; Ige receptor; monoclonal antibody; C11; mouse; human;
 XX KW monoclonal antibody; chimeric antibody; humanised antibody;
 XX KW complementarity determining region; CDR; autoimmune disease;
 XX KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 XX KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 XX KW urticaria; nephrotic syndrome; glomerulonephritis;
 XX KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 XX KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 XX KW graft-versus-host disease; COPD; bronchitis; diabetes;
 XX KW B-cell malignancy; therapy.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Region 1..30
 XX FT /note= "framework region 1"
 XX FT Region 31..35
 XX FT /note= "CDR 1"
 XX FT Region 36..49
 XX FT /note= "framework region 2"
 XX FT Region 50..68
 XX FT /note= "CDR 2"
 XX FT Region 69..100
 XX FT /note= "framework region 3"
 XX FT Region 101..103

FT Region /note= "CDR 3"
 FT 104..111
 FT /note= "framework region 4"
 FT 112..444
 FT /note= "constant region"
 XX WO9958679-A1.
 XX 18-NOV-1999.
 XX 07-MAY-1999; 99WO-GB01434.
 XX 09-MAY-1998; 98GB-0009839.
 XX (GLAX) GLAXO GROUP LTD.
 PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 DR WPI; 2000-053101/04.
 DR N-PSDB; AAZ34748.
 XX^a Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis -
 XX PS Claim 9; Fig 4; 81pp; English.
 XX CC This amino acid sequence represents the heavy chain of humanised
 XX CC anti-CD23 (FCERII) monoclonal antibody C11, composed of a human
 XX CC framework (H5IGKVI) and the heavy chain complementarity
 XX CC determining regions (see AAY32257-59) of murine antibody C11. The
 XX CC DNA was constructed by splice overlap PCR. The invention provides
 XX CC altered antibodies, such as chimeric or humanised antibodies, which
 XX CC comprise sufficient of the amino acid sequences of the C11 light
 XX CC and heavy chain complementarity determining regions to render them
 XX CC capable of binding to the CD23 type II molecule expressed on
 XX CC haematopoietic cells. The antibodies are used to block soluble
 XX CC CD23 formation in human therapy, for the treatment of arthritis,
 XX CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 XX CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 XX CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 XX CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 XX CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 XX CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 XX CC (particularly chronic bronchitis) or diabetes (particularly type 1
 XX CC diabetes), and B-cell malignancies (claimed). They are also useful
 XX CC for studying interactions between CD23 and various ligands and
 XX CC determining the binding agents.
 XX SQ Sequence 444 AA;
 Query Match 100.0%; Score 98; DB 21; Length 444;
 Best Local Similarity 100.0%; Pred. No. 5.7e-08;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRKSDNVATHYAESVKG 19
 DB 50 EIRKSDNVATHYAESVKG 68
 RESULT 5
 AA06973
 ID AAE06973 standard; Protein; 100 AA.
 XX AC AAE06973;
 XX DT 16-OCT-2001 (first entry)
 XX DE Mouse germline heavy chain variable (VH) region, V(H)22.1.
 XX KW Mouse; humanised antibody; CC-chemokine receptor 2; CCR2; nephrotropic;
 XX KW neuroprotective; immunosuppressive; human immunodeficiency virus;
 XX KW HIV infection; cytostatic; vasotropic; leukocyte trafficking; allergy;
 XX KW inflammatory disorder; autoimmune disorder; rheumatoid arthritis; shock;

KW multiple sclerosis; atherosclerosis; restenosis; asthma;
 KW anaphylaxis; malignancy; inflammation; stenosis; allograft rejection;
 KW fibrotic disease; angioplasty; acquired immune deficiency syndrome;
 KW AIDS; inflammatory glomerulopathy; vascular intervention;
 KW neointimal hyperplasia; VH; heavy chain variable region.
 XX
 OS Mus sp.
 XX WO200157226-A1.
 PN 09-AUG-2001.
 XX 02-FEB-2001; 2001WO-US03537.
 XX 03-FEB-2000; 2000US-0497625.
 PR (MILL-) MILLENNIUM PHARM INC.
 PA Larosa GJ, Horvath C, Newman W, Jones ST, O'Brien S, O'Keefe T;
 PI WPI; 2001-488888/53.
 DR Humanized immunoglobulin for treating a CC-chemokine receptor
 PT 2-mediated disorder in a patient, comprises a binding specificity for
 PT CCR2, and a non-human antigen binding region and human immunoglobulin
 PT -
 XX Disclosure; Page 152-153; 183pp; English.
 XX The patent discloses a humanized antibody or its antigen-binding
 CC fragment, having binding specificity for CC-chemokine receptor 2
 CC (CCR2), comprising an antigen binding region of non-human origin
 CC and at least a portion of an immunoglobulin of human origin. The
 CC humanized antibodies are useful for inhibiting the interaction of
 CC a cell expressing CCR2. They are useful for inhibiting or treating
 CC HIV infection. The proteins of the invention are useful for inhibiting
 CC leukocyte trafficking, for treating CCR2-mediated disorders such as
 CC inflammatory disorder, autoimmune disorders such as rheumatoid
 CC arthritis and multiple sclerosis, atherosclerosis and arteriosclerosis,
 CC and for inhibiting restenosis. They are useful in therapy or diagnosis,
 CC and in the manufacture of a medicament for treating CCR2 mediated
 CC disease. They are also useful for treating allergy, anaphylaxis,
 CC malignancy, chronic and acute inflammation, histamine and IgE-
 CC mediated allergic reaction, shock, stenosis, allograft rejection,
 CC fibrotic disease, asthma, inflammatory glomerulopathies, acquired
 CC immune deficiency syndrome (AIDS), restenosis associated with vascular
 CC intervention, including angioplasty and/or stent placement in a mammal.
 CC Humanised antibodies are also useful for inhibiting narrowing of the
 CC lumen of a vessel in a mammal, and inhibiting neointimal hyperplasia of
 CC a vessel in a mammal, preferably associated with vascular intervention.
 CC The present sequence is mouse germline heavy chain variable (VH)
 CC region, V(H)22.1.
 XX
 XX Sequence 100 AA;
 SQ
 Query Match 96.9%; Score 95; DB 22; Length 100;
 Best Local Similarity 94.7%; Pred. No. 3.1e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKSNDNYATHYAESVKG 19
 :|||||
 Db 50 QIRLKSNDNYATHYAESVKG 68
 RESULT 6
 AAB50425
 ID AAB50425 standard; Protein; 299 AA.
 XX
 AC AAB50425;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 XX Mouse antibody 38C2 catalytic fragment.

XX Mouse; antibody 38C2; ketone compound; antitumour; cytotoxic;
 KW targeted drug delivery.
 XX Mus sp.
 PN WO2000071556-A1.
 XX 30-NOV-2000.
 XX 24-MAY-2000; 2000WO-US14366.
 XX 25-MAY-1999; 99US-0318661.
 XX (SCRI) SCRIPPS RES INST.
 XX Barbas CF, Shabat D, Rader C, List B, Lerner RA;
 PI WPI; 2001-061339/07.
 XX N-PSDB; AAC90471.
 DR New ketone compounds containing active agents useful as carriers for
 PT e.g. antitumour agents, antibiotics or fluorescent molecules -
 XX Disclosure; Fig 9; 45pp; English.
 XX The present sequence may be used in the activation of new ketone prodrug
 CC compounds containing active agents. The ketone derivatives are useful as
 CC carriers for antitumour agents such as cytotoxic agents, where the
 CC antitumour agent is a microtubule stabilising agent such as paclitaxel,
 CC epothilone or its therapeutically active analogue or an anthracycline
 CC antibiotic such as doxorubicin or its therapeutically active analogue.
 CC The ketone derivatives are useful for targeted drug delivery.
 CC The inactive molecules in the ketone compounds are converted to
 CC active molecules by retro-Michael reaction. The antibody has
 CC bifunctional activity and specifically immunoreacts with cell surface
 CC antigen of a target cell. The active ingredients can be mixed
 CC effectively with excipients as per desired amount along with the
 CC buffering agent to enhance the effectiveness and activity of the
 CC compound.
 XX Sequence 299 AA;
 SQ
 Query Match 96.9%; Score 95; DB 22; Length 299;
 Best Local Similarity 94.7%; Pred. No. 1.1e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKSNDNYATHYAESVKG 19
 :|||||
 Db 205 EIRLKSNDNYATHYAESVKG 223
 RESULT 7
 AAR34018
 ID AAR34018 standard; Protein; 115 AA.
 XX
 AC AAR34018;
 XX
 DT 02-AUG-1993 (first entry)
 XX
 DE BW 835 VH.
 XX Monoclonal antibody; Mab; hybridoma; lung; adenocarcinoma;
 KW mammary; ovary; prostate; polymorphic epithelial mucin; PEM.
 XX Synthetic.
 XX DE4133791-A.
 XX
 XX 15-APR-1993.
 PD
 XX 11-OCT-1991; 91DE-4133791.
 PF
 XX

PR 11-OCT-1991; 91DE-4133791.
 XX (BEHW) BEHRINGWERKE AG.
 XX
 PI Bosslet K, Pfeleiderer P, Seemann G;
 XX
 DR WPI; 1993-127068/16.
 DR N-PSDB; AAQ40046.
 XX
 PT New monoclonal antibody BW835 specific for tumour antigens -
 PT useful for diagnosis and treatment of tumours affecting the
 PT breasts, ovaries, prostate and lungs
 XX
 PS Disclosure; Fig 1a; 24pp; German.
 XX
 CC Monoclonal antibody BW 835 is produced by hybridoma cell line BW 835.
 CC The antibody strongly reacts with lung adenocarcinomas and human
 CC mammary-, ovary- and prostate carcinomas. It additionally reacts
 CC with polymorphic epithelial mucin (PEM) but does not react with
 CC normal human tissue.
 XX
 SQ Sequence 115 AA;
 Query Match 94.9%; Score 93; DB 14; Length 115;
 Best Local Similarity 94.7%; Pred. No. 7.9e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKSNDNYATHYAESVKG 19
 DB 46 EIRLKSNNYATHYAESVKG 64
 EIRLKSNDNYATHYAESVKG 19
 EIRLKSNNYATHYAESVKG 64
 RESULT 8
 AAY03869
 ID AAY03869 standard; Protein; 116 AA.
 AC
 AC AAY03869;
 XX
 DT 16-JUN-1999 (first entry)
 XX
 DE SM3 heavy chain variable region.
 XX
 KW SM3 antibody; epitope; mimic; crystal; tumour; MUC1 epitope; allergy;
 KW immune response; arthritis; multiple sclerosis; asthma; diabetes;
 KW inflammatory disorder; transplant rejection; graft versus host disease.
 XX
 OS Unidentified.
 XX
 XX WO9910379-A1.
 PN
 PD 04-MAR-1999.
 XX
 XX 24-AUG-1998; 98WO-GB02542.
 XX
 XX 22-AUG-1997; 97GB-0017946.
 XX
 PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
 XX
 PI Bates PA, Dokurno P, Freemont PS, Snary D, Sternberg MJE;
 XX
 DR WPI; 1999-204650/17.
 DR N-PSDB; AAX31971.
 XX
 PT New SM3 antibody crystal structures - used to develop agents for
 PT treating e.g. tumors, autoimmune disorders, allergies, inflammatory
 PT disorders or transplant rejection
 XX
 XX Disclosure; Page 279-280; 316pp; English.
 XX
 CC The invention relates to a process for preparing a crystal using cadmium.
 CC Structure factors or structural coordinates obtained from the crystal of
 CC SM3 antibody bound to an epitope can be used to design mimics of the
 CC antibody or the epitope. The crystals comprise at least an epitope

CC binding fragment of the SM3 antibody bound to a peptide recognised by the
 CC epitope binding site of SM3. The products and methods can be used to
 CC develop agents for the detection of tumour cells and for therapy against
 CC tumours. MUC1 epitope mimics can also be used to prevent or decrease an
 CC immune response, e.g. in the therapy of diseases caused by autoimmune
 CC responses (such as arthritis, multiple sclerosis, asthma or diabetes),
 CC allergies, inflammatory disorders or transplant rejections such as graft
 CC versus host disease. The present sequence represents the amino acid
 CC sequence of a heavy chain variable region of SM3 antibody.
 XX
 SQ Sequence 116 AA;
 Query Match 94.9%; Score 93; DB 20; Length 116;
 Best Local Similarity 94.7%; Pred. No. 7.9e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKSNDNYATHYAESVKG 19
 DB 50 EIRLKSNNYATHYAESVKG 68
 EIRLKSNDNYATHYAESVKG 19
 EIRLKSNNYATHYAESVKG 68
 RESULT 9
 AAW46958
 ID AAW46958 standard; Protein; 119 AA.
 XX
 AC AAW46958;
 XX
 DT 06-JUL-1998 (first entry)
 XX
 DE Amino acid sequence of a synthetic branched mucin type glycolipid.
 XX
 KW Branched mucin type glycolipid; V region; heavy chain; antibody;
 KW cancer treatment; diagnosis.
 XX
 OS Synthetic.
 XX
 XX JPI0084963-A.
 PN
 PD 07-APR-1998.
 XX
 XX 12-SEP-1996; 96JP-0241725.
 XX
 XX 12-SEP-1996; 96JP-0241725.
 XX
 PA (TOVJ) TOSOH CORP.
 XX
 DR WPI; 1998-264850/24.
 DR N-PSDB; AAV22331.
 XX
 PT Recognising branched mucin type synthetic glycolipid - using gene
 PT fragment of an antibody, useful in cancer treatment and diagnosis
 XX
 PS Disclosure; Pages 4-5; 6pp; Japanese.
 XX
 CC The present sequence represents a branched mucin type synthetic
 CC glycolipid. A gene fragment encoding the V region of the heavy
 CC chain of an antibody recognising the present protein is claimed.
 CC The antibody gene fragment is useful for the development of cancer
 CC treatments and diagnosing agents.
 XX
 SQ Sequence 119 AA;
 Query Match 94.9%; Score 93; DB 19; Length 119;
 Best Local Similarity 94.7%; Pred. No. 8.2e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKSNDNYATHYAESVKG 19
 DB 50 EIRLKSNNYATHYAESVKG 68
 EIRLKSNDNYATHYAESVKG 19
 EIRLKSNNYATHYAESVKG 68
 RESULT 10
 AAW01589

KW	specific binding assay; affinity purification; drug targeting;
KW	toxin targeting; imaging; genetic; therapeutic.
XX	
OS	Homo sapiens.
XX	
PN	US6054561-A.
XX	
PD	25-APR-2000.
XX	
PF	07-JUN-1995; 95US-0483749.
XX	
XX	21-MAR-1986; 86US-0842476.
PR	08-MAY-1988; 88US-0190778.
PR	08-FEB-1984; 84US-0577976.
PR	11-JAN-1985; 85US-0690750.
PR	11-AUG-1994; 94US-0288981.
XX	
XX	(CHIR) CHIRON CORP.
XX	
XX	Ring DB;
XX	
XX	WPI; 2000-338508/29.
DR	N-PSDB; AAA38896.
XX	
PT	Monoclonal antibody capable of binding to human breast cancer antigen
PT	useful for affinity purification, drug or toxin targeting, imaging, and
PT	treating cancer -
XX	
XX	Disclosure; Fig 1; 57pp; English.
PS	
XX	
CC	The present invention describes a monoclonal antibody (MAB) (I) that
CC	binds to a human breast cancer antigen that is also bound by MAB 454C11
CC	and 520C9 (produced hybridoma ATCC HB8484 and HB8696, respectively). Also
CC	described is a hybridoma that produces (I). (I) is useful in specific
CC	binding assays, affinity purification, drug or toxin targeting, imaging,
CC	and genetic or immunological therapeutics for various cancers. The
CC	present sequence represents a VH domain derived from a 2G3 hybridoma,
CC	which is used in the exemplification of the present invention.
XX	
SQ	Sequence 122 AA;
	Query Match 94.9%; Score 93; DB 21; Length 122;
	Best Local Similarity 94.7%; Pred. No. 8.4e-08;
	Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0
QY	1 EIRLKSNDNYATHYAESVKG 19
	:
Db	50 EIRLKSNNYATHYAESVKG 68
	RESULT 12
	AAW06212
ID	AAW06212 standard; Protein; 142 AA.
XX	
AC	AAW06212;
XX	
DT	12-FEB-1997 (first entry)
XX	
DE	MAB Br-3 heavy chain variable region.
XX	
KW	Chimeric antibody; monoclonal antibody; Br-3; antibody engineering;
KW	tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
KW	ovary carcinoma; cancer; diagnosis; therapy; heavy chain.
XX	
OS	Mus sp.
XX	
XX	US5576184-A.
PN	
PD	19-NOV-1996.
XX	
XX	
PF	06-SEP-1988; 88US-0240624.
XX	
XX	06-MAY-1991; 91US-0659401.

```

PR 06-SEP-1988; 88US-0240624.
PR 08-SEP-1988; 88US-0241744.
PR 13-SEP-1988; 88US-0243739.
PR 04-OCT-1988; 88US-0253002.
PR 19-JUN-1989; 89US-0367641.
PR 21-JUL-1989; 89US-0382768.
PR 27-DEC-1994; 94US-0364001.
XX (XOMA ) XOMA CORP.
XX
XX Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
XX WPI; 1997-011249/01.
XX N-PSDB; AAT43437.
XX
XX Chimeric mouse-human antibodies - recognise a human tumour antigen,
XX used for the treatment and diagnosis of human cancers
XX
XX Example 3; Fig 15; 102pp; English.
XX
XX The heavy chain variable region (AAW06212) of mouse monoclonal
XX antibody Br-3 is the product of a cDNA clone (AAT43437) isolated
XX from a Br-3 hybridoma cDNA library. MAb Br-3 (IgG1) binds to an
XX antigen that is expressed on the surface of human lung, breast,
XX colon and ovary carcinomas, but not on most normal adult tissues.
XX The heavy chain and light chain variable regions (see also AAW06211)
XX of B38-1 can be linked to human constant regions and expressed in
XX transformed host cells. Novel mouse-human chimeric antibodies (see
XX also AAW06209-10 and AAW06213-18) can be produced that have specificity
XX to human tumour antigens and can be used for the treatment and
XX diagnosis of human cancer.
XX
XX Sequence 142 AA;
SQ
Query Match 94.9%; Score 93; DB 18; Length 142;
Best Local Similarity 94.7%; Pred. No. 1e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
DB 69 EIRLKSNNYATHYAESVKG 87
|||||:|||||
|||||:|||||

RESULT 13
AAW85059
ID AAW85059 standard; Protein; 142 AA.
XX
XX AAW85059;
XX
XX 16-APR-1999 (first entry)
XX
XX Mouse Br-3 heavy chain variable region.
XX
XX Heavy chain variable region; murine antibody Br-3; antibody ING-1;
XX chimeric immunoglobulin; human tumour antigen; chimeric antibody;
XX treatment; human cancer.
XX
XX Mus sp.
XX
XX US5843685-A.
XX
XX 01-DEC-1998.
XX
XX 06-JUN-1995; 95US-0466034.
XX
XX 06-SEP-1989; 89WO-US03852.
XX 06-SEP-1988; 88US-0240624.
XX 08-SEP-1988; 88US-0241744.
XX 13-SEP-1988; 88US-0243739.
XX 04-OCT-1988; 88US-0253002.
XX 19-JUN-1989; 89US-0367641.
XX 21-JUL-1989; 89US-0382768.
XX 27-DEC-1994; 94US-0364001.

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```

PR 06-JUN-1995; 95US-0466034.
XX (XOMA ) XOMA CORP.
XX
XX Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
XX WPI; 1999-044574/04.
XX N-PSDB; AAV71155.
XX
XX Chimeric antibody specific for human tumour antigen - useful as
XX immunoassay, imaging or antitumour agent
XX
XX Example 3; Fig 15; 92pp; English.
XX
XX The present sequence represents the heavy chain variable region of
XX murine antibody Br-3. The sequence was used to create chimeric
XX mouse-human immunoglobulins which recognise the human tumour
XX antigen bound by antibody ING-1 (produced by hybridoma cell line
XX ATCC HB 9812). The chimeric antibodies also have an antigen-binding
XX site that competitively inhibits the binding of antibody ING-1, and
XX mediate complement-dependent cytotoxicity of target cells or
XX antibody-dependent cellular cytotoxicity to target cells. The
XX chimeric antibodies can be used for therapeutic purposes in the
XX treatment of human cancer.
XX
XX Sequence 142 AA;
SQ
Query Match 94.9%; Score 93; DB 20; Length 142;
Best Local Similarity 94.7%; Pred. No. 1e-07;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
DB 69 EIRLKSNNYATHYAESVKG 87
|||||:|||||
|||||:|||||

RESULT 14
AAW09423
ID AAW09423 standard; Protein; 143 AA.
XX
XX AAW09423;
XX
XX 04-MAR-1993 (first entry)
XX
XX Br-3 Heavy Chain V Region (mouse).
XX
XX Monoclonal antibody; chimera; light; heavy; chain; constant;
XX variable; antigen; diagnosis; cancer; tumour.
XX
XX Mus musculus.
XX
XX WO9002569-A.
XX
XX 22-MAR-1990.
XX
XX 06-SEP-1989; 89WO-US03852.
XX
XX 06-SEP-1988; 88US-0240624.
XX 08-SEP-1988; 88US-0241744.
XX 13-SEP-1988; 88US-0243739.
XX 04-OCT-1988; 88US-0253002.
XX 19-JUN-1989; 89US-0367641.
XX 21-JUL-1989; 89US-0382768.
XX
XX (ITGE-) INT GENETIC ENG INC.
XX
XX Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX WPI; 1990-115825/15.
XX N-PSDB; AAQ08605.
XX
XX Chimeric mouse-human antibodies - prepd. using genes coding for
XX constant human region murine variable region, esp. to 3 tumour

```

PT antigen
 PS Claim 13; Page 123 + Fig 15; 173pp; English.
 CC The sequence is used in the prodn. of a chimeric antibody mol.
 CC comprising two light chains and two heavy chains, each having a
 CC constant region (human) and a variable region (murine) having
 CC specificity to an antigen bound by murine monoclonal antibody
 CC (Mab) Br-3. The chimeric antibodies can be used for any purpose for
 CC which the original murine MAb can be used, with the advantage that
 CC they are more compatible with the human body. They are esp. used for
 CC the diagnosis and treatment of cancer.
 XX
 XX Sequence 143 AA;
 SQ
 Query Match 94.9%; Score 93; DB 11; Length 143;
 Best Local Similarity 94.7%; Pred. No. 1e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKSNDNYATHYAESVKG 19
 |||||:|||||||
 DB 69 EIRLKSNNYATHYAESVKG 87
 |||||:|||||||
 RESULT 15
 AAU72870
 ID AAU72870 standard; Protein; 255 AA.
 XX
 AC AAU72870;
 XX
 DT 26-FEB-2002 (first entry)
 XX
 DE P5-23 single chain Fv.
 XX
 KW Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour;
 KW autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary;
 KW intrahepatic bile duct; pancreas; lung; larynx; breast; uterus; cervix;
 KW prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv;
 KW sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAPI0;
 KW helminth; cytostatic; antimicrobial; immunomodulatory; 11B2D10; 6H7E7;
 KW 8G7C10; 6E5A7; 11B2D10x4-7; 8G7C10x4-7; 6E5A7x4-7; P4-2; P4-3; P4-14;
 KW P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-23; 3B10xP4-3; 3B10xP4-14;
 KW P53 tetramerisation domain; 3B10xP5-2; 3B10xP5-23.
 XX
 OS Homo sapiens.
 XX
 XX WO200171005-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 26-MAR-2001; 2001WO-EP03414.
 PF
 XX 24-MAR-2000; 2000EP-0106467.
 PR
 XX (KUFE/) KUPER P.
 PA
 XX Kufer P, Riethmuller G, Lutterbues R, Borschert K, Kischel R;
 PI Mayer M, Hofmeister R;
 DR WPI: 2002-055119/07.
 DR N-PSDB; AAS97144.
 DR
 XX Multifunctional polypeptides comprising binding sites that specifically
 PT recognise extracellular groups of the NKG2D receptor complex and
 PT domains which function as receptors or ligands, useful for treating
 PT cancers and infectious diseases -
 XX
 XX Example 7; Fig 16; 114pp; English.
 PS
 XX The invention relates to a multifunctional polypeptide comprising a
 CC domain with a binding site that specifically recognises an extracellular
 CC group of the NKG2D receptor complex and a second domain which functions
 CC as a receptor or ligand. The polypeptide and its associated

CC polynucleotide are used for the preparation of a pharmaceutical
 CC composition for the treatment of cancer, infections and/or autoimmune
 CC conditions. The cancer may be a tumour of the head and neck, stomach,
 CC oesophagus, colon, liver, intrahepatic bile ducts, pancreas, lung,
 CC larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyroid,
 CC bladder or brain, or a melanoma, myeloma, sarcoma, leukaemia or lymphoma.
 CC The infectious diseases can be caused by viruses, bacteria, fungi,
 CC protozoa or helminths. The autoimmune diseases include multiple
 CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior
 CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and
 CC autoimmune hepatitis. Sequences AAU72820-AAU72875 represent the NKG2D
 CC receptor and the polypeptides of the invention.
 XX
 XX Sequence 255 AA;
 SQ
 Query Match 94.9%; Score 93; DB 23; Length 255;
 Best Local Similarity 94.7%; Pred. No. 2e-07;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLKSNDNYATHYAESVKG 19
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 DB 51 EIRLKSNNYATHYAESVKG 69
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 Job time : 49.1786 secs

GenCore version 5.1.4 p5 4578
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Run on: April 22, 2003, 12:53:59 ; Search time 20.0179 Seconds
(without alignments)
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Title: US-09-674-716B-11

Perfect score: 98
Sequence: 1 EIRLKSNDVATHYAESVKG 19

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Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 301932

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

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- 2: /cgn2_6/prodata/1/pubpaa/RCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 11: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	98	100.0	285	10	US-09-883-758-4
2	95	96.9	100	10	US-09-840-459-36
3	95	96.9	298	10	US-09-883-758-2
4	91	92.9	151	10	US-09-564-329A-15
5	91	92.9	151	10	US-09-855-153-15
6	91	92.9	151	10	US-09-854-811-15
7	91	92.9	151	10	US-09-934-773-15
8	91	92.9	151	10	US-09-963-620-15
9	74	75.5	119	9	US-10-043-432-5
10	74	75.5	119	10	US-09-756-301A-5
11	74	75.5	119	10	US-09-927-703-5
12	74	75.5	119	10	US-09-766-535A-5
13	74	75.5	119	10	US-09-756-161A-5
14	74	75.5	119	12	US-10-010-229-5
15	74	75.5	119	12	US-10-043-450-5
16	74	75.5	119	12	US-10-044-534-5
17	68	69.4	19	10	US-09-839-666-4
18	68	69.4	27	10	US-09-839-666-21
19	66	67.3	100	10	US-09-840-459-35

20	65	66.3	19	10	US-09-835-087-18	Sequence 18, Appl
21	65	66.3	101	10	US-09-840-459-34	Sequence 34, Appl
22	65	66.3	117	10	US-09-835-087-8	Sequence 8, Appl
23	65	66.3	117	10	US-09-835-087-10	Sequence 10, Appl
24	65	66.3	117	10	US-09-835-087-11	Sequence 11, Appl
25	65	66.3	117	10	US-09-835-087-12	Sequence 12, Appl
26	65	66.3	117	10	US-09-835-087-13	Sequence 13, Appl
27	65	66.3	117	10	US-09-803-739-12	Sequence 12, Appl
28	65	66.3	117	10	US-09-803-739-20	Sequence 20, Appl
29	65	66.3	117	10	US-09-803-739-21	Sequence 21, Appl
30	65	66.3	117	10	US-09-803-739-22	Sequence 22, Appl
31	65	66.3	117	10	US-09-803-739-23	Sequence 23, Appl
32	65	66.3	117	10	US-09-840-459-10	Sequence 10, Appl
33	65	66.3	117	10	US-09-840-459-17	Sequence 17, Appl
34	65	66.3	117	10	US-09-840-459-18	Sequence 18, Appl
35	65	66.3	117	10	US-09-840-459-19	Sequence 19, Appl
36	65	66.3	117	10	US-09-840-459-20	Sequence 20, Appl
37	65	66.3	119	10	US-09-840-459-104	Sequence 104, App
38	65	66.3	148	10	US-09-840-459-100	Sequence 100, App
39	64	65.3	123	10	US-09-893-615-87	Sequence 87, Appl
40	63	64.3	143	10	US-09-881-823-16	Sequence 16, Appl
41	60	61.2	115	10	US-09-840-459-75	Sequence 75, Appl
42	58	59.2	126	10	US-09-840-459-74	Sequence 74, Appl
43	57	58.2	35	9	US-09-956-206A-33	Sequence 33, Appl
44	57	58.2	245	9	US-09-880-748-1979	Sequence 1979, Ap
45	56	57.1	127	10	US-09-840-459-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-09-883-758-4
; Sequence 4, Application US/09883758
; Patent No. US2002058804A1
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/883,758
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: US/09/318,661
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment
US-09-883-758-4
Query Match 100.0%; Score 98; DB 10; Length 285;
Best Local Similarity 100.0%; Pred. No. 6e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIRLKSNDVATHYAESVKG 19
|||
Db 203 EIRLKSNDVATHYAESVKG 221
RESULT 2
US-09-840-459-36
; Sequence 36, Application US/09840459
; Patent No. US20020150576A1
; GENERAL INFORMATION:
; APPLICANT: LaRosa, Gregory J.


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; PRIOR FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1998-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-855-153-15

Query Match          92.9%; Score 91; DB 10; Length 151;
Best Local Similarity 89.5%; Pred. No. 3.8e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
||||:|||||
DB 69 EIRLRSYNYATHYAESVKG 87

RESULT 6
US-09-854-811-15
; Sequence 15, Application US/09854811
; Patent No. US20020119157A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCT: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/854,811
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-854-811-15

Query Match          92.9%; Score 91; DB 10; Length 151;
Best Local Similarity 89.5%; Pred. No. 3.8e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
||||:|||||
DB 69 EIRLRSYNYATHYAESVKG 87

RESULT 7
US-09-934-773-15
; Sequence 15, Application US/09934773
; Patent No. US20020136689A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCT: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/934,773
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03

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; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 09/308,503
; PRIOR FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 151
; TYPE: PRT
; ORGANISM: SCID Mice
US-09-934-773-15

Query Match          92.9%; Score 91; DB 10; Length 151;
Best Local Similarity 89.5%; Pred. No. 3.8e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
||||:|||||
DB 69 EIRLRSYNYATHYAESVKG 87

RESULT 8
US-09-963-620-15
; Sequence 15, Application US/09963620
; Patent No. US20020141941A1
; GENERAL INFORMATION:
; APPLICANT: Reiter, Robert E.
; APPLICANT: Witte, Owen N.
; APPLICANT: Saffran, Douglas C.
; TITLE OF INVENTION: PSCT: PROSTATE STEM CELL ANTIGEN AND USES THEREOF
; FILE REFERENCE: 30435.54US14
; CURRENT APPLICATION NUMBER: US/09/963,620
; CURRENT FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 09/564,329
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/359,326
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 08/814,279
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: 60/071,141
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/074,675
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: 60/113,230
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: 60/120,536
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: 60/124,658
; PRIOR FILING DATE: 1999-03-16
; PRIOR APPLICATION NUMBER: 09/038,261
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 09/203,939
; PRIOR FILING DATE: 1998-12-02
; PRIOR APPLICATION NUMBER: 09/251,835
; PRIOR FILING DATE: 1999-02-17

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;; PRIOR APPLICATION NUMBER: 09/308,503
;; PRIOR FILING DATE: 1999-05-25
;; NUMBER OF SEQ ID NOS: 27
;; SOFTWARE: PatentIn Ver. 2.0
;; SEQ ID NO 15
;; LENGTH: 151
;; TYPE: PRT
;; ORGANISM: SCID Mice
US-09-963-620-15

Query Match 92.9%; Score 91; DB 10; Length 151;
Best Local Similarity 89.5%; Pred. No. 3.8e-07;
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
Db 69 EIRLSENATHYAESVKG 87

RESULT 9
US-10-043-432-5
; Sequence 5, Application US/10043432
; Publication No. US20030054004A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US/10/043,432
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-043-432-5

Query Match 75.5%; Score 74; DB 9; Length 119;
Best Local Similarity 84.2%; Pred. No. 0.00014;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
Db 69 EIRLSENATHYAESVKG 87

RESULT 9
US-10-043-432-5
; Sequence 5, Application US/10043432
; Publication No. US20030054004A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US/10/043,432
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-10-043-432-5

QY 1 EIRLSDNYATHYAESVKG 19
Db 50 EIRSKSINSATHYAESVKG 68

RESULT 10
US-09-756-301A-5
; Sequence 5, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-008
; CURRENT FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: US/09/756,301A
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-756-301A-5

Query Match 75.5%; Score 74; DB 10; Length 119;
Best Local Similarity 84.2%; Pred. No. 0.00014;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
Db 50 EIRSKSINSATHYAESVKG 68

RESULT 11
US-09-927-703-5
; Sequence 5, Application US/09927703
; Patent No. US2002002720A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-927-703-5

Query Match 75.5%; Score 74; DB 10; Length 119;
Best Local Similarity 84.2%; Pred. No. 0.00014;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
Db 50 EIRSKSINSATHYAESVKG 68

RESULT 11
US-09-927-703-5
; Sequence 5, Application US/09927703
; Patent No. US2002002720A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-927-703-5

Query Match 75.5%; Score 74; DB 9; Length 119;
Best Local Similarity 84.2%; Pred. No. 0.00014;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EIRLSDNYATHYAESVKG 19
Db 50 EIRSKSINSATHYAESVKG 68

RESULT 11
US-09-927-703-5
; Sequence 5, Application US/09927703
; Patent No. US2002002720A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; TITLE OF INVENTION: Human Tumor Necrosis Factor
; FILE REFERENCE: 0975.1005-013
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US/09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,093
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/010,406
; PRIOR FILING DATE: 1993-01-29
; PRIOR APPLICATION NUMBER: U.S. 08/013,413
; PRIOR FILING DATE: 1993-02-02
; PRIOR APPLICATION NUMBER: U.S. 07/943,852
; PRIOR FILING DATE: 1992-09-11
; PRIOR APPLICATION NUMBER: U.S. 07/853,606
; PRIOR FILING DATE: 1992-03-18
; PRIOR APPLICATION NUMBER: U.S. 07/670,827
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Mus Balb/c
US-09-927-703-5

	PRIOR FILING DATE:	1998-08-12	08/570,674
	PRIOR APPLICATION NUMBER:	U.S.	
	PRIOR FILING DATE:	1995-12-11	08/324,799
	PRIOR APPLICATION NUMBER:	U.S.	
	PRIOR FILING DATE:	1994-10-18	08/192,102
	PRIOR APPLICATION NUMBER:	U.S.	
	PRIOR FILING DATE:	1994-02-04	08/192,861
	PRIOR APPLICATION NUMBER:	U.S.	
	PRIOR FILING DATE:	1994-02-04	08/192,093
	PRIOR APPLICATION NUMBER:	U.S.	
	PRIOR FILING DATE:	1994-02-04	08/010,406
	PRIOR APPLICATION NUMBER:	U.S.	

Query Match 75.5%; Score 74; DB 10; Length 119;

RESULT 15
US-10-043-450-5
; Sequence 5, Application US/10043450
; Patent No. US20020141996A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
; APPLICANT: Wilcek, Peter
; APPLICANT: Daddona, Peter
; APPLICANT: Ghrayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott
; TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
; FILE REFERENCE: 0975.1005-013
; CURRENT APPLICATION NUMBER: US/10/043,450
; CURRENT FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 09/927,703
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/756,398
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: U.S. 09/133,119
; PRIOR FILING DATE: 1998-08-12
; PRIOR APPLICATION NUMBER: U.S. 08/570,674
; PRIOR FILING DATE: 1995-12-11
; PRIOR APPLICATION NUMBER: U.S. 08/324,799
; PRIOR FILING DATE: 1994-10-18
; PRIOR APPLICATION NUMBER: U.S. 08/192,102
; PRIOR FILING DATE: 1994-02-04
; PRIOR APPLICATION NUMBER: U.S. 08/192,861
; PRIOR FILING DATE: 1994-02-04

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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:07:14 ; Search time 15 seconds
(without alignments)
102.543 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81

Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 2770

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	33.3	15	2 C44101	calmodulin, vasoac
2	27	33.3	16	2 S09732	photosystem I prot
3	26	32.1	12	2 S09082	proteasome chain 1
4	25	30.9	13	2 S09733	photosystem I prot
5	22	27.2	10	2 B24736	inhibin beta-B cha
6	22	27.2	13	2 S54344	glyceraldehyde-3-p
7	22	27.2	14	2 A28018	very late antigen-
8	22	27.2	15	2 S21240	alpha-glucosidase
9	22	27.2	15	2 S21202	glucan 1,4-alpha-g
10	22	27.2	16	2 A44101	calmodulin, vasoac
11	21	25.9	11	2 PH0914	T-cell receptor be
12	21	25.9	14	2 PC2373	probable IMP dehyd
13	21	25.9	14	2 PH1311	Ig heavy chain DJ
14	21	25.9	15	2 A47146	topoisomerase I -
15	21	25.9	15	2 A36279	chemoattractant pr
16	21	25.9	15	2 B26501	lipoprotein lipase
17	20	24.7	10	2 PT0243	Ig heavy chain CRD
18	20	24.7	13	2 J02309	hypothetical 1.6K
19	20	24.7	13	2 J02319	hypothetical 1.6K
20	20	24.7	15	2 I46512	troponin - rabbit
21	20	24.7	15	2 JF0101	fibrinogen alpha c
22	20	24.7	15	2 PH1314	Ig heavy chain DJ
23	20	24.7	15	2 PH1616	Ig H chain V-D-J r
24	20	24.7	15	2 S71396	dihydropyrimidine
25	20	24.7	16	2 C39509	mannose-specific 1
26	19.5	24.1	16	2 E28027	protein p8 - curle
27	19	23.5	10	2 A60476	S-layer protein -
28	19	23.5	11	2 A29806	acidic proline-ric
29	19	23.5	12	2 S68402	NAD(+)-glycohydrol

30	19	23.5	12	2 PH0930	T-cell receptor be
31	19	23.5	13	2 G83988	hypothetical prote
32	19	23.5	16	2 G45681	orf 61.1 - phage T
33	18	22.2	8	2 A28719	thymic humoral fac
34	18	22.2	9	2 B20569	serum amyloid P-co
35	18	22.2	10	2 S10926	inhibin beta-A cha
36	18	22.2	10	2 G58501	48K bile/gallblad
37	18	22.2	11	2 B29806	acidic proline-ric
38	18	22.2	11	2 PD0441	translation elonga
39	18	22.2	13	2 B26093	microbial collagen
40	18	22.2	13	2 S47390	T-cell antigen rec
41	18	22.2	14	1 NTKN1M	alpha-conotoxin M1
42	18	22.2	14	2 E33098	214K exoantigen (v
43	18	22.2	15	2 S32677	nitrogenase cofact
44	18	22.2	15	2 PA0058	protein QF200022 -
45	18	22.2	15	2 G35141	T-cell receptor de

ALIGNMENTS

RESULT 1

C44101
calmodulin, vasoactive intestinal peptide-binding protein, VIP binding protein, p18 - gu
C:Species: Cavia porcellus (guinea pig)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: C44101
R:Stallwood, D.; Brugger, C.H.; Baggenstoss, B.A.; Stemmer, P.M.; Shiraga, H.; Landers, J. Biol. Chem. 267, 19617-19621, 1992
A:Title: Identity of a membrane-bound vasoactive intestinal peptide-binding protein with
A:Reference number: A44101; MUID:92406918; PMID:1527080
A:Accession: C44101
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <STA>
A:Experimental source: lung membranes
A:Note: sequence extracted from NCBI backbone (NCBIP:114109)
C:Keywords: intestine

Query Match 33.3%; Score 27; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 KDGKTYLN 16
||| |:
Db 4 KDGNYVIS 11

RESULT 2

S09732
photosystem I protein psaJ - spinach chloroplast (fragment)
C:Species: chloroplast Spinacia oleracea (spinach)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Feb-1997
C:Accession: S09732
R:Ikeuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y. FEBS Lett. 263, 274-278, 1990
A:Title: Polypeptide composition of higher plant photosystem I complex. Identification
A:Reference number: S09730; MUID:90242987; PMID:2185953
A:Accession: S09732
A:Molecule type: protein
A:Residues: 1-16 <IKE>
C:Genetics:
A:Gene: psaJ
A:Genome: chloroplast
C:Keywords: chloroplast; photosynthesis; photosystem I; transmembrane protein

Query Match 33.3%; Score 27; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 4.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 KDGKTYLN 16
:|:|:|:
Db 2 RDKFTYLS 9

RESULT 3

S09082

proteasome chain 1 - rat (fragment)

N;Alternate names: multicatalytic proteinase chain 1

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Aug-1998

C;Accession: S09082

R;Lilley, K.S.; Davison, M.D.; Rivett, A.J.

FEBS Lett. 262, 327-329, 1990

A;Title: N-terminal sequence similarities between components of the multicatalytic prote

A;Reference number: S09082; MUID:90242957; PMID:2335214

A;Accession: S09082

A;Molecule type: protein

A;Residues: 1-12 <LIL>

C;Superfamily: multicatalytic endopeptidase, complex chain C9

Query Match 32.1%; Score 26; DB 2; Length 12;

Best Local Similarity 66.7%; Pred. No. 4.4e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 LLYKDG 11

: : : : : :

DB 6 VVYKDG 11

RESULT 4

S09733

photosystem I protein psaJ - garden pea chloroplast (fragment)

C;Species: chloroplast Pium sativum (garden pea)

C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Feb-1997

C;Accession: S09733

R;Kueuchi, M.; Hirano, A.; Hiyama, T.; Inoue, Y.

FEBS Lett. 263, 274-278, 1990

A;Title: Polypeptide composition of higher plant photosystem I complex. Identification c

A;Reference number: S09733; MUID:90242987; PMID:2185953

A;Accession: S09733

A;Molecule type: protein

A;Residues: 1-13 <LKE>

C;Genetics:

A;Gene: psaJ

A;Genome: chloroplast

C;Keywords: chloroplast; photosynthesis; photosystem I; transmembrane protein

Query Match 30.9%; Score 25; DB 2; Length 13;

Best Local Similarity 71.4%; Pred. No. 7.1e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 KDGKTYL 15

: : : : : :

DB 2 RDLKTYL 8

RESULT 5

B24736

inhibin beta-B chain - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 30-Sep-1993

C;Accession: B24736

R;King, N.; Ying, S.Y.; Ueno, N.; Esch, F.; Denoroy, L.; Guillemin, R.

Proc. Natl. Acad. Sci. U.S.A. 82, 7217-7221, 1985

A;Reference number: A24736; MUID:86042637; PMID:3864157

A;Accession: B24736

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-10 <LIN>

Query Match 27.2%; Score 22; DB 2; Length 10;

Best Local Similarity 55.6%; Pred. No. 1.7e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 LYDKGKTYL 15

Db 2 LEXDGRNL 10

RESULT 6

S54344

glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - bovine (fragm

C;Species: Bos primigenius taurus (cattle)

C;Date: 27-Oct-1995 #sequence_revision 30-Jan-1998 #text_change 03-Jun-2002

C;Accession: S54344

R;Okazaki, K.; Obata, N.H.; Inoue, S.; Hidaka, H.

Biochem. J. 306, 551-555, 1995

A;Title: S100-beta is a target protein of neurocalcin delta, an abundant isoform in glia

A;Reference number: S54343; MUID:95194333; PMID:7887910

A;Accession: S54344

A;Molecule type: protein

A;Residues: 1-13 <OKA>

C;Keywords: oxidoreductase

Query Match 27.2%; Score 22; DB 2; Length 13;

Best Local Similarity 50.0%; Pred. No. 2.2e+03;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 LYKDGK 12

: : : : : :

DB 7 LWRDGR 12

RESULT 7

A28018

very late antigen-1 alpha chain - human (fragment)

N;Alternate names: VLA-1 alpha chain

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994

C;Accession: A28018

R;Takada, Y.; Strominger, J.L.; Hemler, M.E.

Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987

A;Title: The very late antigen family of heterodimers is part of a superfamily of molecu

A;Reference number: A94151; MUID:87204112; PMID:3033641

A;Accession: A28018

A;Molecule type: protein

A;Residues: 1-14 <TAK>

C;Keywords: duplication; heterodimer; membrane protein

Query Match 27.2%; Score 22; DB 2; Length 14;

Best Local Similarity 57.1%; Pred. No. 2.4e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 KDGKTYL 15

: : : : : :

DB 6 KDSMTFL 12

RESULT 8

S21240

alpha-glucosidase (EC 3.2.1.20) I - Bacillus "thermoamyloliquefaciens" (fragment)

C;Species: Bacillus "thermoamyloliquefaciens"

C;Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 21-Aug-1998

C;Accession: S21240

R;Suzuki, Y.; Yonezawa, K.; Hattori, M.; Takii, Y.

Eur. J. Biochem. 205, 249-256, 1992

A;Title: Assignment of Bacillus thermoamyloliquefaciens KP1071 alpha-glucosidase I to an

nce and in structural parameters calculated from the amino acid composition.

A;Reference number: S21202; MUID:92209510; PMID:155585

A;Accession: S21240

A;Molecule type: protein

A;Residues: 1-15 <SUZ>

A;Experimental source: strain KP1071

C;Superfamily: alpha-glucosidase; alpha-amylase core homology

C;Keywords: glycosidase; hydrolase

Query Match 27.2%; Score 22; DB 2; Length 15;

Best Local Similarity 36.4%; Pred. No. 2.6e+03;

Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KSLLYKDGKTY 14
| : | : |
Db 2 KKAWKKEGVVY 12

RESULT 9
S21202
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - Bacillus stearothermophilus (fragment)
N:Alternate names: exo-alpha-1-4-glucosidase I
C:Species: Bacillus stearothermophilus
C:Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 21-Aug-1998
C:Accession: S21202
R:Suzuki, Y.; Yonezawa, K.; Hattori, M.; Takii, Y.
Eur. J. Biochem. 205, 249-256, 1992
A:Title: Assignment of Bacillus thermoamylioliquefaciens KP1071 alpha-glucosidase I to an
nase and in structural parameters calculated from the amino acid composition.
A:Reference number: S21202; MUID:92209510; PMID:1555585
C:Accession: S21202
A:Molecule type: protein
A:Residues: 1-15 <SUZ>
A:Experimental source: ATCC 12016
C:Superfamily: alpha-glucosidase; alpha-amylase core homology
C:Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 2.6e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KSLLYKDGKTY 14
| : | : |
Db 2 KKTWKEGVAY 12

RESULT 10
A44101
calmodulin, vasoactive intestinal peptide-binding protein, VIP binding protein, p18 - gu
C:Species: Cavia porcellus (guinea pig)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 29-Sep-1999
C:Accession: A44101
R:Stallwood, D.; Brugger, C.H.; Baggenstoss, B.A.; Stemmer, P.M.; Shiraga, H.; Landers,
J. Biol. Chem. 267, 19617-19621, 1992
A:Title: Identity of a membrane-bound vasoactive intestinal peptide-binding protein with
A:Reference number: A44101; MUID:92406918; PMID:1527080
C:Accession: A44101
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <STA>
A:Experimental source: lung membranes
A:Note: sequence extracted from NCBI backbone (NCBI:114120)
C:Superfamily: calmodulin; calmodulin repeat homology
C:Keywords: EF hand; intestine

Query Match 27.2%; Score 22; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 SLLYKDG 11
| : | : |
Db 4 SLFDKDG 10

RESULT 11
PH0914
T-cell receptor beta chain V-D-J region (isolate 7) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0914
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A:Reference number: PH0914; MUID:92078857; PMID:1836012

A:Accession: PH0914
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Experimental source: myelin basic protein-immunized lymph node
C:Keywords: T-cell receptor

Query Match 25.9%; Score 21; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.8e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SSKSLLYK 9
| : | : |
Db 3 SSDSLSYE 10

RESULT 12
PC2373
probable IMP dehydrogenase (EC 1.1.1.205) [similarity] - Bacillus cereus (strain ts-4)
C:Species: Bacillus Cereus
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: PC2373
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Saved, M.A.; Kajiwar, T.; Hatano, S.
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporulation i
A:Reference number: PC2369; MUID:95218265; PMID:7766022
C:Accession: PC2373
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <MAS>
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

Query Match 25.9%; Score 21; DB 2; Length 14;
Best Local Similarity 36.4%; Pred. No. 3.5e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 KSLLYKDGKTY 14
| : | : | : |
Db 3 ESKFWKEGLTF 13

RESULT 13
PH1311
Ig heavy chain DJ region (clone C68-101) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1311
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
C:Accession: PH1311
A:Molecule type: DNA
A:Residues: 1-14 <WAS>
C:Keywords: heterotetramer; immunoglobulin

Query Match 25.9%; Score 21; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 LLYKDGKT 13
| : | : | : |
Db 2 ILYHPGTT 9

RESULT 14
A47146
topoisomerase I - vaccinia virus (fragment)
C:Species: vaccinia virus
C:Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 31-Oct-1997
C:Accession: A47146
R:Klempner, N.; Traktman, P.
J. Biol. Chem. 269, 15887-15899, 1994

A;Title: Biochemical analysis of mutant alleles of the vaccinia virus topoisomerase I cd
 A;Reference number: A47146; MUID:93340198; PMID:8393454

A;Accession: A47146

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-15 <KLE>

A;Cross-references: GB:L13447

C;Superfamily: vaccinia virus DNA topoisomerase

Query Match 25.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 3.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 KDGKTY 14

DB 5 KDLRTY 10

RESULT 15

A36279

chemoattractant protein - earthworm (Lumbricus terrestris) (fragment)

C;Species: Lumbricus terrestris (common earthworm)

C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 30-Sep-1993

C;Accession: A36279

R;Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.

J. Biol. Chem. 265, 8736-8744, 1990

A;Title: Purification and characterization of a chemoattractant from electric shock-induced snakes.

A;Reference number: A36279; MUID:90256800; PMID:2160465

A;Accession: A36279

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-15 <JIA>

Query Match 25.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 45.5%; Pred. No. 3.7e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 SLLYKDGKTYL 15

DB 1 ALVCPFGFTYL 11

Search completed: April 22, 2003, 13:13:24

Job time : 16 secs

GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:55:49 ; Search time 24 Seconds
(without alignments)
27.651 Million cell updates/sec

Title: US-09-674-716B-3
Perfect score: 81
Sequence: 1 RSSKSLLYKDKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues 822

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	30.9	13	PSAJ_PEA	P17229 pisum sativ
2	22	27.2	15	MALT_BACTQ	P80072 bacillus th
3	21	25.9	15	MM01_RAT	P81563 rattus norv
4	20	24.7	14	MY14_BISFO	P46979 eisenia foe
5	20	24.7	15	FIBA_NAPL	P12801 anas platyr
6	19	23.5	10	SLAP_BACTG	P43325 bacillus th
7	18	22.2	9	SAMP_MUSCA	P19095 mustelus ca
8	18	22.2	10	PPCK_FASHE	P80525 fasciola he
9	18	22.2	10	SPI_HALRO	Q10997 halocynthia
10	18	22.2	14	CXA1_CONMA	P01521 conus magus
11	18	22.2	14	EFTU_CANFA	P54835 canis famil
12	18	22.2	14	MCRZ_METTM	P58816 methanobact
13	18	22.2	15	NIS1_ANAVA	Q44507 anabaena va
14	17	21.0	10	GONI_PETMA	P04378 petromyzon
15	17	21.0	10	SP34_DICMU	P81545 dictyosteli
16	17	21.0	10	TEMK_RANTE	P56923 rana tempor
17	17	21.0	10	UXA6_CHLTR	P38007 chlamydia t
18	17	21.0	11	CS15_BACSU	P81095 bacillus su
19	17	21.0	11	TKN2_UFERU	P08616 uperoeteia r
20	17	21.0	12	V14K_WSSV	P82006 white spot
21	17	21.0	13	LIGA_TRAVE	P20011 trameses ve
22	17	21.0	14	MY14_PHEVI	P46980 pheretima v
23	17	21.0	14	NEJ2_FASHE	P80526 fasciola he
24	17	21.0	14	UN07_CLOPA	P81352 clostridium
25	17	21.0	15	ATP2_PINPS	P81663 pinus pinas
26	17	21.0	15	CIQA_RAT	P31720 rattus norv
27	17	21.0	15	PC20_BRANA	P81096 brassica na
28	17	21.0	15	UC14_MAIZE	P80620 zea mays (m
29	17	21.0	16	MLB_SQUAC	P01207 squalus aca
30	16	19.8	10	COX0_RAT	P80432 rattus norv
31	16	19.8	10	TKNE_RANCA	P22689 rana catesb
32	16	19.8	10	TP1S_NICPL	P91118 nicotiana p
33	16	19.8	11	MORN_HUMAN	P01163 homo sapien

34 16 19.8 14 1 CXA1_CONCN P56973 conus conso
35 16 19.8 14 1 RS19_PPWBP Q52093 pigeon pea
36 16 19.8 15 1 MILT_ONCKE P81037 oncorhynchu
37 15 18.5 9 1 OXYA_SCYCA P42996 scyllorhinu
38 15 18.5 9 1 OXYA_SQUAC P42999 squalus aca
39 15 18.5 10 1 SYK_CAMUP Q46464 campylobact
40 15 18.5 13 1 LMT4_LOCMC P41490 locusta mig
41 15 18.5 13 1 MPI_MICOC P81532 microplitis
42 15 18.5 15 1 CXA1_CONGE P01519 conus geogr
43 15 18.5 15 1 FGF1_CANFA P18651 canis famil
44 15 18.5 15 1 PGKH_PHYPA P80659 physcomitre
45 15 18.5 15 1 UCI9_MAIZE P80625 zea mays (m

ALIGNMENTS

RESULT 1
PSAJ_PEA
ID PSAJ_PEA STANDARD; PRT; 13 AA.
AC P17229; 1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit IX (P81-J) (Fragment).
GN PSAJ.
OS Pisum sativum (Garden pea).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE
RX MEDLINE=90242987; PubMed=2185953;
RA Ikeuchi M., Hirano A., Hiyama T., Inoue Y.;
RT "Polypeptide composition of higher plant photosystem I complex.
RT Identification of psal, psaj and psak gene products.";
RL FEBS Lett. 263:274-278(1990).
CC -1- FUNCTION: May help in the organization of the psae and psaf
CC subunits.
CC -1- SIMILARITY: BELONGS TO THE PSAJ FAMILY.
CC PIR; S09733; S09733.
KW Chloroplast; Photosystem I; Photosynthesis; Transmembrane.
FT TRANSMEM 7 >13 POTENTIAL.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1516 MW; 9E2E45D11FDE3B41 CRC64;
Query Match 30.9%; Score 25; DB 1; Length 13;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 9 KDKTYL 15
DB 2 RDLKTYL 8
RESULT 2
MALT_BACTQ
ID MALT_BACTQ STANDARD; PRT; 15 AA.
AC P80072;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Maltase (EC 3.2.1.20) (Alpha-glucosidase I) (Fragment).
OS Bacillus thermoamyloliquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1425;
RN [1]
RP SEQUENCE.
RC STRAIN=KPI071 / FERM P8477;
RX MEDLINE=92209510; PubMed=1555585;
RA Suzuki Y., Yonezawa K., Hattori M., Takii Y.;

```

RT "Assignment of Bacillus thermoamylioliquefaciens KP1071
RT alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
RT similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence
RT and in structural parameters calculated from the amino acid
RT composition."
RL Eur. J. Biochem. 205:249-256(1992).
CC -|- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducing 1,4-
CC linked D-glucose residues with release of D-glucose.
CC -|- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
DR PIR; S21240; S21240.
KW Hydrolase; Glycosidase.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1929 MW; 62B4CE501F2D3042 CRC64;

Query Match 27.2%; Score 22; DB 1; Length 15;
Best Local Similarity 36.4%; Pred. No. 6.6e+02;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 KSLLYKDGKTY 14
DB 2 KKAWKKEGVVY 12

RESULT 3
MM01_RAT STANDARD; PRT; 15 AA.
AC P81563;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interstitial collagenase (EC 3.4.24.7) (Matrix metalloproteinase-1)
DE (MMP-1) (Fibroblast collagenase) (Myocardial collagenase) (fragment).
GN MMP1.
OS Rattus norvegicus (Rat).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=96201136; PubMed=8605638;
RA Tyagi S.C.; Cleutjens J.P.M.;
RT "Myocardial collagenase: purification and structural
RT characterization."
RL Can. J. Cardiol. 12:165-171(1996).
CC -|- FUNCTION: CLEAVES COLLAGENS OF TYPES I, II, AND III AT ONE SITE IN
CC THE HELICAL DOMAIN. ALSO CLEAVES COLLAGENS OF TYPES VII AND X. MAY
CC PLAY A ROLE IN THE DETERIORATION OF THE HEART WALL EXTRACELLULAR
CC MATRIX PROTEINS DURING THE ONSET OF DIALATED CARDIOMYOPATHY.
CC -|- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -|- COFACTOR: REQUIRES CALCIUM AND ZINC FOR ACTIVITY.
CC -|- ENZYME REGULATION: CAN BE ACTIVATED WITHOUT REMOVAL OF THE
CC ACTIVATION PEPTIDE.
CC -|- PTM: THE N-TERMINAL IS BLOCKED.
CC -|- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M10A.
KW Hydrolase; Metalloprotease; Zinc; Calcium; Collagen degradation;
KW Extracellular matrix.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1787 MW; 15A57D24C0F6FD80 CRC64;

Query Match 25.9%; Score 21; DB 1; Length 15;
Best Local Similarity 40.0%; Pred. No. 9.8e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLYKVD 10
:|:|:|

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Db 4 KSEKNADFKD 13

RESULT 4
MY14_EISFO STANDARD; PRT; 14 AA.
AC P46979;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myoactive tetradecapeptide (ETP).
OS Eisenia foetida (Common brandling worm) (Common dung-worm).
CC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
CC Lumbricina; Lumbricidae; Eisenia.
OX NCBI_TaxID=6396;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Gut;
RX MEDLINE=96087879; PubMed=8532604;
RA Ukena K.; Umi T.; Matsushima O.; Ikeda T.; Fujita T.; Minakata H.;
RA Nomoto K.;
RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
RT foetida."
RL Peptides 16:995-999(1995).
CC -|- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
CC MUSCLES.
CC -|- SIMILARITY: TO INSECTS ALLATOTROPIN.
CC Neuropeptide; Amidation.
FT MOD_RES 14 14
SQ SEQUENCE 14 AA; 1478 MW; CC9ABEF941CD91AD CRC64;

Query Match 24.7%; Score 20; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 YKDG 11
:|:|:|
DB 2 FKDG 5

RESULT 5
FIBA_ANAPL STANDARD; PRT; 15 AA.
AC P12801;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Anas platyrhynchos (Domestic duck).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RP SEQUENCE.
RX MEDLINE=85168193; PubMed=3983613;
RA Min Y.; Ping Z.; Yaoshi Z.;
RT "Purification and primary structures of duck fibrinopeptides A and
RT B."
RL Sci. Sin., B, Chem. Biol. Agric. Med. Earth Sci. 28:31-35(1985).
CC -|- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
CC AGGREGATION.
CC -|- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -|- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
DR PIR; JP0101; JP0101.
KW Blood coagulation; Plasma.
FT PEPTIDE 1 15
FT MOD_RES 1 1
FIBRINOPEPTIDE A.
PYRROLIDONE CARBOXYLIC ACID.

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FT NON TER 15 15
SQ SEQUENCE 15 AA; 1580 MW; D78A51FF88B40373 CRC64;

Query Match 24.7%; Score 20; DB 1; Length 15;
Best Local Similarity 36.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 RSKSLLYKDG 11
: |||:|
Db 1 QDGKSSFOKEG 11

RESULT 6
SLAP_BACTG
ID SLAP_BACTG STANDARD; PRT; 10 AA.
AC P49325;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE S-layer protein (Surface layer protein) (Fragment).
OS Bacillus thuringiensis (subsp. galleriae).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=29338;
RN [1]
RP SEQUENCE.
RC STRAIN=NRRL 4045; PubMed=2592346;
RX MEDLINE=90078111; Beveridge T.J.;
RA Luckevid M.D.;
RT "Characterization of a dynamic S layer on Bacillus thuringiensis.";
RL J. Bacteriol. 171:6656-6667(1989).
CC -I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH OBLIQUE (P2) SYMMETRY.
CC Cell wall; S-layer.
KW NON TER 10 10
SQ SEQUENCE 10 AA; 1080 MW; 57AECACAB769D1A3 CRC64;

Query Match 23.5%; Score 19; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 GKTY 14
|||:
Db 2 GKTF 5

RESULT 7
SAMP MUSCA
ID -SAMP MUSCA STANDARD; PRT; 9 AA.
AC P19055;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serum amyloid P-component (SAP) (Fragment).
OS Mustelus canis (Smooth dogfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes; Triakidae;
OC Mustelus.
OX NCBI_TaxID=7812;
RN [1]
RP SEQUENCE.
RX MEDLINE=83160932; PubMed=6403520;
RA Robey F.A., Tanaka T., Liu T.-Y.;
RT "Isolation and characterization of two major serum proteins from the
RT dogfish, Mustelus canis, C-reactive protein and amyloid P
RT component.";
RL J. Biol. Chem. 258:3889-3894(1983).
CC -I- SUBUNIT: HOMOPENTAMER. PENTAXIN (OR PENTRAXIN) HAVE A DISCOID
CC ARRANGEMENT OF 5 NONCOVALENTLY BOUND SUBUNITS.
CC -I- DISEASE: SAP IS A PRECURSOR OF AMYLOID COMPONENT P WHICH IS FOUND
CC IN BASEMENT MEMBRANE AND ASSOCIATED WITH AMYLOID DEPOSITS.
CC -I- SIMILARITY: BELONGS TO THE PENTAXIN FAMILY.

DR PIR; B20569; B20569.
DR InterPro; IPR001759; Pentaxin.
DR PROSITE; PS00289; PENTAXIN; PARTIAL.
KW Lectin; Amyloid; Glycoprotein; Plasma; Pentaxin.
FT DOMAIN 1 >9 PENTAXIN.
FT NON TER 9 9
SQ SEQUENCE 9 AA; 965 MW; D05B5735B3386769 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 KSLLY 8
|||:
Db 5 KSLIF 9

RESULT 8
PPCK_FASHE
ID -PPCK_FASHE STANDARD; PRT; 10 AA.
AC P80525; 1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE Putative phosphoenolpyruvate carboxylase [GTP] (EC 4.1.1.32)
DE (Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile
DE protein 1) (Fragment).
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Fasciola.
OC Echinostomida; Echinostomata; Fascioloides; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Tkalcovic J., Ashman K., Meeusen E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proteins.";
RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC -I- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
CC + CO(2).
CC -I- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE [GTP]
CC FAMILY.
DR InterPro; IPR000364; PEP_carboxykin.
DR PROSITE; PS00505; PEPCK GTP; PARTIAL.
KW Lyase; Decarboxylase; GTP-binding.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1069 MW; 8393A6187AA9C87A CRC64;

Query Match 22.2%; Score 18; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 YKDG 11
|||:
Db 1 YPDG 4

RESULT 9
SPI_HALRO
ID SPI_HALRO STANDARD; PRT; 10 AA.
AC Q10597;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Serine proteinase inhibitor (Fragment).
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyruidae; Halocynthia.
OX NCBI_TaxID=7729;
RN [1]
RP SEQUENCE.
RX TISSUE=Hemolymph;
RX MEDLINE=96321313; PubMed=8759295;

RA Shishikura F., Abe T., Ohtake S.-I., Tanaka K.;
 RT "Purification and characterization of a 58,000-Da proteinase
 RT inhibitor from the hemolymph of a solitary ascidian, Halocynthia
 roretzi.";
 RL Comp. Biochem. Physiol. 114B:1-9(1996).
 CC -1- FUNCTION: STRONGLY INHIBITS TRYPSIN AND PLASMA ENZYME(S) ACTIVITY.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Serpin; Serine protease inhibitor; glycoprotein; Plasma.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1104 MW; 4225C73B1B187AA3 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 10;
 Best Local Similarity 75.0%; Pred. No. 2.1e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 KCKK 12
 DB 3 KCKK 6

RESULT 10
 ID CXAL_CONMA STANDARD; PRT; 14 AA.
 AC P01521;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Alpha-conotoxin MI (MI).
 OS Conus magus (Magus cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID=6492;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=83073458; PubMed=7149738;
 RA McIntosh J.M., Cruz L.J., Hunkapiller M.W., Gray W.R., Olivera B.M.;
 RT "Isolation and structure of a peptide toxin from the marine snail
 RT Conus magus.";
 RL Arch. Biochem. Biophys. 218:329-334(1982).
 RN [2]

DISULFIDE BONDS.
 RX MEDLINE=84032400; PubMed=6630187;
 RA Gray W.R., Rivier J.E., Galyean R., Cruz L.J., Olivera B.M.;
 RT "Conotoxin MI. Disulfide bonding and conformational states.";
 RL J. Biol. Chem. 258:12247-12251(1983).
 CC -1- FUNCTION: ALPHA-CONOTOXINS ACT ON POSTSYNAPTIC MEMBRANES, THEY
 CC BIND TO THE NICOTINIC ACETYLCHOLINE RECEPTORS (NACHR) AND THUS
 CC INHIBIT THEM.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- SIMILARITY: BELONGS TO THE A-SUPERFAMILY OF CONOTOXINS. ALPHA-TYPE
 CC FAMILY.
 DR PIR; A01784; NTKNIM.
 DR HSSP; P56973; I845.
 KW Postsynaptic neurotoxin; Neurotoxin; Toxin;
 KW Acetylcholine receptor inhibitor; Amidation.
 FT DISULFID 3 8
 FT MOD_RES 14 14
 FT MOD_RES 14 14
 SQ SEQUENCE 14 AA; 1499 MW; DEE91898B8F5E5BD CRC64;

Query Match 22.2%; Score 18; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GKTY 14
 DB 9 GKTY 12

RESULT 11
 ID EFTU_CANFA STANDARD; PRT; 14 AA.
 AC P54835;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Elongation factor Tu, mitochondrial (Fragment).
 GN TUFM.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";
 RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
 CC AMINOACYL-TRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
 CC BIOSYNTHESIS.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
 CC EF-TU/EF-1A SUBFAMILY.
 DR HSC-2DPAGE; P54835; DOG.
 DR InterPro: IPR000795; EF_GTPbind.
 DR PROSITE: PS00301; EFACFOR_GTP; PARTIAL.
 KW Elongation factor; Protein biosynthesis; Mitochondrion; GTP-binding.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1600 MW; 8CAF0B6AE7CDE41 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 3e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 KTYL 15
 DB 6 KTYV 9

RESULT 12
 ID MCRZ_METTM STANDARD; PRT; 14 AA.
 AC P58816;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Methyl-coenzyme M reductase II gamma subunit (EC 1.8.-.-) (MCR II
 DE gamma) (Fragment).
 GN MRTG.
 OS Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=79929;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=9109370; PubMed=2269306;
 RA Rospert S., Linder D., Ellermann J., Thauer R.K.;
 RT "Two genetically distinct methyl-coenzyme M reductases in
 RT Methanobacterium thermoautotrophicum strain Marburg and Delta H.";
 RL Eur. J. Biochem. 194:871-877(1990).
 CC -1- FUNCTION: Reduction of methyl-coenzyme M (2-(methylthio)
 CC ethanesulfonic acid) with 7-mercaptoheptanoylthreonine phosphate
 CC to methane and an heterodisulfide.
 CC -1- CATALYTIC ACTIVITY: CH(3)-S-CoM + H-S-HTP = CH(4) + CoM-S-S-HTP.
 CC -1- COFACTOR: THE ENZYME COMPLEX BINDS TIGHTLY (BUT NOT COVALENTLY)
 CC TO TWO MOLECULES OF COENZYME F430. F430 IS A YELLOW NICKEL
 CC PORPHINOID.
 CC -1- PATHWAY: Methanogenesis; last step.
 CC -1- SUBUNIT: HEXAMER OF TWO ALPHA, TWO BETA, AND TWO GAMMA CHAINS.

CC -1- DEVELOPMENTAL STAGE: THERE ARE TWO MCR COMPLEXES IN THIS BACTERIA.
 CC MCR II IS EXPRESSED IN THE EARLY GROWTH PHASE. LATE GROWTH CELLS
 CC CONTAINS MOSTLY MCR I.
 KW Methanogenesis; Oxidoreductase; Multigene family.
 FT INIT MET 0
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1557 MW; 97E9439C4223B871 CRC64;

Query Match 22.2%; Score 18; DB 1; Length 14;
 Best Local Similarity 37.5%; Pred. No. 3e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 8 YKDGKTYL 15
 | : : |
 DB 6 YTPGETQI 13

RESULT 13
 NIS1_ANAVA STANDARD; PRT; 15 AA.
 AC Q44507;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cysteine desulfurase 1 (EC 4.4.1.-) (Nitrogenase metalloclusters
 DE biosynthesis protein nifS1) (Fragment).
 GN NIFS1 OR NIFS.
 OS Anabaena variabilis.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=1172;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ECC 7937 / ATCC 29413;
 RA Monnerjahn U.; Boehme H.;
 RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP EXPRESSION PATTERN.
 RC STRAIN=PCC 7937 / ATCC 29413;
 RX MEDLINE=96016168; PubMed=7568132;
 RA Thiel T.; Lyons E.M.; Erker J.C.; Ernst A.;
 RT "A second nitrogenase in vegetative cells of a heterocyst-forming
 RT cyanobacterium."
 CC -1- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM
 CC CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE
 CC BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE
 CC INORGANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY
 CC SIMILARITY).
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- MISCELLANEOUS: BELONGS TO THE NIF1 GENE CLUSTER WHICH IS EXPRESSED
 CC IN HETEROCYSTS UNDER ANAEROBIC AND AEROBIC CONDITIONS.
 CC -1- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES. NIFS/ISCS SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL: X69898; CAA49523.1; -;
 DR InterPro: IPR000192; AminoTransf.
 DR PROSITE: PS00595; AA_TRANSFER CLASS_5; PARTIAL.
 KW Nitrogen fixation; Lyase; Pyridoxal phosphate.
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1684 MW; 08B8F106DE65547D CRC64;

Query Match 22.2%; Score 18; DB 1; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 SLLYKD 10
 | : : |
 DB 2 SVIYLD 7

RESULT 14
 GONI_PETMA STANDARD; PRT; 10 AA.
 AC P04378;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 20-MAR-1987 (Rel. 04, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Gonadoliberin I (Gonadotropin-releasing hormone I) (GNRH-I)
 DE (Luliberin I).
 OS Petromyzon marinus (Sea lamprey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Petromyzon.
 OX NCBI_TaxID=7757;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=86168192; PubMed=3514603;
 RA Sherwood N.M.; Sower S.A.; Marshak D.R.; Fraser B.A.; Brownstein M.J.;
 RT "Primary structure of gonadotropin-releasing hormone from lamprey
 RT brain."
 RL J. Biol. Chem. 261:4812-4819 (1986).
 CC -1- FUNCTION: STIMULATES THE SECRETION OF BOTH LUTEINIZING AND
 CC FOLLICLE-STIMULATING HORMONES.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE GNRH FAMILY.
 DR PIR; A01412; RHLMSG.
 DR InterPro: IPR002012; GNRH.
 DR Pfam: PF00446; GNRH; 1.
 DR PROSITE: PS00473; GNRH; 1.
 KW Hormone; Amidation; Hypothalamus.
 FT MOD RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1244 MW; 1E4B36237B1735AB CRC64;

Query Match 21.0%; Score 17; DB 1; Length 10;
 Best Local Similarity 57.1%; Pred. No. 3.1e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 SLLYKDG 11
 | : : |
 DB 4 SLEWKP 10

RESULT 15
 SP34_DICMU STANDARD; PRT; 10 AA.
 AC P81545;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Surface protein P34 (Fragment).
 GN P34.
 OS Dictyostelium mucoroides (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 OX NCBI_TaxID=31287;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DM-7;
 RA Schreiner S.J.;
 RT "Characterization of a surface protein in macrocysts of Dictyostelium
 RT mucoroides."
 RL Submitted (NOV-1998) to the SWISS-PROT data bank.
 CC -1- FUNCTION: THIS PROTEIN IS PRESENT IN THE MACROCYST PRIMARY WALL
 CC WHICH IS PRODUCED BY AMOEBAE DURING THE ONSET OF SEXUAL
 CC REPRODUCTION.
 CC -1- SUBCELLULAR LOCATION: MACROCYST PRIMARY WALL.
 KW Cell wall.

FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1190 MW; 1B6A707AA3345B50 CRC64;
Query Match 21.0%; Score 17; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 9 KDG 11
Db 6 KDG 8

Search completed: April 22, 2003, 13:13:03
Job time : 25 secs

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	27	33.3		12	11	G61331	mus musculus
2	27	33.3		15	5	P82207	bombyx mori
3	23	28.4		8	4	Q9UJ50	homo sapien
4	23	28.4		16	2	Q9X7K1	rhodobacter
5	22	27.2		12	11	Q9Y1P5	mus musculus
6	22	27.2		13	4	Q16141	homo sapien
7	22	27.2		15	2	Q9R5L9	bacillus et
8	22	27.2		15	5	Q9TWR6	rapana thom
9	22	27.2		16	4	Q16183	homo sapien
10	21	25.9		12	8	P82164	spinacia ol
11	21	25.9		15	2	P82468	pseudomonas
12	21	25.9		15	7	Q9TNP2	homo sapien
13	20	24.7		11	2	Q9JL47	bacillus ce
14	20	24.7		14	5	Q9NFK8	brugia paha
15	20	24.7		15	10	Q9S8R5	gossypium h
16	20	24.7		16	4	Q9UD47	homo sapien

RESULT 2	
P82207	
ID P82207	PRELIMINARY;
AC P82207;	PRT; 15 AA.

DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Unknown protein from 2D-page (Fragment).
 OS Bombyx mori (silk moth).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Bombycoidea; Bombycidae; Bombyx.
 OX NCBI_TaxID=7091;
 RN [1]
 RN SEQUENCE.
 RP STRAIN=XINHANG X KEMING; TISSUE=BODY WALL, AND FAT BODY;
 RX MEDLINE=21177481; PubMed=11280994;
 RA Zhong B.X.;
 RT "Protein database for several tissues derived from five instar of
 RT silkworm".
 RL i Chuan Hsueh Pao 28:217-224 (2001).
 FT NON_TER 15 15
 SQ SEQUENCE 15 AA; 1877 MW; 590F6BD4703CA70C CRC64;
 Query Match 33.3%; Score 27f DB 5; Length 15;
 Best Local Similarity 57.1%; Pred. No. 6.5e+02;
 Matches 8; Conservative 1; Mismatches 3; Indels 2; Gaps 1;
 QY 3 SKSLFYQ--KQYDN 12
 DB 1 SKSLFYQ--KQYDN 12
 RESULT 3
 QYUJ50 PRELIMINARY; PRT; 8 AA.
 AC Q9UJ50;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE Latrophilin-2 (Fragment).
 GN LPFH1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=99153747; PubMed=10030676;
 RA White G.R.M., Varley J.M., Heighway J.;
 RT "Isolation and characterisation of a human homologue of the
 RT latrophilin gene from a region of lp31.1 implicated in breast
 RT cancer.";
 RL Oncogene 17:3513-3519 (1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=20225451; PubMed=10760572;
 RA White G.R.M., Varley J.M., Heighway J.;
 RT "Genomic structure and expression profile of LPFH1, a 7TM gene
 RT variably expressed in breast cancer cell lines.";
 RL Biochim. Biophys. Acta 1491:75-92 (2000).
 DR EMBL; AJ244509; CAB60204.1; --
 FT NON_TER 1 1
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 1025 MW; 4D59D763344AAB0B CRC64;
 Query Match 28.4%; Score 23; DB 4; Length 8;
 Best Local Similarity 37.5%; Pred. No. 6.7e+05;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 8 YKDGKTYL 15
 DB 1 YEDNKPEI 8
 RESULT 4
 Q9X7K1 PRELIMINARY; PRT; 16 AA.
 AC Q9X7K1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Molybdopterin cofactor biosynthesis protein C C-terminus
 DE (Fragment).
 GN MOBC.
 OS Rhodobacter capsulatus (Rhodospseudomonas capsulata).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
 OC Rhodobacter.
 OX NCBI_TaxID=1061;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=B10S;
 RC Lemkueller S., Klipp W.;
 RT "The molybdenum cofactor biosynthesis protein MoBa from Rhodobacter
 RT capsulatus is required for the activity of molybdenum enzymes binding
 RT MGD, but not for xanthine dehydrogenase harbouring the MPT cofactor.";
 RL FEBS Lett. 174:239-246 (1999).
 DR EMBL; AJ1131528; CAB43542.1; --
 FT NON_TER 1 1
 SQ SEQUENCE 16 AA; 1692 MW; 1DFE0534394788F8 CRC64;
 Query Match 28.4%; Score 23; DB 2; Length 16;
 Best Local Similarity 83.3%; Pred. No. 3.2e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 LLYKDG 11
 DB 3 LLYKDG 8
 RESULT 5
 Q91YF5 PRELIMINARY; PRT; 12 AA.
 AC Q91YF5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE GM3 synthase protein (Fragment).
 GN GM3 SYNTHASE.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=ICR; TISSUE=BRAIN;
 RA Shuichi T.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y18020; CAC79652.1; --
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1445 MW; 84E7876609572735 CRC64;
 Query Match 27.2%; Score 22; DB 11; Length 12;
 Best Local Similarity 83.3%; Pred. No. 3.5e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 SLLYKD 10
 DB 5 SLLYKD 10
 RESULT 6
 Q16141 PRELIMINARY; PRT; 13 AA.
 AC Q16141;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Mutant DNA polymerase beta (Fragment).
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94220089; PubMed=7545922;
 RA Sadakane Y., Maeda K., Kuroda Y., Hori K.;
 RT "Identification of mutations in DNA polymerase beta mRNAs from
 RT patients with Werner syndrome";
 RL Biochem. Biophys. Res. Commun. 200:219-225(1994).
 DR EMBL; S69873; AAD14051.1; --
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1568 MW; D88C62798C9542CD CRC64;
 Query Match 27.2%; Score 22; DB 4; Length 13;
 Best Local Similarity 37.5%; Pred. No. 3.8e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 9 KDGKTYLN 16
 Db :|||:|
 3 RDSAVYIN 10
 RESULT 7
 Q9R5L9 PRELIMINARY; PRT; 15 AA.
 AC Q9R5L9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE EXO-alpha-1,4-glucosidase [EC 3.2.1.20] (Fragment).
 OS Bacillus stearothermophilus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Geobacillus.
 OX NCBI_TaxID=1422;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92209510; PubMed=1555585;
 RA Suzuki Y., Yonezawa K., Hattori M., Takii Y.;
 RT "Assignment of Bacillus thermoamyloliquefaciens KP1071 alpha-
 RT glucosidase I to an exo-alpha-1,4-glucosidase, and its striking
 RT similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence
 RT and in structural parameters calculated from the amino acid
 RT composition";
 RL Eur. J. Biochem. 205:249-256(1992).
 SQ SEQUENCE 15 AA; 1931 MW; 62B4CE40013D3042 CRC64;
 Query Match 27.2%; Score 22; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 4.4e+03;
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 4 KSLLYKDGKTY 14
 Db :|||:|
 2 KKTWKEGVAY 12
 RESULT 8
 Q9TWR6 PRELIMINARY; PRT; 15 AA.
 AC Q9TWR6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE Hemocyanin RH51 subunit (Fragment).
 OS Rapana thomasi (Marine snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Muricoidea; Muricidae; Rapana.
 OX NCBI_TaxID=29165;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=94007762; PubMed=8403854;
 RA Idakieva K., Severov S., Svendsen I., Genov N., Stoeva S.,
 RA Beltramini M., Tognon G., Di Muro P., Salvato B.;

RT "Structural properties of Rapana thomasi grose hemocyanin:
 RT isolation, characterization and N-terminal amino acid sequence of two
 RT different dissociation products."; (1993).
 RL Comp. Biochem. Physiol. 106B:53-59 (1993).
 FT NON_TER 1
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1735 MW; 78985413C9E90B6B CRC64;
 Query Match 27.2%; Score 22; DB 5; Length 15;
 Best Local Similarity 55.6%; Pred. No. 4.4e+03;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 SLLYKDGKT 13
 Db :|||:|
 1 SLPYKRVRT 9
 RESULT 9
 Q16183 PRELIMINARY; PRT; 16 AA.
 AC Q16183;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE GPIa protein (Fragment).
 GN GPIA.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94378189; PubMed=7916494;
 RA Kaib R., Santoso S., Unkelbach K., Kiesel V., Mueller-Eckhardt C.;
 RT "Localization of the Br polymorphism on a 144 bp exon of the GPIa gene
 RT and its application in platelet DNA typing.";
 RL Thromb. Haemost. 71:651-654(1994).
 DR EMBL; S72155; AAD14096.1; --
 FT NON_TER 1
 SQ SEQUENCE 16 AA; 1968 MW; B31EPE05E038C26A CRC64;
 Query Match 27.2%; Score 22; DB 4; Length 16;
 Best Local Similarity 42.9%; Pred. No. 4.8e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 9 KDGKTYL 15
 Db :|||:|
 5 EGRVYL 11
 RESULT 10
 P82164 PRELIMINARY; PRT; 12 AA.
 ID P82164
 AC P82164;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Chloroplast 30S ribosomal protein S14 beta (Fragment).
 OS Spinacia oleracea (Spinach).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC STRAIN=CV. ALMARO; TISSUE=LEAF;
 RX MEDLINE=20435797; PubMed=10874039;
 RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
 RT "The plastid ribosomal proteins. Identification of all the proteins in
 RT the small subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 274:28455-28465(2000).
 CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.

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CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: S14 ALPHA AND BETA FORMS DIFFER IN PL. S14 ALPHA
CC FORM IS THE LEAST BASIC FORM.
CC -1- MASS SPECTROMETRY: MW=11745.9; METHOD=ELECTROSPRAY.
CC -1- MASS SPECTROMETRY: MW=11947; METHOD=MALDI.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 KDA.
CC -1- SIMILARITY: BELONGS TO THE S14P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR001209; Ribosomal_S14.
DR InterPro: IPR001648; Ribosomal_S18.
DR Pfam: PF00253; Ribosomal_S14; PARTIAL.
DR PROSITE: PS00057; RIBOSOMAL_S18; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1513 MW; 5E84D3F10116D057 CRC64;

Query Match 25.9%; Score 21; DB 8; Length 12;
Best Local Similarity 44.4%; Pred. No. 5.1e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 KSLLYKDGK 12
DB 3 KSLIQREKK 11

RESULT 11
P82468
ID P82468 PRELIMINARY; PRT; 15 AA.
AC P82468;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Lysyl endopeptidase (EC 3.4.21.50) (Fragment).
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]_SEQUENCE.
RP Lammstein J.;
RA Submitted (APR-2000) to the SWISS-PROT data bank.
RL -1- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: LYS-|-XAA, INCLUDING
CC LYS-|-PRO.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S5 (SERINE PROTEASE).
KW Hydrolase; Serine protease.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1483 MW; 3F42C5B66C4F76DD CRC64;

Query Match 25.9%; Score 21; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 6.5e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 YKDG 11
DB 3 YRDG 6

RESULT 12
Q9TNP2
ID Q9TNP2 PRELIMINARY; PRT; 15 AA.
AC Q9TNP2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fraction 60-SHLA BC locus class I-bound peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE.
RP Harris P.E., Colovai A.I., Maffei A., Liu Z., Foca N.S.;
RA MEDLINE=96165039; PubMed=8567028;

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RT "Major histocompatibility complex class I presentation of exogenous
RT and endogenous protein-derived peptides by a transfected human
RT monocyte cell line.";
RL Immunology 86:606-611(1995).
KW MHC.
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1838 MW; 98DCDC01F8F7E15 CRC64;

Query Match 25.9%; Score 21; DB 7; Length 15;
Best Local Similarity 44.4%; Pred. No. 6.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 YKDGKTYLN 16
DB 3 YGVARTYLD 11

RESULT 13
Q9L4F7
ID Q9L4F7 PRELIMINARY; PRT; 11 AA.
AC Q9L4F7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Phosphatidylinositol-specific phospholipase C (PI-PLC)
DE (Fragment).
GN PLCA.
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]_SEQUENCE FROM N.A.
RP STRAIN=ATCC 14579 TYPE STRAIN;
RX MEDLINE=20055637; PubMed=10589720;
RA Oktad O., Gominet M., Purnelle B., Rose M., Lereclus D., Kolsto A.B.;
RT "Sequence analysis of three Bacillus cereus loci under PicR-regulated
RT genes encoding degradative enzymes and enterotoxin.";
RL Microbiology 145:3129-3138(1999).
DR EMBL; AJ243711; CAB69804.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1335 MW; 4277A30E20572333 CRC64;

Query Match 24.7%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 SSKSLLYK 9
DB 2 SNKKLILK 9

RESULT 14
Q9NFK8
ID Q9NFK8 PRELIMINARY; PRT; 14 AA.
AC Q9NFK8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE MmcI protein (Fragment).
GN MMC1.
OS Brugia pahangi.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Brugia.
OX NCBI_TaxID=6280;
RN [1]_SEQUENCE FROM N.A.
RP Ems R.D., Thompson F., Devaney E.;
RT "A novel mRNA up-regulated in mammalian-derived microfilaria of
RT Brugia.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ277990; CAB93515.1; -.

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FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1602 MW; 5C4C62C55AB89397 CRC64;

Query Match      24.7%; Score 20; DB 5; Length 14;
Best Local Similarity 45.5%; Pred. No. 8.8e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 SSKSLLYKDGK 12
   |: ||: ||
Db 3 SATSLMMQMK 13

RESULT 15
Q9S8R5 PRELIMINARY; PRT; 15 AA.
AC Q9S8R5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Fiber annexin (Fragment).
OS Gossypium hirsutum (Upland cotton).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Malvales; Malvaceae; Gossypium.
OX NCBI_TaxID=3635;
RN [1]
RP SEQUENCE.
RX MEDLINE=94004990; PubMed=8401609;
RA Andrawis A., Solomon M., Delmer D.P.;
RT "Cotton fiber annexins: a potential role in the regulation of callose
  synthase.";
RL Plant J. 3:763-772(1993).
SQ SEQUENCE 15 AA; 1689 MW; 1087950BAC4F69F9 CRC64;

Query Match      24.7%; Score 20; DB 10; Length 15;
Best Local Similarity 50.0%; Pred. No. 9.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSKSLLY 8
   |: ||: ||
Db 5 RSANQLLH 12

Search completed: April 22, 2003, 13:14:00
Job time : 30 secs
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GenCore version 5.1.4 p5-4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:54:59 / Search time 73 Seconds
(without alignments)
29.206 Million cell updates/sec

Title: US-09-674-716B-3
Perfect score: 81
Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 255767

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	16	AAV32254	Light chain CDR L1
2	77	95.1	16	AAV39818	Light chain CDR1 o
3	75	92.6	16	AAV39815	Light chain CDR1 o
4	75	92.6	16	AAV39824	Light chain CDR1 o
5	69	85.2	16	AAV39875	Light chain CDR1 o
6	69	85.2	16	AAV39839	Light chain CDR1 o
7	62.5	77.2	15	AAV39821	Light chain CDR1 o
8	61	75.3	16	AAU70328	Human Kappa II lig
9	60	74.1	16	AAV14404	Peptide CDR-L1 der
10	59	72.8	16	AAB86292	Murine derived ant

11	59	72.8	16	22	AAB73652	Murine monoclonal
12	57	70.4	16	13	AAR24704	Sequence of an ant
13	55	67.9	16	14	AAR30448	C242-11 MAb kappa
14	55	67.9	16	22	AAU07734	Human light chain
15	55	67.9	16	23	AAO14984	Mouse mAb 1D9 anti
16	53	65.4	16	18	AAW31747	CDRL1 region of L
17	53	65.4	16	19	AAW71894	Anti-human Fas mon
18	53	65.4	16	21	AAAB12905	Anti-human Fas ant
19	53	65.4	16	21	AAW80281	Humanised anti-Fas
20	52	64.2	16	21	AAV92169	Murine 13H10 light
21	51	63.0	16	19	AAW70926	CDR1 of the light
22	49	60.5	16	16	AAR75487	Mouse antibody var
23	49	60.5	16	21	AAB21364	Mouse antibody 13G
24	49	60.5	16	22	AAB97198	Murine anti-PI-3,4
25	48	59.3	16	23	AAU70349	Mouse Kappa II lig
26	47	58.0	16	19	AAW50213	Sequence from the
27	46	56.8	16	16	AAR70451	VL sequence of ant
28	46	56.8	16	19	AAW58534	CDR-1 of the L cha
29	46	56.8	16	21	AAW51154	Murine CD4/CD34 re
30	45	55.6	16	19	AAW70920	CDR1 of the light
31	45	55.6	16	21	AAV95222	Anti-platelet glyc
32	45	55.6	16	22	AAB50790	Murine antibody S2
33	43	53.1	16	15	AAR59420	6D9 antibody light
34	43	53.1	16	22	AAG64460	Mouse 6D9 catalyti
35	41	50.6	16	22	AAG64463	L27ey catalytic an
36	40	49.4	16	14	AAR40216	Sequence of light
37	40	49.4	16	22	AAG67670	Complementarity de
38	39	48.1	16	22	AG64461	3H5 catalytic ant
39	39	48.1	16	23	AAU11180	Mouse antibody Act
40	36	44.4	13	22	AAB82174	H-2Kd MHC-Class I
41	34	42.0	16	22	AAG64462	5H3 catalytic ant
42	32.5	40.1	15	16	AAR70195	MAB 3B9 light chai
43	32.5	40.1	15	19	AAW83027	Anti-Fas MAb HFET7A
44	32.5	40.1	15	20	AAV23772	CDR of the light c
45	32.5	40.1	15	20	AAV18114	Light chain CDR fo

ALIGNMENTS

RESULT 1
AAV32254
ID AAV32254 standard; Peptide; 16 AA.
XX
AC AAV32254;
XX
DT 15-FEB-2000 (first entry)
XX
DE Light chain CDR L1 of mouse anti-CD23 MAb C11.
XX
KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy.

OS Mus musculus.

XX WO9958679-A1.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-GB01434.

XX 09-MAY-1998; 98GB-0009839.

XX (GLAX) GLAXO GROUP LTD.

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 DR N-PSDB; AA234739.
 XX
 PT Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis -
 XX Claim 1; Page 40; 81pp; English.
 XX
 CC This sequence represents complementarity determining region 1
 CC (CDR L1) of the light chain of murine anti-CD23 (FCBRII) monoclonal
 CC antibody C11 (see also AA32262). The invention provides altered
 CC antibodies, such as chimeric or humanised antibodies, which comprise
 CC sufficient of the amino acid sequences of C11 light and heavy chain
 CC CDRs (see AA32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies
 CC are used to block soluble CD23 formation for treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 81; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 1 RSSKSLLYKDGKTYLN 16
 RESULT 2
 AAW39818
 ID AAW39818 standard; peptide; 16 AA.
 AC AAW39818;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Light chain CDR1 of catalytic antibody 6A12.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US10965.
 XX
 PR 25-JUN-1996; 96US-0672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 XX
 PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX
 PS Claim 11; Page 80; 147pp; English.
 XX
 CC AAW39815-17 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was
 CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 6A12 has a per minute Kcat
 CC of 0.072. The antibodies reduce the concentration of cocaine in a
 CC subject, and are used particularly for the treatment of an overdose. They
 CC are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved).
 XX
 SQ Sequence 16 AA;
 Query Match 95.1%; Score 77; DB 19; Length 16;
 Best Local Similarity 93.8%; Pred. No. 2.4e-06;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 DB 1 RSSKSLLYKDGKTYLN 16
 RESULT 3
 AAW39815
 ID AAW39815 standard; peptide; 16 AA.
 XX
 AC AAW39815;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Light chain CDR1 of catalytic antibody 3B9.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US10965.
 XX
 PR 25-JUN-1996; 96US-0672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 XX
 PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX
 PS Claim 11; Page 80; 147pp; English.
 XX
 CC AAW39815-17 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was

CC identified using TSA1, which is an immunogenic conjugate of a phosphate monoester transition state analogue. Antibody 3B9 has a per minute Kcat of 0.11. The antibodies reduce the concentration of cocaine in a subject, CC and are used particularly for the treatment of an overdose. They are also CC used for treating addiction (by reducing the in vivo concentration that CC can be achieved).

SQ Sequence 16 AA;
Query Match 92.6%; Score 75; DB 19; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYXDKGKTYLN 16
|||:||||:|||||
Db 1 RSSRSLLYRDKGKTYLN 16

RESULT 4
AAW39824
ID AAW39824 standard; peptide; 16 AA.

AC AAW39824;
XX
DT 16-JUN-1998 (first entry)

XX Light chain CDR1 of catalytic antibody 12H1.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.

XX Mus sp.
XX WO9749800-A1.
XX 31-DEC-1997.
XX 25-JUN-1997; 97WO-US10965.
XX 25-JUN-1996; 96US-0672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding

XX Claim 17; Page 83; 147pp; English.

XX AAW39824-26 represent the sequences of the light chain complementarity
CC determining regions (CDRs) of the catalytic antibody 12H1, which is able
CC to degrade cocaine. A series of cocaine transition state analogues
CC (TSAs) were prepared and used to immunise mice for production of
CC hybridomas. Catalytic antibodies were identified by their capacity to
CC release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was
CC identified using TSA2, and has a per minute Kcat of 0.16. The antibodies
CC reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved).

XX Sequence 16 AA;

Query Match 92.6%; Score 75; DB 19; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.2e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYXDKGKTYLN 16
|||:||||:|||||
Db 1 RSSRSLLYRDKGKTYLN 16

RESULT 5

AAW39875
ID AAW39875 standard; peptide; 16 AA.

XX AAW39875;

XX 16-JUN-1998 (first entry)

XX Light chain CDR1 of a catalytic antibody capable of degrading cocaine.
XX Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.

XX Mus sp.

XX Key Location/Qualifiers

XX Misc-difference 4 /note= "not specified"

XX Misc-difference 9 /note= "not specified"

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US10965.

XX 25-JUN-1996; 96US-0672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding

XX Claim 10; Page 5; 147pp; English.

XX AAW39875-77 represent the sequences of the light chain complementarity
CC determining regions (CDRs) of a catalytic antibody which is capable of
CC degrading cocaine. A series of cocaine transition state analogues (TSAs)
CC were prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release
CC 3H-benzoic acid from 3H-phenyl cocaine. These antibodies were found
CC to have CDRs of the present sequence. The antibodies reduce the
CC concentration of cocaine in a subject, and are used particularly for the
CC treatment of an overdose. They are also used for treating addiction (by
CC reducing the in vivo concentration that can be achieved).

XX Sequence 16 AA;

Query Match 85.2%; Score 69; DB 19; Length 16;
Best Local Similarity 87.5%; Pred. No. 5.4e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYXDKGKTYLN 16
|||:||||:|||||
Db 1 RSSRSLLYRDKGKTYLN 16

RESULT 6

```

AAW39839
ID AAW39839 standard; peptide; 16 AA.
XX
AC AAW39839;
XX
DT 16-JUN-1998 (first entry)
XX
DE Light chain CDR1 of catalytic antibody 8G4E.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
FN WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US10965.
XX
PR 25-JUN-1996; 96US-0672345.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Landry DW;
XX
DR WPI; 1998-077166/07.
XX
PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
PS Claim 15; Page 82; 147pp; English.
XX
CC AAW39821-23 represent the sequences of the light chain complementarity
CC determining regions (CDRs) of the catalytic antibody 2A10, which is able
CC to degrade cocaine. A series of cocaine transition state analogues
CC (TSAs) were prepared and used to immunise mice for production of
CC hybridomas. Catalytic antibodies were identified by their capacity to
CC release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was
CC identified using TSA1, which is an immunogenic conjugate of a phosphate
CC monoester transition state analogue. Antibody 2A10 has a per minute Kcat
CC of 0.011. The antibodies reduce the concentration of cocaine in a
CC subject, and are used particularly for the treatment of an overdose. They
CC are also used for treating addiction (by reducing the in vivo
CC concentration that can be achieved).
XX
SQ Sequence 15 AA;
Query Match 77.2%; Score 62.5; DB 19; Length 15;
Best Local Similarity 87.5%; Pred. NO. 0.00064;
Matches 14; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
QY 1 RSSKSLLYKDGKTYLN 16
DB 1 RSSKS-LYEDGKTYLN 15
:|||||:|||||
:|||||:|||||

RESULT 8
AAU70328
ID AAU70328 standard; Peptide; 16 AA.
XX
AC AAU70328;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human Kappa II light chain CDR1.
XX
KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
KW complementarity determining region; framework region; IgBP;
KW transgenic plant; immunoglobulin binding protein array;
KW IgM; IgG; IgA; IgD; IgE; IgY; IgW; kappa; lambda; CHBP.
XX
OS Homo sapiens.
XX
PN WO200183806-A1.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US14349.
XX
PR 02-MAY-2000; 2000US-0563222.

AAW39839
ID AAW39839 standard; peptide; 16 AA.
XX
AC AAW39839;
XX
DT 16-JUN-1998 (first entry)
XX
DE Light chain CDR1 of catalytic antibody 8G4E.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
XX
OS Mus sp.
XX
FN WO9749800-A1.
XX
PD 31-DEC-1997.
XX
PF 25-JUN-1997; 97WO-US10965.
XX
PR 25-JUN-1996; 96US-0672345.
XX
PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX
PI Landry DW;
XX
DR WPI; 1998-077166/07.
XX
PT New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required
PT in far smaller doses than antibodies that antagonise cocaine by
PT simply binding
XX
PS Claim 19; Page 87; 147pp; English.
XX
CC AAW39839-41 represent the sequences of the light chain complementarity
CC determining regions (CDRs) of the catalytic antibody 8G4E, which is able
CC to degrade cocaine. A series of cocaine transition state analogues
CC (TSAs) were prepared and used to immunise mice for production of
CC hybridomas. Catalytic antibodies were identified by their capacity to
CC release 3H-benzoic acid from 3H-phenyl cocaine. The 8G4E antibody was
CC identified using TSA3, and has a per minute Kcat of 0.12. The antibodies
CC reduce the concentration of cocaine in a subject, and are used
CC particularly for the treatment of an overdose. They are also used for
CC treating addiction (by reducing the in vivo concentration that can be
CC achieved).
XX
SQ Sequence 16 AA;
Query Match 85.2%; Score 69; DB 19; Length 16;
Best Local Similarity 81.2%; Pred. NO. 5.4e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 RSSKSLLYKDGKTYLN 16
DB 1 KSSQSLLYSDGKTYLN 16
:|||||:|||||
:|||||:|||||

RESULT 7
AAW39821
ID AAW39821 standard; peptide; 15 AA.
XX
AC AAW39821;
XX
DT 16-JUN-1998 (first entry)
XX
DE Light chain CDR1 of catalytic antibody 2A10.
XX
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;

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XX (EPIC-) EPICYTE PHARM INC.
 XX
 XX Hiatt AC, Hein MB;
 XX
 XX WPI; 2002-055482/07.
 XX
 XX Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array -
 XX
 XX Disclosure; Page 14; 129pp; English.
 XX
 XX The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that
 CC binds to a ligand, and transformed plant cells are selected, and
 CC preparing an IgBP array in plant cells. At least one peptide sequence has
 CC at least 75% sequence identity to a framework region (FR) of a native
 CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
 CC The method is useful for preparing an immunoglobulin binding protein
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 CC cells, especially plant cells (e.g. Agrobacterium tumefaciens or maize)
 CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
 CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
 CC desired characteristics. The present sequence is a mammalian
 CC immunoglobulin derived peptide that may be incorporated into an IgBP of
 CC the invention.
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 75.3%; Score 61; DB 23; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.0012;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 16
 |||:||||:|||||
 Db 1 RSSQSLHSDGDTYLN 16
 RESULT 9
 AAY14404
 ID AAY14404 standard; peptide; 16 AA.
 XX
 XX AAY14404;
 XX
 XX 17-AUG-1999 (first entry)
 XX
 XX Peptide CDR-L1 derived from anti-HCV Ser/Thr protease MAB 8D4.
 DE
 XX Complementarity determining region; CDR; monoclonal antibody; MAb;
 KW hepatitis C virus; HCV; protease; binding site.
 KW
 XX Synthetic.
 OS
 XX JP1127861-A.
 PN
 XX 18-MAY-1999.
 XX
 XX 29-OCT-1997; 97JP-0297451.
 PF
 XX 29-OCT-1997; 97JP-0297451.
 PR
 XX (NIHA) JAPAN ENERGY CORP.
 PA
 XX WPI; 1999-350322/30.
 XX
 XX Neutralized antibody partial peptide derived from hepatitis C virus
 PT - useful for inhibiting Hepatitis C Virus (HCV) serine protease
 PT activity

XX
 PS Example 1; Page 13; 32pp; Japanese.
 XX
 XX This sequence represents a peptide derived for the sequence of the light
 CC chain variable region complementarity determining region (CDR)-1 of the
 CC anti-hepatitis C virus (HCV) Ser/Thr protease monoclonal antibody (MAb)
 CC 8D4 protein. The invention relates to the use of partial peptides
 CC (AAY14348-Y14353) from the MAB 8D4 for inhibiting HCV serine protease
 CC activity.
 XX
 XX Sequence 16 AA;
 SQ
 Query Match 74.1%; Score 60; DB 20; Length 16;
 Best Local Similarity 80.0%; Pred. No. 0.0018;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RSSKSLLYKDGKTYLN 15
 |||:||||:|||||
 Db 1 RSSKSLHSDGNTYL 15
 RESULT 10
 AAB86292
 ID AAB86292 standard; peptide; 16 AA.
 XX
 XX AAB86292;
 AC
 XX 13-SEP-2001 (first entry)
 DT*
 DE Murine derived antibody Wue-1 light chain variable region CDR-1.
 DE
 XX Antibody; Wue-1; variable region; light chain; heavy chain; antitumor;
 KW immunomodulatory; cognate antigen identification; autoimmune disease;
 KW tumor; multiple myeloma; lymphoma; plasmacytoma; CDR-1.
 KW
 XX Mus sp.
 OS
 XX DE19962583-A1.
 PN
 XX 28-JUN-2001.
 PD
 XX 23-DEC-1999; 99DE-1062583.
 PF
 XX 23-DEC-1999; 99DE-1062583.
 PR
 XX (MUEL/) MUELLER-HERMELINK H K.
 PA (GREI/) GREINER A.
 XX
 XX Mueller-Hermelink HK, Greiner A;
 PI
 XX WPI; 2001-426596/46.
 DR
 XX New antibodies specific for plasma cells; useful for treatment and
 PT diagnosis of autoimmune diseases and plasma cell tumors -
 PT
 XX Claim 1; Page 9; 18pp; German.
 PS
 XX This invention describes novel antibodies (Ab) in which the variable
 CC region (VR) of at least one chain and/or the VR of at least one heavy
 CC chain includes at least one of 7 specified sequences, or fragments of
 CC these sequences, or contain at least one light chain and/or heavy
 CC chain encoded by specific nucleic acid sequences (I) and (II),
 CC reproduced, or their fragments. The products of the invention have
 CC antitumor and immunomodulatory activity. Ab, or other antibodies that
 CC recognize the same antigen, are used: (i) to identify cognate antigens;
 CC (ii) for specific labeling of plasma cells (PC) for generating or
 CC separation, e.g. in an extracorporeal system; (iii) for generating
 CC additional antibodies able to label PC; and (iv) for treating autoimmune
 CC diseases and/or tumors, e.g. multiple myeloma, lymphoma and/or
 CC plasmacytoma. Ab are specific for mature PC, i.e. they do not recognize
 CC precursor stages, even though these precursors are used as immunogens. As
 CC therapeutic agents, they should show fewer side effects than conventional
 CC chemotherapeutic agents. This sequence represents the Wue-1 antibody

CC variable region light chain complementarity determining region CDR1
 CC fragment described in the method of the invention.
 XX
 SQ Sequence 16 AA;
 Query Match 72.8%; Score 59; DB 22; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.0027;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RSKSKLLYDKGKTYLN 16
 :||:|||||
 Db 1 KSSQSLDSDGKTYLN 16
 RESULT 11
 AAB73652
 ID AAB73652 standard; peptide; 16 AA.
 XX
 AC AAB73652;
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE Murine monoclonal antibody IOR C5 light chain variable region CDR1.
 XX
 KW Monoclonal antibody IOR C5; hybridoma ECCC 97061101; mouse; humanised;
 KW IOR C2 antigen; colorectal cancer; tumour; metastasis; therapy;
 KW drug targeting; imaging; diagnosis; cytostatic; VL;
 KW light chain variable region;
 XX
 OS Mus sp.
 OS Synthetic.
 OS
 FN WO200136485-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 16-NOV-2000; 2000WO-CU000004.
 XX
 PR 16-NOV-1999; 99CU-0000196.
 XX
 PA (IMMU-) CENT IMMUNOLOGIA MOLECULAR.
 XX
 PI Mateo De Acosta Del Rio CM, Roque Navarro LT, Morales Morales A;
 PI Perez Rodriguez R, Ayala Avila M, Gavilondo Cowley JV;
 PI Duenas Porto M, Bell Garcia H, Rengifo Calzado E, Iznaga Escobar N;
 PI Ramos Zuzarte M;
 XX
 WPI; 2001-343804/36.
 XX
 PT New recombinant antibody, or single-chain fragment, derived from murine
 PT monoclonal IOR C5, useful for treatment and diagnosis of colo-rectal
 PT cancer -
 XX
 PS Claim 2; Page 24; 30pp; Spanish.
 XX
 CC The invention relates to a chimeric antibody, or an Fv-type
 CC single-chain fragment, derived from the murine monoclonal antibody
 CC IOR C5 expressed by hybridoma ECCC 97061101. It contains the CDRs
 CC (complementarity determining regions) of IOR C5 and human constant
 CC regions, in both heavy and light chains. The IOR C5 antibody specifically
 CC binds to the IOR C2 antigen and light chains. The IOR C5 antibody specifically
 CC colorectal cells. The invention also encompasses a cell line which
 CC expresses the humanised IOR C5 antibody; host cells which express the
 CC Fv fragment; a pharmaceutical composition for treatment, location or
 CC in vivo identification of malignant tumours of colon and rectum,
 CC including their metastases and recurrences, containing the humanised
 CC antibody or the Fv fragment thereof, plus an excipient; and a method
 CC for the in vivo diagnosis of tumours comprising the administration of
 CC a 99m-technetium-labelled humanised IOR C5 antibody or Fv fragment, and
 CC monitoring biodistribution by radiography. The humanised IOR C5 antibody
 CC and/or its Fv fragment are used to treat malignant tumours of the colon
 CC or rectum, including their metastases or recurrences, and for in vivo
 CC diagnosis (imaging) of tumours, particularly when radiolabelled.

CC Sequences AAB73652-AAB73654 represent, respectively, CDRs 1-3 of the
 CC light chain variable region (LH) of antibody IOR C5.
 XX
 SQ Sequence 16 AA;
 Query Match 72.8%; Score 59; DB 22; Length 16;
 Best Local Similarity 75.0%; Pred. No. 0.0027;
 Matches 12; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 RSKSKLLYDKGKTYLN 16
 :||:|||||
 Db 1 KSSQSLDSDGKTYLN 16
 RESULT 12
 AAR24704
 ID AAR24704 standard; peptide; 16 AA.
 XX
 AC AAR24704;
 XX
 DT 28-DEC-1992 (first entry)
 XX
 DE Sequence of an anti-human fibrin antibody light chain variable
 DE region chain designated 'A'.
 XX
 KW Chimeric monoclonal antibody; anti-fibrin antibody;
 KW antithrombotic agent; myocardial infarction therapy.
 XX
 OS Mus musculus.
 XX
 FN EP491351-A.
 XX
 PD 24-JUN-1992.
 XX
 PF 17-DEC-1991; 91EP-0121591.
 XX
 PR 18-DEC-1990; 90JP-0413829.
 PR 11-NOV-1991; 91JP-0294464.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Iwasa S, Taka H, Watanabe T, Tada H;
 XX
 WPI; 1992-209528/26.
 XX
 PT Chimeric monoclonal antibodies - contain anti-human fibrin
 PT antibody light and heavy chain variable and constant for treating
 PT thrombotic conditions e.g. myocardial infarction
 XX
 PS Claim 1; Page 49; 87pp; English.
 XX
 CC The inventors claim a chimeric monoclonal antibody which contains an
 CC anti-human fibrin antibody light chain variable region contg. at
 CC least one of the polypeptide chains A, B and C
 CC (AAR24704, R24705, AAR24706) and a human antibody light chain constant
 CC region. The chimeric Abs can be used both in vivo and in vitro and, since
 CC they have very low immunogenicity as compared with mouse Abs, they can be
 CC administered to humans for diagnostic and therapeutic purposes. They are
 CC also more stable and show a longer half-life in the blood as compared
 CC with the original mouse Abs.
 XX
 SQ Sequence 16 AA;
 Query Match 70.4%; Score 57; DB 13; Length 16;
 Best Local Similarity 80.0%; Pred. No. 0.0059;
 Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 SSKSKLLYDKGKTYLN 16
 :||:|||||
 Db 2 SSQSLDSDGKTYLN 16
 RESULT 13

AAR30448
ID AAR30448 standard; peptide; 16 AA.
XX
AC AAR30448;
XX
DT 06-MAY-1993 (first entry)
XX
DE C242:11 MAb kappa chain CDR1.
XX
KW Kappa; chain; heavy; complementarity determining region; CDR; MAb;
KW monoclonal antibody; C242:II; murine; IgG; hybridoma; cell line;
KW spleen; human; colonic; adenocarcinoma; myeloma; Sp2/0; antigen;
KW endocytosis.
XX
OS Synthetic.
XX
PN EP521842-A.
XX
PD 07-JAN-1993.
XX
PF 03-JUL-1992; 92EP-0850166.
XX
PR 03-JUL-1991; 91SE-0002074.
XX
PA (KABI) KABI PHARMACIA AB.
XX
PI Holmgren J, Lind P, Lindholm L;
XX
DR WPI; 1993-002345/01.
XX
PT Monoclonal antibody reacting with CA-242 antigen - obt'd. by
PT culturing hybridoma cell line C242:11 or mutants, useful for
PT diagnosis and therapy of pancreatic or colorectal cancers
XX
PS Claim 5; Page 11; 15pp; English.
XX
CC The sequences given in AAR30448-50 represent the kappa chain and
CC AAR30451-53 the heavy chain complementarity determining regions (CDR)
CC of a monoclonal antibody (MAB), C242:II. C242:II is a monoclonal
CC murine Ab of IgG class produced when culturing in an appropriate
CC medium a hybridoma cell line obtained by fusing spleen cells from a
CC mouse, which has been immunised with a human colonic adenocarcinoma
CC cell line, with the murine myeloma cell line Sp2/0. C242:II when
CC bound to a cell surface antigen is capable of being endocytosed or
CC internalised into cells.
XX
SQ Sequence 16 AA;
Query Match 67.9%; Score 55; DB 14; Length 16;
Best Local Similarity 73.3%; Pred. No. 0.013;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 RSKSKLLYKDGKTYL 15
DB 1 RSKSKLLHSGNGTYL 15
RESULT 14
AAU07734
ID AAU07734 standard; peptide; 16 AA.
XX
AC AAU07734;
XX
DT 04-DEC-2001 (first entry)
XX
DE Human light chain complementarity determining region, CDR1.
XX
KW Complementarity determining region; CDR1; Hu266; nootropic;
KW neuroprotective; Abeta peptide; Alzheimer's disease; Down's syndrome;
KW cerebral amyloid angiopathy; antibody; gene therapy.
XX
OS Homo sapiens.
OS Synthetic.

XX
PN WO200162801-A2.
XX
PD 30-AUG-2001.
XX
PF 26-FEB-2001; 2001WO-US06191.
XX
PR 24-FEB-2000; 2000US-0184601.
PR 08-DEC-2000; 2000US-0254465.
PR 08-DEC-2000; 2000US-0254498.
XX
PA (UNIW) UNIV WASHINGTON.
PA (ELIL) LILLY & CO ELI.
XX
PI Holtzman DM, Demattos R, Bales KR, Paul SM, Tsurushita N;
PI Vasquez M;
XX
DR WPI; 2001-550087/61.
XX
PT New humanised antibody for the treatment of Alzheimer's comprises the
PT inhibition and reduction of the formation of amyloid plaques -
XX
PS Claim 14; Page 45; 63pp; English.
XX
CC The invention relates a humanised antibody that specifically binds
CC an epitope contained within positions 13-28 of amyloid beta peptide,
CC Abeta. The antibody is useful to inhibit and reduce the formation of
CC amyloid plaques or the effects of toxic soluble Abeta species in humans
CC their fragments are used for the manufacture of a medicament. This includes
CC the prolonged expression of recombinant sequences of them in human
CC tissues for the treatment of clinical/pre-clinical Alzheimer's disease,
CC Down's syndrome or pre clinical cerebral amyloid angiopathy.
CC Specifically, the antibody is used to sequester Abeta into plasma, brain
CC or cerebrospinal fluid to prevent/reverse accumulation of the Abeta
CC peptide within the brain thereby improving cognition. The present
CC sequence is human light chain CDR1 (complementarity determining region 1)
CC used to humanise the mouse monoclonal antibody 266 to produce Hu266.
XX
SQ Sequence 16 AA;
Query Match 67.9%; Score 55; DB 22; Length 16;
Best Local Similarity 62.5%; Pred. No. 0.013;
Matches 10; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 RSKSKLLYKDGKTYL 16
DB 1 RSKSKLLYSDGNAYLH 16
RESULT 15
AAO14984
ID AAO14984 standard; peptide; 16 AA.
XX
AC AAO14984;
XX
DT 05-SEP-2002 (first entry)
XX
DE Mouse mAb 1D9 antibody light chain complementarity determining region 1.
XX
KW Mouse; graft rejection; CC chemokine receptor 2 antagonist;
KW CCR2 antagonist; anti-CCR2 antibody; kidney transplant; liver transplant;
KW lung transplant; heart-lung transplant; pancreas transplant;
KW bowel transplant; heart transplant; graft versus host disease;
KW chronic graft rejection; antibody light chain; mAb 1D9; CDR1;
KW complementarity determining region 1.
XX
OS Mus musculus.
XX
PN US2002042370-A1.
XX
PD 11-APR-2002.
XX
PF 13-APR-2001; 2001US-0835087.

XX	
PR	14-APR-2000; 2000US-0549448.
XX	(MILL-) MILLENNIUM PHARM INC.
PA	Hancock WW;
XX	
PI	
XX	
DR	WFI; 2002-351265/38.
XX	
PT	Inhibiting graft rejection, graft versus host disease or chronic
PT	rejection of a transplanted graft, involves administering a CCR2
PT	antagonist -
XX	
XX	Claim 25; Page 12; 16pp; English.
PS	
CC	The invention comprises a method of inhibiting graft rejection, graft
CC	versus host disease or chronic rejection of a transplanted graft. The
CC	method involves administering an antagonist of CC chemokine receptor 2
CC	(CCR2) and optionally an immunosuppressive agent. The CCR2 antagonist may
CC	be an anti-CCR2 antibody (i.e. containing light and heavy chain
CC	complementarity determining regions from various non-human origins). CCR2
CC	is known to be involved in the rejection of transplanted grafts. The
CC	method of the invention is useful for inhibiting graft rejection -
CC	particularly allografts such as kidney, liver, lung, heart-lung,
CC	pancreas, bowel and heart. The method of the invention is also useful for
CC	inhibiting graft versus host disease and for inhibiting chronic rejection
CC	of a transplanted graft. The present amino acid sequence represents a
CC	mouse mAb ID9 antibody light chain complementarity determining region 1
CC	(CDR1).
XX	
SQ	Sequence 16 AA;
	Query Match 67.9%; Score 55; DB 23; Length 16;
	Best Local Similarity 68.8%; Pred. No. 0.013;
	Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0
Qy	1 RSKSLLYKDGKTYLN 16
	: : :
Db	1 KSSQLLSDSGKTFN 16

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Job time : 74 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:13:30 ; Search time 41 Seconds
(without alignments)
31.270 Million cell updates/sec

Title: US-09-674-716B-3
Perfect score: 81
Sequence: 1 RSSKSLLYKDGKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues
Total number of hits satisfying chosen parameters: 48364

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	67.9	16	10	US-09-835-087-14
2	49	60.5	16	9	US-09-518-737-8
3	43	53.1	15	10	US-09-217-268B-29
4	40	49.4	16	10	US-09-796-744-8
5	39	48.1	16	9	US-10-091-236-14
6	39	48.1	16	9	US-10-091-313-4
7	39	48.1	16	9	US-10-091-268-4
8	39	48.1	16	10	US-09-748-960-9
9	32.5	40.1	15	9	US-09-879-461-16
10	32	39.5	9	9	US-10-205-150-4
11	30	37.0	16	9	US-09-876-904A-343
12	29	35.8	10	9	US-09-809-638-497
13	27	33.3	12	9	US-10-084-813-328
14	27	33.3	15	9	US-10-084-813-692
15	27	33.3	15	9	US-10-084-813-693
16	27	33.3	15	9	US-10-084-813-694
17	27	33.3	15	9	US-10-084-813-695
18	26	32.1	9	9	US-09-809-638-622
19	26	32.1	10	9	US-09-809-638-704

20	26	32.1	12	10	US-09-850-351A-61	Sequence 61, Appl
21	26	32.1	14	9	US-09-736-968A-18	Sequence 18, Appl
22	26	32.1	14	10	US-09-736-969A-18	Sequence 18, Appl
23	26	32.1	14	10	US-09-736-960-18	Sequence 18, Appl
24	26	32.1	16	9	US-09-876-904A-344	Sequence 344, App
25	25	30.9	10	10	US-09-780-053-103	Sequence 103, App
26	25	30.9	10	10	US-09-780-053-670	Sequence 670, App
27	25	30.9	10	10	US-09-308-511-3	Sequence 3, Appli
28	25	30.9	11	9	US-09-969-037-1	Sequence 1, Appli
29	25	30.9	11	9	US-09-969-037-2	Sequence 2, Appli
30	25	30.9	12	9	US-10-084-813-927	Sequence 927, App
31	25	30.9	15	9	US-09-912-414-37	Sequence 37, Appl
32	25	30.9	15	9	US-10-161-499-26	Sequence 26, Appl
33	25	30.9	15	9	US-10-084-813-691	Sequence 691, App
34	24	29.6	12	9	US-09-818-991-9	Sequence 9, Appli
35	24	29.6	13	9	US-10-216-408-25	Sequence 25, Appl
36	24	29.6	15	10	US-09-861-294-23	Sequence 23, Appl
37	24	29.6	16	9	US-09-996-288-25	Sequence 25, Appl
38	24	29.6	16	9	US-09-996-288-106	Sequence 106, App
39	24	29.6	16	9	US-10-023-896-113	Sequence 113, App
40	24	29.6	16	10	US-09-796-848A-27	Sequence 27, Appl
41	23.5	29.0	11	9	US-09-968-561A-184	Sequence 184, App
42	23.5	29.0	11	10	US-09-192-854-105	Sequence 105, App
43	23	28.4	10	10	US-09-973-145-17	Sequence 17, Appl
44	23	28.4	12	9	US-10-057-505-26	Sequence 26, Appl
45	23	28.4	12	9	US-09-912-414-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-09-835-087-14
; Sequence 14, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; FILE REFERENCE: 1855-2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; * PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus Musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(16)
; OTHER INFORMATION: CDR1 of murine mAb 1D9 light chain variable region
US-09-835-087-14

Query Match 67.9%; Score 55; DB 10; Length 16;
Best Local Similarity 68.8%; Pred. No. 0.007;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
:|||||
Db 1 KSSQSLSDSGKTFN 16

RESULT 2
US-09-518-737-8
; Sequence 8, Application US/09518737
; Publication NO. US20030008321A1
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIRO
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI


```

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-091-313-4

Query Match      48.1%; Score 39; DB 9; Length 16;
Best Local Similarity 61.5%; Pred. No. 3;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKT 13
DB 1 RSSQSLHSSGNT 13

RESULT 7
US-10-091-268-4
; Sequence 4, Application US/10091268
; Publication No. US20030068320A1
; GENERAL INFORMATION:
; APPLICANT: DINGIVAN, CHRISTINE A
; TITLE OF INVENTION: METHODS OF ADMINISTERING/DOSING CD2 ANTAGONISTS FOR THE PREVENTIO
; FILE REFERENCE: 10271-054-999
; CURRENT APPLICATION NUMBER: US/10/091,268
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/273,098
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/346,918
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-091-268-4

Query Match      48.1%; Score 39; DB 9; Length 16;
Best Local Similarity 61.5%; Pred. No. 3;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKT 13
DB 1 RSSQSLHSSGNT 13

RESULT 8
US-09-748-960-9
; Sequence 9, Application US/09748960
; Patent No. US20010046496A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Judith A.
; APPLICANT: Brettman, Lee R.
; APPLICANT: Allison, David Edward
; TITLE OF INVENTION: Method of Administering an Antibody
; FILE REFERENCE: 1855-2007-001
; CURRENT APPLICATION NUMBER: US/09/748,960
; CURRENT FILING DATE: 2000-12-27
; PRIOR FILING DATE: 2000-12-27
; PRIOR APPLICATION NUMBER: US 09/550,082
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(16)
; OTHER INFORMATION: CDR1 of the light chain of antibodies Act-1 and

```

```

; OTHER INFORMATION: LDP-02
US-09-748-960-9

Query Match      48.1%; Score 39; DB 10; Length 16;
Best Local Similarity 56.2%; Pred. No. 3;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
DB 1 RSSQSLAKSYGNTYLS 16

RESULT 9
US-09-879-461-16
; Sequence 16, Application US/09879461
; Publication No. US20020193575A1
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; Gross, Mitchell S.
; Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: Corporate Intellectual Property, UW2220 - 709
; Swedeland Rd.
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-2799
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/879,461
; FILING DATE: 12-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/612,929
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/136,783
; FILING DATE: 14-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-879-461-16

Query Match      40.1%; Score 32.5; DB 9; Length 15;
Best Local Similarity 43.8%; Pred. No. 33;
Matches 7; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 1 RSSKSLLYKDGKTYLN 16
DB 1 KASQSDVY-DGDSYNN 15

RESULT 10
US-10-205-150-4
; Sequence 4, Application US/10205150

```

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; Publication No. US20020197269A1
; GENERAL INFORMATION:
; APPLICANT: LINGNAU, KAREN ET AL.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR IMMUNOMODULATION AND PREPARATION
; TITLE OF INVENTION: OF VACCINES COMPRISING AN ANTIGEN AND AN IMMUNOGENIC OLIGODEOXYN
; FILE REFERENCE: 129 35US01
; CURRENT APPLICATION NUMBER: US/09/809,638
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 746
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 497
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-809-638-497

Query Match 35.8%; Score 29; DB 9; Length 10;
Best Local Similarity 55.6%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 YKDGKTYL 16
Db 2 YKEGHNYEN 10

RESULT 13
US-10-084-813-928
; Sequence 928, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 928
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
; US-10-084-813-928

Query Match 33.3%; Score 27; DB 9; Length 12;
Best Local Similarity 41.7%; Pred. No. 2,1e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 KSLLYKDGKTYL 15
Db 1 KNLKIEDSDTYI 12

RESULT 14
US-10-084-813-692
; Sequence 692, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27

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; Publication No. US20020197269A1
; GENERAL INFORMATION:
; APPLICANT: LINGNAU, KAREN ET AL.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION FOR IMMUNOMODULATION AND PREPARATION
; TITLE OF INVENTION: OF VACCINES COMPRISING AN ANTIGEN AND AN IMMUNOGENIC OLIGODEOXYN
; FILE REFERENCE: 129 35US01
; CURRENT APPLICATION NUMBER: US/09/809,638
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 746
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 497
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-809-638-497

Query Match 39.5%; Score 32; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 2,7e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YKDGKTYL 15
Db 2 YKDGNEYI 9

RESULT 11
US-09-876-904A-343
; Sequence 343, Application US/09876904A
; Publication No. US20030072794A1
; GENERAL INFORMATION:
; APPLICANT: BOULIKAS, TENI
; TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
; TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
; FILE REFERENCE: TB-2002.00
; CURRENT APPLICATION NUMBER: US/09/876,904A
; CURRENT FILING DATE: 2001-06-08
; PRIOR FILING DATE: 2000-06-09
; NUMBER OF SEQ ID NOS: 629
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 343
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; OTHER INFORMATION: Ser/Thr protein kinase
; US-09-876-904A-343

Query Match 37.0%; Score 30; DB 9; Length 16;
Best Local Similarity 55.6%; Pred. No. 93;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 8 YKDGKTYL 16
Db 6 YRDHKTHLH 14

RESULT 12
US-09-809-638-497
; Sequence 497, Application US/09809638
; Publication No. US20030059895A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Bid
; APPLICANT: Steve Chappell Michell
; APPLICANT: Daniel E.H. Afar

```

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; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 692
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-692
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Query Match      33.3%; Score 27; DB 9; Length 15;
Best Local Similarity 41.7%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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```
QY 4 KSLLYKDGKTYL 15
   |:|:|:|:|:|:|:
Db 4 KNLKIEDSDTYI 15
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RESULT 15
US-10-084-813-693
; Sequence 693, Application US/10084813
; Publication No. US20030068615A1
; GENERAL INFORMATION:
; APPLICANT: SAXINGER, CARL
; TITLE OF INVENTION: POLYPEPTIDES THAT BIND HIV GP120 AND RELATED NUCLEIC
; FILE REFERENCE: 215875
; CURRENT APPLICATION NUMBER: US/10/084,813
; CURRENT FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: PCT/US00/23505
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,270
; PRIOR FILING DATE: 1999-08-27
; NUMBER OF SEQ ID NOS: 1242
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 693
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: binding peptide
US-10-084-813-693
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```
Query Match      33.3%; Score 27; DB 9; Length 15;
Best Local Similarity 41.7%; Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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QY 4 KSLLYKDGKTYL 15
   |:|:|:|:|:|:|:
Db 3 KNLKIEDSDTYI 14
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Job time : 41 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:11:19 ; Search time 14 Seconds
(without alignments)
33.626 Million cell updates/sec

Title: US-09-674-716B-3
Perfect score: 81
Sequence: 1 RSKSKLLYKDGKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 116189

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A-COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B-COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A-COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B-COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCFUS-COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77	95.1	16	2	US-08-672-345C-22
2	77	95.1	16	2	US-08-672-345C-25
3	77	95.1	16	4	US-09-214-095D-22
4	77	95.1	16	4	US-09-214-095D-25
5	75	92.6	16	2	US-08-672-345C-19
6	75	92.6	16	2	US-08-672-345C-28
7	75	92.6	16	4	US-09-214-095D-19
8	75	92.6	16	4	US-09-214-095D-28
9	69	85.2	16	2	US-08-672-345C-43
10	69	85.2	16	2	US-08-672-345C-79
11	69	85.2	16	4	US-09-214-095D-43
12	69	85.2	16	4	US-09-214-095D-79
13	55	67.9	16	1	US-08-438-123-1
14	52	64.2	16	4	US-09-406-532-18
15	49	60.5	16	1	US-08-244-626-4
16	46	56.8	16	1	US-08-053-171-27
17	46	56.8	16	1	US-07-977-696C-30
18	46	56.8	16	1	US-08-129-930B-30
19	46	56.8	16	4	US-08-134-346A-17
20	46	56.8	16	4	US-08-976-288A-30
21	45	55.6	16	1	US-07-977-696C-68
22	45	55.6	16	1	US-08-129-930B-68
23	45	55.6	16	4	US-08-976-288A-68
24	44	54.3	16	2	US-08-560-558E-29
25	32.5	40.1	15	2	US-08-483-636-16
26	32.5	40.1	15	2	US-08-483-632-16
27	32	39.5	9	5	PCT-US95-04975-6

28	30	37.0	9	3	US-08-159-339A-133	Sequence 133, Appl
29	30	37.0	14	1	US-08-360-125-23	Sequence 23, Appl
30	30	37.0	14	2	US-08-450-578-23	Sequence 23, Appl
31	30	37.0	14	2	US-09-017-628-23	Sequence 23, Appl
32	30	37.0	14	2	US-09-014-880-23	Sequence 23, Appl
33	30	37.0	14	4	US-08-450-363-23	Sequence 23, Appl
34	30	37.0	16	2	US-08-647-960-18	Sequence 18, Appl
35	29	35.8	12	6	5443956-15	Patent No. 5443956
36	28	34.6	15	1	US-07-720-189-11	Sequence 11, Appl
37	27	33.3	9	3	US-08-159-339A-219	Sequence 219, Appl
38	27	33.3	14	1	US-08-337-615A-16	Sequence 16, Appl
39	26	32.1	9	1	US-08-080-073-15	Sequence 15, Appl
40	26	32.1	11	2	US-08-765-536-3	Sequence 3, Appl
41	26	32.1	11	5	PCT-US95-08401-3	Sequence 3, Appl
42	26	32.1	12	1	US-07-620-669-16	Sequence 16, Appl
43	26	32.1	12	1	US-07-803-624-16	Sequence 16, Appl
44	26	32.1	12	1	US-07-998-361-16	Sequence 16, Appl
45	26	32.1	12	4	US-08-960-780-61	Sequence 61, Appl

ALIGNMENTS

RESULT 1
US-08-672-345C-22
; Sequence 22, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-22

Query Match 95.1%; Score 77; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSKSKLLYKDGKTYLN 16

DB 1 RSKSKLLYKDGKTYLN 16

RESULT 2

US-08-672-345C-25
; Sequence 25, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-25

Query Match 95.1%; Score 77; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYDKGKTYLN 16
| | | | | | | | | | | | | | | |
Db 1 RSSKSLLYEDGKTYLN 16

RESULT 3
US-09-214-095D-22
; Sequence 22, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-22

Query Match 95.1%; Score 77; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-09-214-095D-25
; Sequence 25, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-25

Query Match 95.1%; Score 77; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSSKSLLYDKGKTYLN 16
| | | | | | | | | | | | | | | |
Db 1 RSSKSLLYEDGKTYLN 16

RESULT 5
US-08-672-345C-19
; Sequence 19, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-19

Query Match 92.6%; Score 75; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.8e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSKSLLYKDGKTYLN 16
|||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 6

US-08-672-345C-28
; Sequence 28, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-28

Query Match 92.6%; Score 75; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.8e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSKSLLYKDGKTYLN 16
|||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 7

US-09-214-095D-19
; Sequence 19, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-19

Query Match 92.6%; Score 75; DB 4; Length 16;

Best Local Similarity 87.5%; Pred. No. 2.8e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSKSLLYKDGKTYLN 16
|||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 8

US-09-214-095D-28
; Sequence 28, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-28

Query Match 92.6%; Score 75; DB 4; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.8e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSKSLLYKDGKTYLN 16
|||:||||:|||||
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 9

US-08-672-345C-43
; Sequence 43, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

US-08-672-345C-43

Query Match 85.2%; Score 69; DB 2; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.7e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
:|||||
Db 1 KSSQSLLYSDGKTYLN 16

RESULT 10

US-08-672-345C-79
; Sequence 79, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 79:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-79

Query Match 85.2%; Score 69; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
:|||||
Db 1 RSSKSLLYSDGKTYLN 16

RESULT 11

US-09-214-095D-43
; Sequence 43, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 43

; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-43

Query Match 85.2%; Score 69; DB 4; Length 16;
Best Local Similarity 81.2%; Pred. No. 2.7e-05;
Matches 13; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
:|||||
Db 1 KSSQSLLYSDGKTYLN 16

RESULT 12

US-09-214-095D-79
; Sequence 79, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 79
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (4)-(9)
; OTHER INFORMATION: X at positions 4 and 9 represents any amino acid
US-09-214-095D-79

Query Match 85.2%; Score 69; DB 4; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
:|||||
Db 1 RSSKSLLYSDGKTYLN 16

RESULT 13

US-08-438-123-1
; Sequence 1, Application US/08438123
; Patent No. 5552293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, LeBlanc & Becker
; STREET: Suite 300, 99 Canal Center Plaza
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: DOS Text File
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,123
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/906,350
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```
; NAME: J.G. Mullins
; REGISTRATION NUMBER: 33073
; REFERENCE/DOCKET NUMBER: 149-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 684 1111
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Polypeptide
US-08-438-123-1

Query Match 67.9%; Score 55; DB 1; Length 16;
Best Local Similarity 73.3%; Pred. No. 0.0056;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYL 15
   |||||..:||||
Db 1 RSSKSLHSHNGNTYL 15

RESULT 14
US-09-406-532-18
; Sequence 18, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; PRIORITY FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(16)
; OTHER INFORMATION: light chain CDR 1
US-09-406-532-18

Query Match 64.2%; Score 52; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 0.018;
Matches 10; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYL 15
   |||||..:||||
Db 1 RSSKSLHSHNGNTYL 15

RESULT 15
US-08-244-626-4
; Sequence 4, Application US/08244626
; Patent No. 5502167
; GENERAL INFORMATION:
; APPLICANT: Waldmann, Herman
; APPLICANT: Walsh, Louise
; APPLICANT: Crowe, James Scott
; APPLICANT: Lewis, Alan Peter
; TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, p.c.
; STREET: 555 Thirteenth Street, N. W.
```

```
; CITY: Washington
; STATE: D. C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/244,626
; FILING DATE: July 15, 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02251
; FILING DATE: December 4, 1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Ernst, Barbara G.
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-153A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-244-626-4

Query Match 60.5%; Score 49; DB 1; Length 16;
Best Local Similarity 56.2%; Pred. No. 0.055;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
   |||||..:||||
Db 1 RSSKSLVSHNGNTYLH 16
```

Search completed: April 22, 2003, 13:14:20
Job time : 15 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:20:30 ; Search time 43 seconds
(without alignments)
15.650 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 456

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	14	45.2	3	I50412	gene p20K protein
2	13	41.9	6	A11490	pyruvate kinase (E
3	12	38.7	5	I40469	dnazX-like protein
4	12	38.7	6	I51434	H4 histone - Afric
5	12	38.7	6	PT0518	T-cell receptor be
6	11	35.5	5	B31836	20K protein - Rick
7	11	35.5	5	H44817	34.5K structural p
8	11	35.5	5	F44817	34.5K structural p
9	11	35.5	5	A58728	serawettin W2 - S
10	11	35.5	7	S42620	aggrecan - bovine
11	10	32.3	5	A37114	hypoxanthine phosph
12	10	32.3	5	PT0295	Ig heavy chain CRD
13	10	32.3	5	PT0577	T-cell receptor be
14	10	32.3	5	PT0565	T-cell receptor be
15	10	32.3	5	PT0700	surface protein te
16	10	32.3	5	S69237	hypothetical prote
17	10	32.3	6	A37765	hypothetical prote
18	10	32.3	6	S14159	parasporal crystal
19	10	32.3	6	B26206	alpha-1,4-glucan-p
20	10	32.3	6	A45474	PC epsilon RIIB -
21	10	32.3	7	A34026	acetylcholinestera
22	10	32.3	7	B33541	hypothetical prote
23	10	32.3	7	I55382	hypothetical pepti
24	9	29.0	3	I78890	tyrosine protein k
25	9	29.0	5	S70154	URP2 protein - Xan
26	9	29.0	5	I40702	primase - Citrobac
27	9	29.0	5	B37325	pap fibmbrial regul
28	9	29.0	5	T14910	hypothetical prote
29	9	29.0	5	PT0686	T-cell receptor be

T-cell receptor be
dnAA protein - pse
hypothetical 6 pro
D-Sp2.5 region - m
T-cell receptor be
T-cell receptor ga
laminin B1 - weste
orf 3 rara 5'-regi
microcin C7 - Esch
piliE protein - Esc
mabinlin II chain
seed protein ws-5
myomodulin - Calif
neuromodulatory pe
neuromodulatory pe
neuromodulatory pe

ALIGNMENTS

RESULT 1

I50412

gene p20K protein - chicken (fragment)

C;Species: Gallus gallus (chicken)

C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001

C;Accession: I50412

R;Mao, P.L.; Beauchemin, M.; Bedard, P.A.

J. Biol. Chem. 268, 8131-8139, 1993

A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken

A;Reference number: A46643; MUID:93216790; PMID:8463325

A;Accession: I50412

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-3 <MAO>

A;Cross-references: GB:L02537; NID:g212616; PID:g212617

C;Genetics:

A;Gene: p20K

Query Match 45.2%; Score 14; DB 3; Length 3;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4

Db 1 MST 3

RESULT 2

A11490

pyruvate kinase (EC 2.7.1.40) - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 03-Mar-1995

C;Accession: A11490

R;Hjelmlquist, G.; Andersson, J.; Edlund, B.; Engstrom, L.

Biochem. Biophys. Res. Commun. 61, 559-563, 1974

A;Title: Amino acid sequence of a (32-P)phosphopeptide from pig liver pyruvate kinase ph

A;Reference number: A11490; MUID:75127438; PMID:4375989

A;Accession: A11490

A;Molecule type: protein

A;Residues: 1-6 <HJE>

A;Experimental source: liver

C;Keywords: glycolysis; phosphotransferase

Query Match 41.9%; Score 13; DB 2; Length 6;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RAS 7

Db 3 RAS 5

RESULT 3
I40469
dnaXZ-like protein - Bacillus subtilis (fragment)
C:Species: Bacillus subtilis
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C:Accession: I40469
R:Struck, J.C.; Hartmann, R.K.; Toschka, H.Y.; Erdmann, V.A.
Mol. Gen. Genet. 215, 478-482, 1989
A:Title: Transcription and processing of Bacillus subtilis small cytoplasmic RNA.
A:Reference number: I40469; MUID:89218958; PMID:2468993
A:Accession: I40469
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5 <RES>
A:Cross-references: EMBL:X14796; NID:940130; PIDN:CAA32902.1; PID:94376204
C:Genetics:
A:Start codon: GTG

Query Match 38.7%; Score 12; DB 2; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MSTR 6
DB 1 MSYQA 5

RESULT 4
I51434
H4 histone - African clawed frog (fragment)
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C:Accession: I51434
R:Woodland, H.R.; Warrington, J.R.; Ballantine, J.E.M.; Turner, P.C.
Nucleic Acids Res. 12, 4939-4958, 1984
A:Title: Are there major developmentally regulated H4 gene classes in Xenopus?
A:Reference number: I51391; MUID:84247348; PMID:6330691
A:Accession: I51434
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-6 <WOO>
A:Cross-references: GB:K02304; NID:9214227; PIDN:AAA49738.1; PID:9555517

Query Match 38.7%; Score 12; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MSTR 5
DB 1 MSGR 4

RESULT 5
PT0518
T-cell receptor beta chain V-D-J region (100-4B) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0518
R:Peeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0518
A>Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-6 <FEE>
A:Experimental source: adult thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 38.7%; Score 12; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
DB 1 ASRAT 5

RESULT 6
B31836
20K protein - Rickettsia rickettsii (fragment)
C:Species: Rickettsia rickettsii
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
C:Accession: B31836
R:Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.
J. Bacteriol. 170, 4493-4500, 1988
A:Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii.
A:Reference number: A91885; MUID:8908059; PMID:3139629
A:Accession: B31836
A:Molecule type: DNA
A:Residues: 1-5 <AND>
A:Cross-references: GB:J03371; NID:9152455; PIDN:AA015030.1; PID:94262874

Query Match 35.5%; Score 11; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 MSTR 6
DB 1 MDTNS 5

RESULT 7
H44817
34.5K structural protein - Leuconostoc oenos phage P32 (fragment)
C:Species: Leuconostoc oenos phage P32
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: H44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: H44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A>Note: sequence extracted from NCBI backbone (NCBI:70332)

Query Match 35.5%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4
DB 1 MAT 3

RESULT 8
F44817
34.5K structural protein - Leuconostoc oenos phage P54 (fragment)
C:Species: Leuconostoc oenos phage P54
C:Date: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C:Accession: F44817
R:Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A:Title: Lysogeny in Leuconostoc oenos.
A:Reference number: A44817; MUID:92085033; PMID:1748868
A:Accession: F44817
A:Molecule type: protein
A:Residues: 1-5 <ARE>
A>Note: sequence extracted from NCBI backbone (NCBI:70335)

Query Match 35.5%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4
DB 1 MAT 3


```

Db      1 MAT 3
|:|
RESULT 9
A58728
Serrawettin W2 - Serratia marcescens
C:Species: Serratia marcescens
C>Date: 10-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 12-Feb-1998
C:Accession: A58728
R:Matsumura, T.; Kaneda, K.; Nakagawa, Y.; Isa, K.; Hara-Hotta, H.; Yano, I.
J. Bacteriol. 174, 1769-1776, 1992
A:Title: A novel extracellular cyclic lipopeptide which promotes flagellum-dependent and
A:Reference number: A58728; MUID:92193260; PMID:1548227
A:Accession: A58728
A:Status: unencoded polypeptide
A:Molecule type: protein
A:Residues: 1-5 <MAT>
A:Experimental source: strain NS 25
C:Comment: A surfactant lipopeptide promoting flagellum-independent surface translocation
C:Keywords: blocked amino end; blocked carboxyl end; D-amino acid; lipoprotein; unencoded
F:1/Modified site: D-leucine (Leu) #status experimental
F:4/Modified site: D-phenylalanine (Phe) #status experimental
F:1-5/Cross-link: 3-hydroxydecanoyl amino end, ester carboxyl end (Leu-Ile) #status experimental

Query Match      35.5%; Score 11; DB 4; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  2 MST 4
    |||
Db   1 LST 3

RESULT 10
A42620
aggreccan - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
C:Accession: S42620
R:Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
Matrix Biol. 14, 171-179, 1994
A:Title: Aggreccan in bovine tendon.
A:Reference number: S42620; MUID:94340214; PMID:7520336
A:Accession: S42620
A:Molecule type: protein
A:Residues: 1-7 <VOG>
A:Experimental source: flexor tendon
C:Keywords: cartilage

Query Match      35.5%; Score 11; DB 2; Length 7;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1 LMSTR 5
    :|||
Db   3 IVSPR 7

RESULT 11
A37114
hypoxanthine phosphoribosyltransferase (EC 2.4.2.8) - fluke (Schistosoma mansoni) (fragment)
C:Species: Schistosoma mansoni
C>Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 23-Jun-1993
C:Accession: A37114
R:Yuan, L.; Craig, S.P.; McKerrow, J.H.; Wang, C.C.
J. Biol. Chem. 265, 13528-13532, 1990
A:Title: The hypoxanthine-guanine phosphoribosyltransferase of Schistosoma mansoni. Further
A:Reference number: A37114; MUID:90337955; PMID:2199439
A:Accession: A37114
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <YUA>

```

C:Keywords: glycosyltransferase; pentosyltransferase

Query Match 32.3%; Score 10; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MST 4
 |||
 Db 1 MSS 3

RESULT 12
 PT0295

IG heavy chain CDR3 region (clone 5-91) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PT0295
 R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A:Reference number: PT0222; MUID:91108337; PMID:1893102
 A:Accession: PT0295
 A:Molecule type: DNA
 A:Residues: 1-5 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match 32.3%; Score 10; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TR 5
 |||
 Db 3 TR 4

RESULT 13
 PT0577

T-cell receptor beta chain V-D-J region (141-1BC) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0577; PT0574
 R:Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A:Reference number: PT0509; MUID:91277601; PMID:1711558
 A:Accession: PT0577
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FEE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1BC
 A:Accession: PT0574
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-5 <FEE>
 A:Experimental source: day 19 fetal thymus, strain BALB/c, clone 141-1Q
 C:Keywords: T-cell receptor

Query Match 32.3%; Score 10; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STR 5
 |||
 Db 2 SSR 4

RESULT 14
 PT0565

T-cell receptor beta chain V-D-J region (141-1CF) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C:Accession: PT0565

R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0565
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-5 <PEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 32.3%; Score 10; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STR 5
|:|
Db 2 SSR 4

RESULT 15

PT0700
T-cell receptor beta chain V-D-J region (161-2A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0700
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0700
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <PEE>
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match 32.3%; Score 10; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STR 5
|:|
Db 2 SSR 4

Search completed: April 22, 2003, 13:24:30
Job time : 43 secs

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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:14:25 ; Search time 11 Seconds
(without alignments)
26.394 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 85

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	45.2	7	1	P99025 mus musculus
2	11	35.5	5	1	P13071 citrobacter
3	11	35.5	7	1	P80630 zea mays (m
4	10	32.3	6	1	P23210 herpes simp
5	9	29.0	7	1	P56576 rattus norv
6	9	29.0	7	1	P35919 achatina fu
7	9	29.0	7	1	P35920 achatina fu
8	9	29.0	7	1	P35921 achatina fu
9	8	25.8	7	1	P11932 enterococcu
10	7	22.6	4	1	P01858 homo sapien
11	7	22.6	7	1	P06294 dactylium d
12	6	19.4	4	1	P19918 pseudomonas
13	6	19.4	4	1	P58705 anthopleura
14	6	19.4	5	1	P12997 citrobacter
15	6	19.4	5	1	P01373 periplaneta
16	6	19.4	5	1	P58261 daucus caro
17	6	19.4	6	1	P36414 pseudomonas
18	6	19.4	6	1	P81351 clostridium
19	6	19.4	7	1	P20184 enterococcu
20	6	19.4	7	1	CCF1 ENTFA
21	5	16.1	4	1	P16101 alcaligenes
22	5	16.1	4	1	P19916 pseudomonas
23	5	16.1	4	1	P42562 hirudo medi
24	5	16.1	4	1	P42563 hirudo medi
25	5	16.1	4	1	P58707 anthopleura
26	5	16.1	4	1	P01162 macrocallis
27	5	16.1	4	1	P58706 anthopleura
28	5	16.1	4	1	P36515 saccharomyc
29	5	16.1	5	1	P82099 litoria rub
30	5	16.1	5	1	P82100 litoria rub
31	5	16.1	5	1	P41853 artiopeathi
32	5	16.1	5	1	P82072 litoria rub
33	5	16.1	5	1	P82073 litoria rub

P19991 acheta dome
P38639 mus musculus
P25154 oryctolagus
P13736 mytilus edu
P13737 mytilus edu
P82096 litoria rub
P41966 moniezia ex
P41491 locusta mig
P41495 sarcophaga
P82158 cydia pomon
P58803 conus imper
P10420 mytilus edu

ALIGNMENTS

RESULT 1
GFRP MOUSE STANDARD; PRT; 7 AA.
AC P99025;1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE GTP cyclohydrolase I feedback regulatory protein (P15) (Fragment).
GN GCHFR OR GFRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
RA Cowthorne M.;
RL Submitted (AUG-1998) to the SWISS-PROT data bank.
CC -!- FUNCTION: MEDIATES TETRAHYDROBIOTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
(BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC SWISS-2DPAGE; P99025; MOUSE.
FT INIT MET 0
FT NON TER 7
SQ SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;
Query Match 45.2%; Score 14; DB 1; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMST 4
Db 4 LIST 7

RESULT 2
BIOA CITFR STANDARD; PRT; 5 AA.
ID BIOA CITFR
AC P13071;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adenosylmethionine-8-amino-7-oxononanoate aminotransferase
(EC 2.6.1.62) (7,8-diamino-pelargonic acid aminotransferase) (DAPA
aminotransferase) (Fragment).
DE BIOA.
GN Citrobacter freundii.
OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89006280; PubMed=2971595;

```

RA Shuan D., Campbell A.;
RT "transcriptional regulation and gene arrangement of Escherichia coli,
RL Citrobacter freundii and Salmonella typhimurium biotin operons.";
GC Gene 67:203-211(1988).
CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + 8-amino-7-
CC oxononanoate = S-adenosyl-4-methylthio-2-oxobutanoate + 7,8-
CC oximinonanoate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: Biotin biosynthesis.
CC -1- SUBUNIT: Biotin biosynthesis.
CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC AMINOTRANSFERASES.
CC -----
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CC -----
DR EMBL; M21922; -; NOT ANNOTATED CDS.
DR InterPro; IPR000954; AminoTransfer_3.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
KW Biotin biosynthesis; Transferase; AminoTransferase;
KW Pyridoxal phosphate; 5
FT NON TER 5
SQ SEQUENCE 5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;

Query Match 35.5%; Score 11; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 MST 4
| |
| |
Db 1 MTT 3

RESULT 3
UC24 MAIZE STANDARD; PRT; 7 AA.
ID UC24 MAIZE
AC P80630;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 447)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.0. ITS MW IS: 30.0 kDa.
CC Maize-2DPAGE; P80630; COLEOPTILE.
DR MaizeDB; 123956; -.
FT NON TER 1
FT NON TER 7
SQ SEQUENCE 7 AA; 665 MW; 6DC1B5B33DC1B5D0 CRC64;

Query Match 35.5%; Score 11; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 STRAS 7

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Db 1 STAKS 5
| |
| |
RESULT 4
VP19 HSV1K STANDARD; PRT; 6 AA.
ID VP19 HSV1K
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavassiliou A.G., Rice M., Hecht L.B.,
RA Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
RT expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -1- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
CC EMBEDDED. BINDS DNA.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC -----
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CC -----
DR EMBL; M57646; AAA45830.1; -
DR Capsid assembly; Coat protein; DNA-binding.
FT NON TER 6
SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 32.3%; Score 10; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MST 4
| |
| |
Db 1 MKT 3

RESULT 5
UH11 RAT STANDARD; PRT; 7 AA.
ID UH11 RAT
AC P56576;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot P11) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE.
RC STRAIN=Wistar; TISSUE=Heart;
RA Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov J.,
RA Jungblut P.R.;
RL Submitted (SEP-1998) to the SWISS-PROT data bank.
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 8.5. ITS MW IS: 42 kDa.
FT UNSURE 2 OR A.

```

FT NON TER 7 7
SQ SEQUENCE 7 AA; 775 MW; 6866DB040DC5A6B0 CRC64;
Query Match 29.0%; Score 9; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 STR 5
DB 2 SAR 4
RESULT 6
WMA1_ACHFU
ID WMA1_ACHFU STANDARD; PRT; 7 AA.
AC P35919;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMA1-1.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WMA1-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
CC -1- FUNCTION: EXHIBITS MODULATORY EFFECTS ON THE PERIPHERAL NERVOUS
CC SYSTEM. INHIBITS ACTIVITY ON A CENTRAL NEURON.
DR PIR; S33245; S33245.
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 993 MW; 7362D5B6B041310 CRC64;
Query Match 29.0%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 MS 3
DB 4 MS 5
RESULT 7
WMA2_ACHFU
ID WMA2_ACHFU STANDARD; PRT; 7 AA.
AC P35920;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMA2-2.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WMA2-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 964 MW; 7362D5B6B6D32310 CRC64;
Query Match 29.0%; Score 9; DB 1; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 MS 3
DB 4 MS 5
RESULT 8
WMA3_ACHFU
ID WMA3_ACHFU STANDARD; PRT; 7 AA.
AC P35921;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE WMA3-3.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE.
RC TISSUE=Ganglion;
RX MEDLINE=93265912; PubMed=8495720;
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;
RT "WMA3-1, -2 and -3: novel neuromodulatory peptides isolated from
RT ganglia of the African giant snail, Achatina fulica.";
RL FEBS Lett. 323:104-108(1993).
DR PIR; S33244; S33244.
KW Neuropeptide; Amidation.
FT MOD RES 7
SQ SEQUENCE 7 AA; 965 MW; 7362D5B6B132310 CRC64;
Query Match 29.0%; Score 9; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 MS 3
DB 4 MS 5
RESULT 9
CIA_ENTFA
ID CIA_ENTFA STANDARD; PRT; 7 AA.
AC P11932;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE Sex pheromone CAM373 (clumping-inducing agent) (CIA).
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE.
RX MEDLINE=87005252; PubMed=3093276;
RA Mori M., Tanaka H., Sakagami Y., Isogai A., Fujino M., Kitada C.,
RA White B.A., An F.Y., Clewell D.B., Suzuki A.;
RT "Isolation and structure of the Streptococcus faecalis sex pheromone,
RT CAM373.";
RL FEBS Lett. 206:69-72(1986).
CC -1- FUNCTION: CAM373 INDUCES MATING RESPONSE OF DONOR CELLS
CC HARBORING PAM373.
CC -1- MISCELLANEOUS: THE N-TERMINUS IS POSSIBLY RESPONSIBLE FOR
CC SPECIFICITY OF PHEROMONES TO PLASMIDS.
CC -1- SIMILARITY: C-TERMINAL TO THE PHEROMONES CPD1 AND CAD1.
DR PIR; A25269; A25269.
KW Pheromone.
FT MOD RES 7
SQ SEQUENCE 7 AA; 734 MW; 75BDD72059C05DB0 CRC64;
Query Match 25.8%; Score 8; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 AS 7
DB 6 AS 7

RESULT 10
TUFT HUMAN
ID TUFT HUMAN STANDARD; PRT; 4 AA.
AC P01858;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phagocytosis-stimulating peptide (Tuftsin).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]_SEQUENCE.
RP MEDLINE=72187087; PubMed=4112769;
RA Nishioka K., Constantopoulos A., Satoh P.S., Najjar V.A.;
RT "The characteristics, isolation and synthesis of the phagocytosis
stimulating peptide tuftsin.";
RL Biochem. Biophys. Res. Commun. 47:172-179(1972).
RN [2]
RP IMMUNOGLOBULIN CLASS.
RX MEDLINE=68091045; PubMed=4169272;
RA Fidalgo B.V., Najjar V.A.;
RT "The physiological role of the lymphoid system. VI. The stimulatory
effect of leucophilic gamma globulin (leucokinin) on the phagocytic
activity of human polymorphonuclear leucocyte.";
RL Biochemistry 6:3386-3392(1967).
CC -!- MISCELLANEOUS: AN IGG (CALLED LEUCOKININ) BINDS REVERSIBLY TO THE
CELL MEMBRANE OF NEUTROPHILS IN THE BLOOD. LEUCOKININASE ON THE
MEMBRANE RELEASES THE ACTIVE PEPTIDE TUFTSIN FROM THE GAMMA CHAIN.
CC TUFTSIN IS ESSENTIAL FOR MAXIMUM STIMULATION OF THE PHAGOCYTIC
ACTIVITY OF NEUTROPHILS.
CR PIR; A02147; A02147.
DR MIM; 191150; -
SQ SEQUENCE 4 AA; 501 MW; 74176321C000000000 CRC64;

Query Match 22.6%; Score 7; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TR 5
DB 1 TK 2

RESULT 11
IGAO DACDE
ID IGAO DACDE STANDARD; PRT; 7 AA.
AC P06234;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Galactose oxidase inhibitor.
OS Dactylium dendroideae (Cladobotryum dendroideae).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreales; Hypocreaceae; Hypomyces.
ON NCBI_TaxID=5132;
RN [1]_SEQUENCE.
RP Avigad G., Markus Z.;
RT "Identification of a peptide inhibitor of galactose oxidase from
Dactylium dendroideae.";
RL Fed. Proc. 31:447-447(1972).
CC -!- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE
GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY
BINDING TO ITS PROSTHETIC COPPER GROUP.
DR PIR; A0134; KEYDGD.

KW Copper; Metalloenzyme inhibitor.
SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;

Query Match 22.6%; Score 7; DB 1; Length 7;
Best Local Similarity 25.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRA 6
DB 4 NTES 7

RESULT 12
DCMS_PSECH
ID DCMS_PSECH STANDARD; PRT; 4 AA.
AC P19918;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase small chain (EC 1.2.99.2) (CO
dehydrogenase subunit S) (CO-DH S) (Fragment).
ON CUTS.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group.
ON NCBI_TaxID=290;
RN [1]_SEQUENCE.
RP MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
carboxydrotrophic bacteria.";
RL Arch. Microbiol. 152:335-341(1989).
CC -!- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
dioxide.
CC -!- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
acceptor.
CC -!- COFACTOR: BINDS TWO 2FE-2S CLUSTERS.
CC -!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
SMALL.
DR PIR; P10146; P10146.
KW Oxidoreductase; Iron-sulfur.
FT NON_TER 4
SQ SEQUENCE 4 AA; 420 MW; 6DD33DD6F000000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MS 3
DB 1 MA 2

RESULT 13
FFKA ANTEL
ID FFKA ANTEL STANDARD; PRT; 4 AA.
AC P58705;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antho-Kamide.
OS Anthopleura elegantissima (Sea anemone).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC Nynanthaeae; Actiniidae; Anthopleura.
ON NCBI_TaxID=6110;
RN [1]_SEQUENCE.
RP MEDLINE=92028952; PubMed=1681803;
RA Nethacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.;
RT "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-Kamide), a
novel neuropeptide from sea anemones.";
RL Biochem. Biophys. Res. Commun. 179:1205-1211(1991).

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RN FUNCTION.
RX MEDLINE=93391436; PubMed=8397415;
RA McFarlane I.D., Hudman D., Nockacker H.-P., Grimmelikhuijzen C.J.P.;
RT "The expansion behaviour of sea anemones may be coordinated by two
RT inhibitory neuropeptides, Antho-Xamide and Antho-Kamide.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle
CC groups. May be involved in the expansion phase of feeding
CC behaviour in sea anemones.
CC -!- SURCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Neuron-specific.
KW Neuropeptide; Amidation.
FT MOD RES 1 1 L-3-PHENYLACTYL.
FT MOD RES 4 4 AMIDATION.
SQ SEQUENCE 4 AA; 512 MW; 6DD339C9A0000000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 RA 6
DB 3 KA 4

RESULT 14
BIOB CITFR
ID BIOB CITFR STANDARD; PRT; 5 AA.
AC P12997;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Biotin synthase [EC 2.8.1.6] (Biotin synthetase) (Fragment).
GN BIOB.
OC Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter.
OX NCBI_TaxID=546;
[1] SEQUENCE FROM N.A.
RN MEDLINE=89006280; PubMed=2971595;
RX Shiuan D., Campbell A.;
RA "Transcriptional regulation and gene arrangement of Escherichia coli,
RT Citrobacter freundii and Salmonella typhimurium biotin operons.";
RL Gene 67:203-211(1988).
CC -!- CATALYTIC ACTIVITY: Dethiobiotin + sulfur = biotin.
CC -!- PATHWAY: Biotin biosynthesis; last step.
CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC FAMILY.
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CC -----
DR EMBL; M21922; -; NOT ANNOTATED CDS.
KW Biotin biosynthesis; Iron-sulfur; Transferase.
FT NON_TER 5
SQ SEQUENCE 5 AA; 532 MW; 75A5B1EDD6F00000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 MS 3
DB 1 MA 2

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RESULT 15
PRCT PERAM STANDARD; PRT; 5 AA.
ID PRCT PERAM STANDARD; PRT; 5 AA.
AC P01373;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattodea; Blattellidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
[1] SEQUENCE.
RN SPECIES=P.americana;
RC MEDLINE=76074708; PubMed=576;
RX Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
RT in insects.";
RL Life Sci. 17:1253-1256(1975).
[2]
RN SPECIES=P.americana;
RC SPECIES=P.americana;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
[3]
RN SPECIES=L.polyphemus;
RC SPECIES=L.polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
RT horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
[4]
RN SPECIES=C.maenas;
RC SPECIES=C.maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
RT pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
CC THE CRAB PERICARDIAL ORGANS.
DR PIR; A01644; HOROHA.
DR PIR; A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 19.4%; Score 6; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 MST 4
DB 3 LPT 5

Search completed: April 22, 2003, 13:22:12
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:20:00 ; Search time 81 Seconds
(without alignments)
17.807 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 58

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21.*

- 1: sp archea.*
- 2: sp bacteria.*
- 3: sp fungi.*
- 4: sp human.*
- 5: sp invertebrate.*
- 6: sp mammal.*
- 7: sp mhc.*
- 8: sp organelle.*
- 9: sp phage.*
- 10: sp plant.*
- 11: sp rodent.*
- 12: sp virus.*
- 13: sp vertebrate.*
- 14: sp unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	11	35.5	6	10 P82541	P82541 spinacia ol
2	10	32.3	7	12 Q65578	Q65578 bovine herp
3	9	29.0	7	2 Q47505	Q47505 escherichia
4	9	29.0	7	2 P70804	P70804 azotobacter
5	9	29.0	7	8 Q95945	Q95945 saccharomyc
6	9	29.0	7	10 P93233	P93233 lycopersico
7	8	25.8	5	10 Q93007	Q93007 hordeum vul
8	7	22.6	6	10 P82181	P82181 spinacia ol
9	7	22.6	6	10 P82182	P82182 spinacia ol
10	7	22.6	7	2 Q47029	Q47029 enterobacte
11	7	22.6	7	2 Q34028	Q34028 sphingomona
12	6	19.4	5	2 P83073	P83073 bacillus ce
13	6	19.4	7	4 Q15897	Q15897 homo sapien
14	6	19.4	7	4 Q15903	Q15903 homo sapien
15	6	19.4	7	8 Q99182	Q99182 gnathotobia
16	6	19.4	7	11 Q63668	Q63668 rattus norv

17	6	19.4	7	12	Q66205	Q66205 transmissib
18	6	19.4	7	12	Q9YQ10	Q9YQ10 transmissib
19	6	19.4	7	12	Q67113	Q67113 influenzavi
20	6	19.4	7	13	Q42564	Q42564 fugu rubrip
21	6	19.4	7	15	Q07624	Q07624 rous sarcom
22	5	16.1	5	13	P83308	P83308 gallus gall
23	5	16.1	7	2	O07354	O07354 synechococc
24	5	16.1	7	2	O50556	O50556 actinobacil
25	5	16.1	7	2	Q47477	Q47477 escherichia
26	5	16.1	7	2	Q54248	Q54248 streptomyc
27	5	16.1	7	2	P72081	P72081 nocardia la
28	5	16.1	7	5	P83274	P83274 macrobrachi
29	5	16.1	7	6	Q28742	Q28742 oryctolagus
30	5	16.1	7	8	P92372	P92372 haynaldia v
31	5	16.1	7	8	P92403	P92403 lophopyrum
32	5	16.1	7	8	P92425	P92425 pseudoroegn
33	5	16.1	7	8	P92387	P92387 nenardia p
34	5	16.1	7	8	P92427	P92427 peridictyon
35	5	16.1	7	8	P92390	P92390 heteranthel
36	5	16.1	7	8	P92226	P92226 crithopsis
37	5	16.1	7	8	P92214	P92214 amblyopyrum
38	5	16.1	7	8	P92430	P92430 aegilops ta
39	5	16.1	7	8	P92221	P92221 bromus iner
40	5	16.1	7	8	P92442	P92442 taeniathecu
41	5	16.1	7	8	P92381	P92381 hordeum bra
42	5	16.1	7	8	P92393	P92393 hordeum vul
43	5	16.1	7	8	P92218	P92218 australopyr
44	5	16.1	7	8	P92440	P92440 thinopyrum
45	5	16.1	7	8	P92210	P92210 agropyron c

ALIGNMENTS

RESULT 1

ID P82541 PRELIMINARY; PRT; 6 AA.
AC P82541;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Chloroplast 30S ribosomal protein S19 beta (Fragment).
OS Spinacia oleracea (Spinach).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=CV. ALVARO; TISSUE=LEAF;
EX MEDLINE=20435797; PubMed=10874039;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the small subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 37:28455-28465(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MASS SPECTROMETRY: MW=10477.0; METHOD=ELECTROSPRAY.
CC -!- MASS SPECTROMETRY: MW=10495; METHOD=MALDI.
CC -!- MISCELLANEOUS: S19 ALPHA AND BETA FORMS DIFFER IN PI. S19 BETA
FORM IS THE MINOR BASIC FORM.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 12 KDA.
CC -!- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR002222; Ribosomal S19
DR Pfam; PF02030; Ribosomal S19; PARTIAL.
DR PRINTS; PR00375; Ribosomal S19; PARTIAL.
DR PROSITE; PS00323; RIBOSOMAL S19; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER
SQ SEQUENCE 6 AA; 732 MW; 63333735A411C000 CRC64;

Query Match 35.5%; Score 11; DB 10; Length 6;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TRA 6
| |
Db 1 TRS 3

RESULT 2

Q65578 PRELIMINARY; PRT; 7 AA.
AC Q65578;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 0.8 kDa protein (Fragment).
OS Bovine herpesvirus 1.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
OX NCBI_TaxID=10320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COOPER;
RX MEDLINE=95313343; PubMed=7793062;
RA Vleck C., Benes V., Lu Z., Kutish G.F., Paces V., Rock D.,
RA Letchworth G.J., Schwyzler M.;
RT "Nucleotide sequence analysis of a 30-kb region of the bovine
herpesvirus 1 genome which exhibits a colinear gene arrangement with
the UL21 to UL4 genes of herpes simplex virus.";
RL Virology 210:100-108(1995).
DR EMBL; Z48053; CAA88130.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 7 AA; 758 MW; 6DD33455B1F1B1C0 CRC64;

Query Match 32.3%; Score 10; DB 12; Length 7;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRA 6
| |
Db 4 SNKA 7

RESULT 3

Q47505 PRELIMINARY; PRT; 7 AA.
AC Q47505;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MCCA protein.
GN MCCA.
OS Escherichia coli.
OG Plasmid pmccC7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96099297; PubMed=8522520;
RA Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F.;
RT "Structure and organization of plasmid genes required to produce the
translation inhibitor microcin C7";
RL J. Bacteriol. 177:7131-7140(1995).
DR EMBL; X57583; CAA40808.1; -.
KW Plasmid.
SQ SEQUENCE 7 AA; 763 MW; 644DD44861B406F0 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 MST 4
| |
Db 1 MRT 3

RESULT 4

P70804 PRELIMINARY; PRT; 7 AA.
ID P70804;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ALG1 protein (Fragment).
GN ALG1.
OS Azotobacter vinelandii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Azotobacter.
OX NCBI_TaxID=354;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E;
RX MEDLINE=96427318; PubMed=8830682;
RA Rehm B.H.A., Ertesvag H., Valla S.;
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algC) is
part of an alg gene cluster physically organized in a manner similar
to that in Pseudomonas aeruginosa.";
RL J. Bacteriol. 178:5884-5889(1996).
DR EMBL; X87973; CAA61230.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A2D1AED0 CRC64;

Query Match 29.0%; Score 9; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ST 4
| |
Db 6 ST 7

RESULT 5

Q95945 PRELIMINARY; PRT; 7 AA.
ID Q95945;
AC Q95945;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Inside intron 5 (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=D273-10B;
RX MEDLINE=81069885; PubMed=6254986;
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Trzagaloff A., Macino G.;
RT "Assembly of the mitochondrial membrane system: Structure and
nucleotide sequence of the gene coding for subunit 1 of yeast
cytochrome oxidase.";
RL J. Biol. Chem. 255:11927-11941(1980).
DR EMBL; V00694; CAA24066.1; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 29.0%; Score 9; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RA 6

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Db          ||
1 RA 2.

RESULT 6
P93233      PRELIMINARY;      PRT;      7 AA.
AC P93233;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
DE (Fragment).
GN LE-ACSIB.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97351561; PubMed=9207843;
RA Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
RT synthase genes by elicitor in suspension cultures of tomato
RT (lycopersicon esculentum)".
RL Plant Mol. Biol. 34:275-286(1997).
DR EMBL; U75692; AAC49682.1; -.
KW Lyase.
FT NON_TER
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match      29.0%; Score 9; DB 10; Length 7;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMST 4
   | : |
Db 4 LVRT 7

RESULT 7
Q99007      PRELIMINARY;      PRT;      5 AA.
AC Q99007;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Alpha-amylase (EC 3.2.1.1) (Fragment).
GN AMY1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers".
RL Plant Mol. Biol. 16:713-721(1991).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -!- COPACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -!- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN
CC BARLEY.
DR EMBL; X54643; CAA38455.1; -.
KW Hydrolase; Glycoisidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON_TER

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SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match      25.8%; Score 8; DB 10; Length 5;
Best Local Similarity 25.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 MSTR 5
   | : |
Db 1 MANK 4

RESULT 8
P82181      PRELIMINARY;      PRT;      6 AA.
ID P82181;
AC P82181;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -!- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -!- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -!- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -!- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro; IPR001790; Ribosomal_L10.
DR Pfam; PF00466; Ribosomal_L10; PARTIAL.
DR PROSITE; PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match      22.6%; Score 7; DB 10; Length 6;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TR 5
   | : |
Db 5 TK 6

RESULT 9
P82182      PRELIMINARY;      PRT;      6 AA.
ID P82182;
AC P82182;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 gamma (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RX STRAIN=CV. ALVARO; TISSUE=LEAF;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in

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RT the 50 S subunit of an organelle ribosome (chloroplast).";
 RL J. Biol. Chem. 275:28466-28482(2000).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
 CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
 DR InterPro: IPR001790; Ribosomal_L10.
 DR InterPro: IPR002363; Ribosomal_L10eub.
 DR Pfam: PF00466; Ribosomal_L10; PARTIAL.
 DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
 KW Ribosomal protein; Chloroplast; rRNA-binding.
 FT NON_TER 6
 SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;
 Query Match 22.6%; Score 7; DB 10; Length 6;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TR 5
 Db 5 TK 6
 RESULT 10
 Q47029 PRELIMINARY; PRT; 7 AA.
 ID Q47029;
 AC Q47029;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Aad A1 protein (Fragment).
 GN Aad A1.
 OS Enterobacter cloacae.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Enterobacter.
 OC NCBI_TaxID=550;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94079349; PubMed=8257126;
 RA Rather P.N., Mann P.A., Mierzwa R., Hare R.S., Miller G.H., Shaw K.J.;
 RT "Analysis of the aac(3)-VIA gene encoding a novel 3-N-
 RT acetyltransferase";
 RL Antimicrob. Agents Chemother. 37:2074-2079(1993).
 EMBL: M88012; AAA16193.1; -.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 744 MW; 633862D2C321A030 CRC64;
 Query Match 22.6%; Score 7; DB 2; Length 7;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 TR 5
 Db 2 TK 3
 RESULT 11
 O34028 PRELIMINARY; PRT; 7 AA.
 ID O34028;
 AC O34028;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Catechol-2,3-dioxygenase (Fragment).
 GN PHNE.
 OS Shingomonas chungkukensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Shingomonadaceae;
 OC Shingomonas.
 OC NCBI_TaxID=56193;
 RN [1]
 RP SEQUENCE FROM N.A.
 FT NON_TER 1
 SQ STRAIN=DJ77;

RA Kim Y.-C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U88298; AAB6311.1; -.
 KW Dioxigenase.
 FT NON_TER 1
 SQ SEQUENCE 7 AA; 868 MW; 71A452D1A699D460 CRC64;
 Query Match 22.6%; Score 7; DB 2; Length 7;
 Best Local Similarity 33.3%; Pred. No. 6.7e+05;
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MST 4
 Db 5 VNT 7
 RESULT 12
 P83073 PRELIMINARY; PRT; 5 AA.
 ID P83073;
 AC P83073;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE 88 kDa protein (Fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OC NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (JUL-2001) to the SWISS-PROT data bank.
 FT NON_TER 5
 SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;
 Query Match 19.4%; Score 6; DB 2; Length 5;
 Best Local Similarity 25.0%; Pred. No. 6.7e+05;
 Matches 1; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LMST 4
 Db 1 MKDT 4
 RESULT 13
 Q15897 PRELIMINARY; PRT; 7 AA.
 ID Q15897;
 AC Q15897;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE (clone XP6A11A) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.-C., Yardani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.I., Chinsault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries";
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL: L32077; AAA73887.1; -.
 FT NON_TER 1
 FT NON_TER 7
 SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;
 Query Match 19.4%; Score 6; DB 4; Length 7;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 RA 6
:|
Db 4 KA 5

RESULT 14
Q15903
ID Q15903 PRELIMINARY; PRT; 7 AA.
AC Q15903;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE (clone XP7E7B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinalt C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries."
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32082; AAA73893.1; -.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 849 MW; 6B040339CDD33DB0 CRC64;

Query Match 19.4%; Score 6; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 RA 6
:|
Db 2 KA 3

RESULT 15
O99182
ID O99182 PRELIMINARY; PRT; 7 AA.
AC O99182;
DT 01-MAY-1999 (TREMELrel. 10, Created)
DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMELrel. 19, Last annotation update)
DE Cytochrome oxidase I (Fragment).
GN COI.
OS Gnatholebias zonatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Aplocheilidae; Rivulinae; Gnatholebias.
OX NCBI_TaxID=135316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20072328; PubMed=10603257;
RA Murphy W.J., Thomerson J.E., Collier G.E.;
RT "Phylogeny of the Neotropical killifish family Rivulidae
RT (Cyprinodontiformes, Aplocheiloidei) inferred from mitochondrial DNA
RT sequences."
RL Mol. Phylogenet. Evol. 13:289-301(1999).
DR EMBL; AF002591; AAD01074.1; -.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 899 MW; 672721F6CB572030 CRC64;

Query Match 19.4%; Score 6; DB 8; Length 7;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LM 2
:|
Db 6 LL 7

Search completed: April 22, 2003, 13:23:41
Job time : 82 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:14:05 ; Search time 34 Seconds
(without alignments)
27.434 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 64668

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 101002:*

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6:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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9:	/SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
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22:	/SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	AAW39819	Light chain CDR2 o
2	31	100.0	7	AAW39822	Light chain CDR2 o
3	31	100.0	7	AAW39825	Light chain CDR L2
4	31	100.0	7	AAW32255	Light chain CDR2 o
5	28	90.3	7	AAW39816	Light chain CDR2 o
6	27	87.1	7	AAW39876	Light chain CDR2 o
7	22	71.0	7	AAU70329	Human Kappa II lig
8	19	61.3	4	RAY81430	Amino acids encode
9	19	61.3	7	AAU06840	Peptide Seq ID No:
10	19	61.3	7	AAW05015	Tumour antigen ant

11	18	58.1	6	22	AAW35205	Retroviral recombi
12	18	58.1	7	15	AAW46961	Peptide fused to i
13	18	58.1	7	16	AAW76083	Mab 55.1 light cha
14	18	58.1	7	18	AAW31179	Hepatitis C virus
15	18	58.1	7	20	AAW05016	Tumour antigen ant
16	18	58.1	7	21	AAW95223	Anti-platelet glyc
17	17	54.8	6	20	AAW95268	Anti-progesterone
18	17	54.8	7	14	AAW30157	Mab GAH variable r
19	17	54.8	7	15	AAW57964	Mab NFS2 light cha
20	17	54.8	7	15	AAW57966	Mab NFS2 light cha
21	17	54.8	7	15	AAW50317	Mab NFS2 light cha
22	17	54.8	7	15	AAW54108	Humanised anti-Hiv
23	17	54.8	7	17	AAW03579	G-protein coupled
24	17	54.8	7	17	AAW98485	Anti-IL-5 Mab ligh
25	17	54.8	7	19	AAW68514	Mab MCP603 V1 CDR
26	17	54.8	7	19	AAW42461	Mouse anti-human I
27	17	54.8	7	20	AAW08713	Human milk fat glo
28	17	54.8	7	21	AAW07952	CDR2 sequence from
29	17	54.8	7	21	AAW95234	Human monoclonal a
30	17	54.8	7	21	AAW54529	Human CD4 protein
31	17	54.8	7	21	AAW32227	G-CSF agonist anti
32	17	54.8	7	22	AAW62866	Anti-SAF-1 antibod
33	17	54.8	7	23	ABG68854	CDR2 VL peptide </td
34	17	54.8	7	23	AAU81257	Human trkC antibod
35	17	54.8	7	23	AAU70335	Human Kappa IV lig
36	17	54.8	7	23	AAU70347	Mouse Kappa I ligh
37	16	51.6	4	12	AAW14267	Chromogenic substr
38	16	51.6	4	20	AAW30776	Peptide used to de
39	16	51.6	5	21	AAW19563	Human matrixpase s
40	16	51.6	6	19	AAW57028	Enzyme inhibitor p
41	16	51.6	6	19	AAW56931	Enzyme inhibitor p
42	16	51.6	6	21	AAW524306	Prostate tumour as
43	16	51.6	6	22	AAW55470	Human elastase var
44	16	51.6	7	17	AAW07065	Synthetic peptide
45	16	51.6	7	19	AAW70909	CDR2 of the light

ALIGNMENTS

RESULT 1
AAW39819
ID AAW39819 standard; peptide; 7 AA.
AC AAW39819;
XX
XX
DT 16-JUN-1998 (first entry)
DE Light chain CDR2 of catalytic antibody 6A12.
KW Variable domain; lambda light chain; catalytic antibody; degradation;
KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
KW overdose; addiction.
OS Mus sp.
XX
XX WO9749800-A1.
XX
XX 31-DEC-1997.
XX
XX 25-JUN-1997; 97WO-US10965.
XX 25-JUN-1996; 96US-0672345.
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX Landry DW;
XX WPI; 1998-077166/07.
XX New catalytic antibodies able to decompose cocaine, single-chain
PT analogues - used to treat cocaine overdose and addiction, required

PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding

PS Claim 13; Page 81; 147pp; English.

XX AAW39818-20 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 6A12, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 6A12 antibody was
 CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 6A12 has a per minute Kcat
 CC of 0.072. The antibodies reduce the concentration of cocaine in a
 CC subject, and are used particularly for the treatment of an overdose. They
 CC are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved).

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 |||||

Db 1 LMSTRAS 7

RESULT 2

AAW39822
 ID AAW39822 standard; peptide; 7 AA.

AC AAW39822;

XX 16-JUN-1998 (first entry)

DE Light chain CDR2 of catalytic antibody 2A10.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

OS Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US10965.

XX 25-JUN-1996; 96US-0672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding

XX Claim 15; Page 82; 147pp; English.

XX AAW39821-23 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 2A10, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was

CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 2A10 has a per minute Kcat
 CC of 0.011. The antibodies reduce the concentration of cocaine in a
 CC subject, and are used particularly for the treatment of an overdose. They
 CC are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved).

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 |||||

Db 1 LMSTRAS 7

RESULT 3

AAW39825
 ID AAW39825 standard; peptide; 7 AA.

XX AC AAW39825;

XX 16-JUN-1998 (first entry)

DE Light chain CDR2 of catalytic antibody 12H1.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

OS Mus sp.

XX WO9749800-A1.

XX 31-DEC-1997.

XX 25-JUN-1997; 97WO-US10965.

XX 25-JUN-1996; 96US-0672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.

XX Landry DW;

XX WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding

XX Claim 17; Page 83; 147pp; English.

XX AAW39824-26 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 12H1, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 12H1 antibody was
 CC identified using TSA2, and has a per minute Kcat of 0.16. The antibodies
 CC reduce the concentration of cocaine in a subject, and are used
 CC particularly for the treatment of an overdose. They are also used for
 CC treating addiction (by reducing the in vivo concentration that can be
 CC achieved).

XX Sequence 7 AA;

Query Match 100.0%; Score 31; DB 19; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 Db 1 LMSTRAS 7

RESULT 4

AAV32255
 ID AAV32255 standard; Peptide; 7 AA.

AC AAV32255;

DT 15-FEB-2000 (first entry)

DE Light chain CDR L2 of mouse anti-CD23 Mab C11.

KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
 KW monoclonal antibody; chimeric antibody; humanised antibody;
 KW complementarity determining region; CDR; autoimmune disease;
 KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
 KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
 KW urticaria; nephrotic syndrome; glomerulonephritis;
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
 KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
 KW graft-versus-host disease; COPD; bronchitis; diabetes;
 KW B-cell malignancy; therapy.

OS Mus musculus.

PN WO9958679-A1.

PD 18-NOV-1999.

PF 07-MAY-1999; 99WO-GB01434.

PR 09-MAY-1998; 98GB-0009839.

PA (GLAX) GLAXO GROUP LTD.

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;

DR WPI; 2000-053101/04.

DR N-PSDB; AAZ34749.

CC Cell receptor specific antibodies useful for treating e.g. arthritis,
 diabetes, multiple sclerosis and psoriasis -

PS Claim 1; Page 40; 81pp; English.

CC This sequence represents complementarity determining region 2
 CC (CDR L2) of the light chain of murine anti-CD23 (FCERII) monoclonal
 CC antibody C11 (see also AAV32262). The invention provides altered
 CC antibodies, such as chimeric or humanised antibodies, which comprise
 CC sufficient of the amino acid sequences of C11 light and heavy chain
 CC CDRs (see AAV32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies
 CC are used to block soluble CD23 formation for treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.

SQ Sequence 7 AA;

Query Match 100.0%; Score 31; DB 21; Length 7;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
 Db 1 LMSTRAS 7

RESULT 5

AAW39816

ID AAW39816 standard; peptide; 7 AA.

AC AAW39816;

DT 16-JUN-1998 (first entry)

DE Light chain CDR2 of catalytic antibody 3B9.

KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.

OS Mus sp.

PN WO9749800-A1.

PD 31-DEC-1997.

PF 25-JUN-1997; 97WO-US10965.

PR 25-JUN-1996; 96US-0672345.

PA (UYCO) UNIV COLUMBIA NEW YORK.

PI Landry DW;

DR WPI; 1998-077166/07.

CC New catalytic antibodies able to decompose cocaine, single-chain
 CC analogues used to treat cocaine overdose and addiction, required
 CC in far smaller doses than antibodies that antagonise cocaine by
 CC simply binding

PS Claim 11; Page 80; 147pp; English.

CC AAW39815-17 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was
 CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 3B9 has a per minute Kcat
 CC of 0.11. The antibodies reduce the concentration of cocaine in a subject,
 CC and are used particularly for the treatment of an overdose. They are also
 CC used for treating addiction (by reducing the in vivo concentration that
 CC can be achieved).

SQ Sequence 7 AA;

Query Match 90.3%; Score 28; DB 19; Length 7;

Best Local Similarity 85.7%; Pred. No. 7.8e+05;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7

Db 1 LMSTRSS 7

RESULT 6

AAW39876

ID AAW39876 standard; peptide; 7 AA.

AC AAW39876;

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XX DT 16-JUN-1998 (first entry)
XX DE Light chain CDR2 of a catalytic antibody capable of degrading cocaine.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addiction.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT Misc-difference 6
XX FT /note= "not specified"
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US10965.
XX PR 25-JUN-1996; 96US-0672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX FT New catalytic antibodies able to decompose cocaine, single-chain
XX FT analogues - used to treat cocaine overdose and addiction, required
XX FT in far smaller doses than antibodies that antagonise cocaine by
XX FT simply binding
XX PS Claim 10; Page 5; 147pp; English.
XX CC AA039875-77 represent the sequences of the light chain complementarity
XX CC determining regions (CDRs) of a catalytic antibody which is capable of
XX CC degrading cocaine. A series of cocaine transition state analogues (TSAs)
XX CC were prepared and used to immunise mice for production of hybridomas.
XX CC Catalytic antibodies were identified by their capacity to release
XX CC 3H-benzoic acid from 3H-phenyl cocaine. These antibodies were found
XX CC to have CDRs of the present sequence. The antibodies reduce the
XX CC concentration of cocaine in a subject, and are used particularly for the
XX CC treatment of an overdose. They are also used for treating addiction (by
XX CC reducing the in vivo concentration that can be achieved).
XX SQ Sequence 7 AA;
    Query Match 87.1%; Score 27; DB 19; Length 7;
    Best Local Similarity 85.7%; Pred. No. 7.8e+05;
    Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 1 LMSTRXS 7
    |||||
    |||||

RESULT 7
ID AAU70329 standard; Peptide; 7 AA.
XX AC AAU70329;
XX DT 14-FEB-2002 (first entry)
XX DE Human Kappa II light chain CDR2.
XX KW Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
XX KW complementarity determining region; framework region; IgBP;
XX KW transgenic plant; immunoglobulin binding protein array;
XX KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.

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XX OS Homo sapiens.
XX PN WO200183806-A1.
XX PD 08-NOV-2001.
XX PF 02-MAY-2001; 2001WO-US14349.
XX PR 02-MAY-2000; 2000US-0563222.
XX PA (EPIC-) EPICYTE PHARM INC.
XX PI Hiatt AC, Hein WB;
XX DR WPI; 2002-055482/07.
XX FT Preparing immunoglobulin binding protein array in plant cells by
XX FT transforming the cells with different polynucleotides encoding binding
XX FT protein polypeptides specific to ligand, selecting plant cells for
XX FT preparing array -
XX PS Disclosure; Page 14; 129pp; English.
XX CC The invention relates to transforming a population of cells (e.g. plant
XX CC cells), comprising using a library of two different polynucleotides
XX CC encoding different immunoglobulin binding protein (IgBP) polypeptides
XX CC that specifically bind to a ligand or form one or more disulphide bonds
XX CC with polypeptides in transfected cells, to generate an IgBP that
XX CC binds to a ligand, and transformed plant cells are selected, and
XX CC preparing an IgBP array in plant cells. At least one peptide sequence has
XX CC at least 75% sequence identity to a framework region (FR) of a native
XX CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
XX CC The method is useful for preparing an immunoglobulin binding protein
XX CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
XX CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
XX CC or other eukaryotic cells (e.g. insect cells or mammalian cells). The
XX CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
XX CC desired characteristics. The present sequence is a mammalian
XX CC immunoglobulin derived peptide that may be incorporated into an IgBP of
XX CC the invention.
XX SQ Sequence 7 AA;
    Query Match 71.0%; Score 22; DB 23; Length 7;
    Best Local Similarity 71.4%; Pred. No. 7.8e+05;
    Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
DB 1 LVSNRAS 7
    |||||
    |||||

RESULT 8
ID AA81430 standard; peptide; 4 AA.
XX AC AA81430;
XX DT 19-JUN-2000 (first entry)
XX DE Amino acids encoded by 5' portion of pTugAS vector SacI-HindIII region.
XX KW pTugAS vector; Cellulomonas fimi; endoglucanase C; CBD;
XX KW cellulose binding domain; polysaccharide binding peptide;
XX KW fusion protein; recombinant protein; cell separation;
XX KW affinity phase separation.
XX OS Synthetic.
XX PN US6048715-A.
XX PD 11-APR-2000.

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XX PF 24-JUL-1996; 96US-0685808.
 XX PR 08-JUL-1988; 88US-0216794.
 XX PR 08-APR-1992; 92US-0865095.
 XX PR 25-OCT-1990; 90US-0603987.
 XX PR 24-MAY-1994; 94US-0249037.
 XX PR 24-JUL-1995; 95US-0505860.
 XX PA (UYBR-) UNIV BRITISH COLUMBIA.
 XX PI Haynes CA, Tomme P, Kilburn DG;
 XX XX WPI; 2000-328038/28.
 XX XX Two-phase partition affinity separation system useful for separating
 PT and purifying proteins comprises a phase-forming oligosaccharide
 PT polymer and a phase-separation agent -
 XX Disclosure; Fig 3A; 46pp; English.
 XX CC The invention relates to a novel two-phase partition system for affinity
 CC separation which comprises a phase-forming oligosaccharide polymer to
 CC which a polysaccharide binding peptide (PBP) binds, and a phase
 CC separation inducing agent. The system may be used for the separation and
 CC purification of recombinant proteins from cell cultures. The protein of
 CC interest is expressed in the host cell as a fusion protein with a
 CC polysaccharide binding peptide, and the cell lysate or fermentation
 CC broth (or other composition comprising the fusion protein) is contacted
 CC with the phase separation system. The fusion protein partitions into the
 CC oligosaccharide polymer phase, and can then be isolated e.g., via the
 CC use of a solution with a low ionic strength, high pH or containing a
 CC chaotropic agent, or by the use of chemical cleavage agents such as
 CC cyanogen bromide. If the fusion protein has been engineered such that
 CC there is a protease recognition site between the PBP and the protein of
 CC interest, the protein can be cleaved from the PBP, which remains bound
 CC to the oligosaccharide. Proteins that may be purified using the method
 CC of the invention include a wide variety of medically and industrially
 CC important proteins e.g., interleukin 2, factor X, insulin, lignase.
 CC The system can also be used for cell separation and/or enrichment of a
 CC particular cell type; for example, a fusion protein comprising a PBP and
 CC a ligand of a particular receptor can be used to isolate cells
 CC comprising that receptor. The system is useful for concentrating a
 CC component in a mixture, removing contaminants and for preparing solid
 CC state reagents for diagnostic assays. Oligosaccharide polymers can be
 CC obtained inexpensively and the water-soluble cellulosic substrates offer
 CC a new, cost-effective, highly flexible affinity partition system for
 CC continuous purification. Selective binding of PBP from the
 CC oligosaccharide polymer makes it suitable for purification of a wide
 CC variety of compounds using a single oligosaccharide polymer phase
 CC separation system. Hence it is unnecessary to prepare separate systems
 CC for each compound to be separated. Sequences AAY81430-181431 represent
 CC the amino acids sequences encoded by the 5' and 3' portions of the
 CC SacI-HindIII region of the pTUGAS vector. DNA encoding the Cellulomonas
 CC fimi endoglucanase C cellulose binding domain (CBD) N1 (AAY81423) was
 CC inserted between the 5' and 3' portions of the SacI-HindIII region of the
 CC vector.
 XX SQ Sequence 4 AA;
 Query Match 61.3%; Score 19; DB 21; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 MSTR 5
 Db 1 MSTR 4
 RESULT 9
 AAY06840
 ID AAY06840 standard; peptide; 7 AA.
 XX

AC AAY06840;
 XX 25-JUN-1999 (first entry)
 XX DE Peptide Seq ID No:6 of JP11089576.
 XX DE AntiHbs; monoclonal antibody; Epstein Barr virus; EBV; adr type;
 XX KW human; Hbs antigen; hepatitis C.
 XX OS Homo sapiens.
 XX XX JP11089576-A.
 XX XX 06-APR-1999.
 XX PF 19-SEP-1997; 97JP-0255705.
 XX PR 19-SEP-1997; 97JP-0255705.
 XX PA (NISN) NISSHINBO IND INC.
 XX DR WPI; 1999-281053/24.
 XX XX Anti-HBs monoclonal antibody - produced without the risk of Epstein
 PT Barr virus contamination
 XX PS Claim 4; Page 7; 12pp; Japanese.
 XX CC The invention relates to an antiHbs monoclonal antibody having the
 CC following properties: (A) CDR-3 of H chain variable region; (B) it
 CC contains no Epstein Barr virus (EBV); (C) it binds at least one adr type
 CC among human Hbs antigens. The antiHbs monoclonal antibody is high in
 CC antibody titer and has low risk of EBV contamination. It can be used to
 CC prevent hepatitis C.
 XX SQ Sequence 7 AA;
 Query Match 61.3%; Score 19; DB 20; Length 7;
 Best Local Similarity 80.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 STRAS 7
 Db 3 STRAT 7
 RESULT 10
 AAY05015
 ID AAY05015 standard; peptide; 7 AA.
 XX AC AAY05015;
 XX AC 16-JUN-1999 (first entry)
 XX DE Tumour antigen antibody light chain CDR2 clone F14.
 XX KW Tumour antigen; antibody; CDR; complementarity determining region;
 XX KW binding molecule identification; tumour-specific binding polypeptide;
 XX KW cancer therapy; light chain.
 XX OS Homo sapiens.
 XX XX WO9906834-A2.
 XX XX 11-FEB-1999.
 XX PF 04-AUG-1998; 98WO-US16280.
 XX PR 04-AUG-1997; 97US-0905825.
 XX PR 04-AUG-1997; 97US-1112222.
 XX PA (IXSY-) IXSYS INC.
 XX XX

QY 1 LMSTRA 6
| | | |
Db 2 LSTRS 7

RESULT 13

AAW76083
ID AAR76083 standard; Peptide; 7 AA.

AC AAR76083;

DT 21-NOV-1995 (first entry)

XX MAb 55.1 light chain CDR2.

XX Antigen binding structure; complementarity determining region; CDR;
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin.

OS Mus sp.

XX WO9515382-A.

XX 08-JUN-1995.

XX 29-NOV-1994; 94WO-GB02610.

XX 03-JUN-1994; 94GB-0011089.

PR 03-DEC-1993; 93GB-0024819.

XX (ZENE) ZENECA LTD.

XX Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;

PI Rose MS, Wright AF;

XX WPI; 1995-215262/28.

XX Antigen binding structures containing CDRs recognising the CA55.1
PT antigen - produced by hybridomas and host cells, for use in the
PT diagnosis and therapy of cancer

PS Claim 2; Page 97; 121pp; English.

XX An antigen binding structure is based on the CDRs (given in AAR76078-
CC 84) of the heavy and light chains of Mab 55.1 (ECACC 93081901),
CC which recognises the colorectal tumor-associated antigen CA55.1.
CC It is optionally humanized and in the form F(ab')₂, F(ab)', Fab,
CC Fv, scFv or V-min, and is produced in transgenic animals or plants.

XX Sequence 7 AA;

Query Match 58.1%; Score 18; DB 16; Length 7;
Best Local Similarity 80.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7
| | | |
Db 3 STRTS 7

RESULT 14

AAW31179

ID AAW31179 standard; peptide; 7 AA.

XX AAW31179;

DT 05-FEB-1998 (first entry)

XX Hepatitis C virus genotype 5a peptide, OMM25.

XX Hepatitis C virus; HCV; genotype determination; 1a; 1b; 2a; 2b; 3a;

KW 3b; 4; 5a; 6a; 6b; diagnosis; amplification; PCR; primer.
OS Hepatitis C virus.

XX JP09234072-A.

PN 09-SEP-1997.

XX 01-FEB-1996; 96JP-0038875.

PR 30-DEC-1995; 95JP-0352511.

PR 01-FEB-1995; 95JP-0035997.

XX (SRLS-) SRL KK.

XX WPI; 1997-497313/46.

XX Primers used for determining hepatitis C virus genotype - provide a
PT rapid and accurate method of hepatitis C virus genotyping
XX Example 1; Page 18; 33pp; Japanese.

CC AAW31170-W31181 are peptides derived from various genotypes of
CC hepatitis C virus. The peptides were used for the production of PCR
CC (polymerase chain reaction) primers used for discrimination between
CC hepatitis C virus (HCV) genotypes. Classification of the
CC genotype of HCV can be achieved precisely and simply according to
CC the international standardisation of classification. The primers
CC can be used to distinguish between HCV genotypes 1a, 1b, 2a, 2b,
CC 3a, 3b, 4, 5a, 6a and 6b.

XX Sequence 7 AA;

Query Match 58.1%; Score 18; DB 18; Length 7;
Best Local Similarity 57.1%; Pred. No. 7.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
| | | |
Db 1 LLSPRGS 7

RESULT 15

AAW05016

ID AAY05016 standard; peptide; 7 AA.

XX AAY05016;

DT 16-JUN-1999 (first entry)

XX Tumour antigen antibody light chain CDR2 clone F15.

KW Tumour antigen; antibody; CDR; complementarity determining region;
KW binding molecule identification; tumour-specific binding polypeptide;
KW cancer therapy; light chain.

OS Homo sapiens.

XX WO9906834-A2.

XX 11-FEB-1999.

XX 04-AUG-1998; 98WO-US16280.

PR 04-AUG-1997; 97US-0905825.

PR 04-AUG-1997; 97US-1112222.

XX (IXSY-) IXSYS INC.

XX Huse WD, Watkins JD, Wu H;

XX WPI; 1999-153951/13.

XX N-PSDB; AAX28193.

XX Identifying binding molecules for ligands, particularly tumour
PT antigens - by selectively immobilising a population of binding
PT molecules to a solid support and screening for binding to two or
PT more ligands
XX
PS Claim 15; Page 57; 80pp; English.
XX
CC This sequence represents a light chain complementarity determining
CC region (CDR) from a tumour antigen specific antibody.
CC The invention relates to a method for identifying a binding molecule
CC having selective affinity for a ligand comprising: (a) selectively
CC immobilising a diverse population of binding molecules to a solid
CC support; (b) simultaneously contacting the diverse population immobilised
CC on the solid support with 2 or more ligands; and (c) determining at least
CC one binding molecule which selectively binds to one or more of the
CC ligands. The method allows for the rapid and efficient methods for the
CC identification of binding molecules which exhibit selective affinity for
CC one or more ligands of interest. They are used particularly for
CC identifying tumour-specific binding polypeptides which can be used as
CC targeting agents for cancer therapy that minimises impact on non-tumour
CC tissues.
XX
SQ Sequence 7 AA;
Query Match 58.1%; Score 18; DB 20; Length 7;
Best Local Similarity 80.0%; Pred. No. 7.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 STRAS 7
Db 3 SSRAS 7

Search completed: April 22, 2003, 13:21:55
Job time : 35 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:23:45 ; Search time 15 Seconds
(without alignments)
37.394 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 18120

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	61.3	7	9	US-09-977-797A-30
2	18	58.1	7	9	Sequence 32, Appl
3	17	54.8	7	9	Sequence 30, Appl
4	17	54.8	7	9	Sequence 10, Appl
5	17	54.8	7	9	Sequence 18, Appl
6	17	54.8	7	9	Sequence 11, Appl
7	17	54.8	7	10	US-09-828-708-43
8	16	51.6	7	10	US-09-828-708-46
9	15	48.4	7	10	US-09-947-137-8
10	15	48.4	6	10	US-10-078-458-11
11	15	48.4	6	10	US-09-800-433-8
12	15	48.4	6	12	US-10-014-774-19
13	15	48.4	7	9	US-09-995-973-53
14	15	48.4	7	9	US-10-116-255-58
15	15	48.4	7	9	US-09-913-238-62
16	15	48.4	7	10	US-09-850-351A-75
17	15	48.4	7	10	US-09-839-497A-17
18	15	48.4	7	10	US-09-828-708-45
19	15	48.4	7	10	US-09-828-708-47
19	15	48.4	7	10	US-09-828-708-48

20	15	48.4	7	10	US-09-828-708-49
21	14	45.2	3	10	US-09-982-172-82
22	14	45.2	5	10	US-09-800-433-7
23	14	45.2	5	10	US-09-976-155-63
24	14	45.2	6	9	US-09-858-852A-66
25	14	45.2	6	9	US-09-925-179-35
26	14	45.2	6	10	US-09-802-077-35
27	14	45.2	6	10	US-09-802-096-35
28	14	45.2	6	10	US-09-736-959A-22
29	14	45.2	6	10	US-09-990-762-66
30	14	45.2	7	9	US-09-977-797A-82
31	14	45.2	7	9	US-09-967-237-107
32	14	45.2	7	9	US-10-217-957-3
33	14	45.2	7	9	US-10-217-957-4
34	14	45.2	7	10	US-09-765-086-71
35	14	45.2	7	10	US-09-253-794-21
36	14	45.2	7	10	US-09-947-137-29
37	13	41.9	4	10	US-09-220-920-71
38	13	41.9	4	10	US-09-839-447A-78
39	13	41.9	4	10	US-09-782-980-102
40	13	41.9	4	10	US-09-405-439-3
41	13	41.9	4	10	US-09-872-349-1
42	13	41.9	4	10	US-09-982-172-87
43	13	41.9	4	10	US-09-751-100B-15
44	13	41.9	5	9	US-09-933-999A-30
45	13	41.9	5	10	US-09-287-849-36

ALIGNMENTS

RESULT 1

US-09-977-797A-30
; Sequence 30, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-30

Query Match 61.3%; Score 19; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
| | | | |
Db 3 STRAT 7

RESULT 2

US-09-977-797A-32
; Sequence 32, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules

```
; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-32

Query Match          58.1%; Score 18; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 STRAS 7
   |||||
Db 3 SSRAS 7

RESULT 3
US-10-146-305-10
; Sequence 10, Application US/10146305
; Patent No. US20020173035A1
; GENERAL INFORMATION:
; APPLICANT: YUHAN CORPORATION
; TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST THE HBV
; FILE REFERENCE: OVI7440
; CURRENT APPLICATION NUMBER: US/10/146,305
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: KR 10-2001-26634
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 10
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Escherichia coli
US-10-146-305-10

Query Match          54.8%; Score 17; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7
   |||||
Db 3 STRES 7

RESULT 4
US-09-249-011A-18
; Sequence 18, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, NAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-00000
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; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CDR2 of humanized
; OTHER INFORMATION: murine anti-human B7-2 light chain
US-09-249-011A-18

Query Match          54.8%; Score 17; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7
   |||||
Db 3 STRES 7

RESULT 5
US-10-144-644-11
; Sequence 11, Application US/10144644
; Publication No. US20030059429A1
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp
; STREET: P.O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/144,644
; FILING DATE: 2002-08-08
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470110
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467420
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION: INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5090
; TELEFAX: 610-270-5090
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-144-644-11

Query Match      54.8%; Score 17; DB 9; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7
Db 3 STRES 7

RESULT 6
US-09-828-708-43
; Sequence 43, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Burton, D.
; APPLICANT: Ditzel, H.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-43

Query Match      54.8%; Score 17; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7
Db 3 STRES 7

RESULT 7
US-09-828-708-46
; Sequence 46, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Burton, D.
; APPLICANT: Ditzel, H.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-46

Query Match      54.8%; Score 17; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7
Db 3 STRES 7

RESULT 8
US-09-947-137-8
; Sequence 8, Application US/09947137
; Patent No. US20020137023A1
; GENERAL INFORMATION:
; APPLICANT: Smith, Bruce F.
; APPLICANT: Samoilova, Tatiana
; TITLE OF INVENTION: Methods and Compositions for Targeting
; FILE REFERENCE: 5721-8
; CURRENT APPLICATION NUMBER: US/09/947,137
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: 09/084,605
; PRIOR FILING DATE: 1998-05-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Phage display library peptides
US-09-947-137-8

Query Match      51.6%; Score 16; DB 10; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTRAS 6
Db 1 MSTQS 5

RESULT 9
US-10-078-458-11
; Sequence 11, Application US/10078458
; Publication No. US20020187934A1
; GENERAL INFORMATION:
; APPLICANT: LUKE, Richard William Arthur
; APPLICANT: COTTON, Ronald
; TITLE OF INVENTION: PEPTIDE DERIVATIVES
; FILE REFERENCE: 1991-174
; CURRENT APPLICATION NUMBER: US/10/078,458
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/308,175
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: PCT/GB97/03199
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: GB 9624562.6
; PRIOR FILING DATE: 1996-11-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-078-458-11

Query Match      48.4%; Score 15; DB 9; Length 4;
Best Local Similarity 75.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 TRAS 7
Db 1 TRAA 4

RESULT 10
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US-09-800-433-8

Sequence 8, Application US/09800433

Patent No. US20020106378A1

GENERAL INFORMATION:

APPLICANT: O'Hare and Elliott

TITLE OF INVENTION: Materials and methods for intracellular transport and

TITLE OF INVENTION: their uses

FILE REFERENCE: 49408

CURRENT APPLICATION NUMBER: US/09/800,433

CURRENT FILING DATE: 2000-03-05

PRIOR APPLICATION NUMBER: 09/395,344

PRIOR FILING DATE: 1999-09-13

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 6

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: peptide

US-09-800-433-8

Query Match 48.4%; Score 15; DB 10; Length 6;

Best Local Similarity 75.0%; Pred. No. 2.7e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRAS 7

Db 2 TRAA 5

RESULT 11

US-10-014-774-19

Sequence 19, Application US/10014774

Patent No. US2002009173A1

GENERAL INFORMATION:

APPLICANT: D'Azzo, Alessandra

APPLICANT: Bongiovanni, Antonella

APPLICANT: Nastasi, Tommaso

TITLE OF INVENTION: Protein Specific for Cardiac and Skeletal Muscle

FILE REFERENCE: 2427/1F509-US1

CURRENT APPLICATION NUMBER: US/10/014,774

CURRENT FILING DATE: 2001-10-29

PRIOR APPLICATION NUMBER: PCT/US00/11900

PRIOR FILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: US 60/131,814

PRIOR FILING DATE: 1999-04-29

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 19

LENGTH: 6

TYPE: PRT

ORGANISM: Homo sapiens

US-10-014-774-19

Query Match 48.4%; Score 15; DB 12; Length 6;

Best Local Similarity 75.0%; Pred. No. 2.7e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TRAS 7

Db 2 TRAT 5

RESULT 12

US-09-995-973-53

Sequence 53, Application US/09995973

Publication No. US20030024006A1

GENERAL INFORMATION:

APPLICANT: CHOO, Yen

APPLICANT: ULLMAN, Christopher G.

TITLE OF INVENTION: GENE SWITCHES

FILE REFERENCE: 8325-2003 / G7-US1

US-09-995-973-53

Query Match 48.4%; Score 15; DB 9; Length 7;

Best Local Similarity 60.0%; Pred. No. 2.7e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LMSTR 5

Db 3 LVKTR 7

RESULT 14

US-09-913-238-62

Sequence 62, Application US/09913238

Publication No. US20030049251A1

GENERAL INFORMATION:

APPLICANT: Barbas, Carlos F.

APPLICANT: Steinberger, Peter

TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL FOR

TITLE OF INVENTION: INHIBITING CCR5-DEPENDENT INFECTION OF CELLS BY HIV-1

FILE REFERENCE: TSRI 728.1

CURRENT APPLICATION NUMBER: US/09/913,238

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; CURRENT FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: PCT/EP 0/12419
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/169,653
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthesized
; US-09-913-238-62

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Query Match 48.4%; Score 15; DB 9; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 3 STRAS 7
|:|:|
DB 3 SSRSS 7

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RESULT 15

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US-09-850-351A-75
; Sequence 75, Application US/09850351A
; Patent No. US20020100080A1
; GENERAL INFORMATION:

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; APPLICANT: Feitelson, Gerald S.
; Schnepf, H. Ernest
; Narva, Kenneth E.
; Stockhoff, Brian A.
; Schmeits, James
; Loewer, David
; Dullum, Charles Joseph
; Muller-Cohn, Judy
; Stamp, Lisa
; Morrill, George

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; TITLE OF INVENTION: No. US20020100080A1 Pesticidal Toxins and Nucleotide
; Sequences Which Encode These Toxins

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; NUMBER OF SEQUENCES: 144

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; CORRESPONDENCE ADDRESS:

```

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; ADDRESSER: Saliwanchik, Lloyd & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US

```

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; ZIP: 32606-6669

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; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/09/850,351A

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; FILING DATE: 07-May-2001

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; CLASSIFICATION: <Unknown>

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; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 09/073,898

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; FILING DATE: 06-May-1998

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; APPLICATION NUMBER: US 08/960,780

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; FILING DATE: 30-OCT-1997

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; APPLICATION NUMBER: US 60/029,848

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; FILING DATE: 30-OCT-1996

```

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; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Sanders, Jay M.

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```

; REGISTRATION NUMBER: 39,355

```

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; REFERENCE/DOCKET NUMBER: MA-708CD1

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; TELECOMMUNICATION INFORMATION:

```

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; TELEPHONE: 352-375-8100

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; TELEFAX: 352-372-5800

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; INFORMATION FOR SEQ ID NO: 75:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 75:
US-09-850-351A-75

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Query Match 48.4%; Score 15; DB 10; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 LMST 4
|:|:|
DB 2 LLST 5

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Search completed: April 22, 2003, 13:29:09
Job time : 16 secs

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GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2003, 13:21:20 ; Search time 28 seconds
(without alignments)
7.356 Million cell updates/sec

Title: US-09-674-716B-5

Perfect score: 31

Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 42808

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	2	US-08-672-345C-23
2	31	100.0	7	2	US-08-672-345C-26
3	31	100.0	7	2	US-08-672-345C-29
4	31	100.0	7	4	US-09-214-095D-23
5	31	100.0	7	4	US-09-214-095D-26
6	31	100.0	7	4	US-09-214-095D-29
7	28	90.3	7	2	US-08-672-345C-20
8	28	90.3	7	2	US-09-214-095D-20
9	27	87.1	7	2	US-08-672-345C-80
10	27	87.1	7	4	US-09-214-095D-80
11	19	61.3	4	3	US-08-685-808-9
12	19	61.3	4	4	US-08-505-860C-9
13	18	58.1	7	1	US-08-353-400-31
14	17	54.8	7	1	US-08-264-093-25
15	17	54.8	7	1	US-08-467-420A-11
16	17	54.8	7	1	US-08-470-110A-11
17	17	54.8	7	1	US-08-360-125-20
18	17	54.8	7	1	US-08-667-789A-11
19	17	54.8	7	2	US-08-452-724A-34
20	17	54.8	7	2	US-08-450-578-20
21	17	54.8	7	2	US-08-940-371-11
22	17	54.8	7	2	US-09-017-628-20
23	17	54.8	7	3	US-09-014-880-20
24	17	54.8	7	3	US-09-100-409A-30
25	17	54.8	7	3	US-08-637-647-11
26	17	54.8	7	4	US-07-987-264-5
27	17	54.8	7	4	US-08-450-363-20

28	17	54.8	7	5	PCT-US93-08435-24	Sequence 24, Appl
29	17	54.8	7	5	PCT-US93-08435-37	Sequence 37, Appl
30	17	54.8	7	5	PCT-US93-08435-41	Sequence 41, Appl
31	17	54.8	7	5	PCT-US95-17082A-11	Sequence 11, Appl
32	16	51.6	4	1	US-07-776-257-3	Sequence 3, Appl
33	16	51.6	7	1	US-08-503-062-14	Sequence 14, Appl
34	16	51.6	7	2	US-08-340-283-90	Sequence 90, Appl
35	16	51.6	7	4	US-09-084-605B-8	Sequence 8, Appl
36	16	51.6	7	4	US-09-174-216-1	Sequence 1, Appl
37	16	51.6	7	5	PCT-US96-11495-14	Sequence 14, Appl
38	15	48.4	4	4	US-09-308-175A-11	Sequence 11, Appl
39	15	48.4	4	4	US-09-082-358B-47	Sequence 47, Appl
40	15	48.4	4	5	PCT-US93-01669-38	Sequence 38, Appl
41	15	48.4	5	1	US-08-064-111C-10	Sequence 10, Appl
42	15	48.4	6	2	US-08-729-152-7	Sequence 7, Appl
43	15	48.4	6	2	US-08-729-152-28	Sequence 28, Appl
44	15	48.4	6	3	US-09-012-126-8	Sequence 8, Appl
45	15	48.4	6	4	US-09-395-344-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-08-672-345C-23
; Sequence 23, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-23

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
| | | | |
Db 1 LMSTRAS 7

RESULT 2

<p>US-08-672-345C-26 ; NAME: White, John P. ; REGISTRATION NUMBER: 28,678 ; REFERENCE/DOCKET NUMBER: 0575/51400 ; TELECOMMUNICATION INFORMATION: ; APPLICANT: Landry Donald, W. ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY ; NUMBER OF SEQUENCES: 108 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Cooper and Dunham LLP ; STREET: 1185 Avenue of the Americas ; CITY: New York ; STATE: New York ; COUNTRY: USA ; ZIP: 10036 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS. ; SOFTWARE: PatentIn Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/672,345C ; FILING DATE: 24-JUN-1996 ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: White, John P. ; REGISTRATION NUMBER: 28,678 ; REFERENCE/DOCKET NUMBER: 0575/51400 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 212-278-0400 ; TELEFAX: 212-391-0525 ; INFORMATION FOR SEQ ID NO: 26: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 7 amino acids ; TYPE: amino acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: peptide ; US-08-672-345C-26</p>	<p>Query Match 100.0%; Score 31; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 1 LMSTRAS 7 Db 1 LMSTRAS 7</p> <p>RESULT 3 US-09-214-095D-23 ; Sequence 23, Application US/09214095D ; Patent No. 6280987 ; GENERAL INFORMATION: ; APPLICANT: Landry, Donald ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY ; FILE REFERENCE: 51400-A-PCT-US ; CURRENT APPLICATION NUMBER: US/09/214,095D ; CURRENT FILING DATE: 1999-07-19 ; NUMBER OF SEQ ID NOS: 121 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 23 ; LENGTH: 7 ; TYPE: PRT ; ORGANISM: Murinae gen. sp. US-09-214-095D-23</p> <p>Query Match 100.0%; Score 31; DB 4; Length 7; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 1 LMSTRAS 7 Db 1 LMSTRAS 7</p> <p>RESULT 5 US-09-214-095D-26 ; Sequence 26, Application US/09214095D ; Patent No. 6280987 ; GENERAL INFORMATION: ; APPLICANT: Landry, Donald ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY ; FILE REFERENCE: 51400-A-PCT-US ; CURRENT APPLICATION NUMBER: US/09/214,095D ; CURRENT FILING DATE: 1999-07-19 ; NUMBER OF SEQ ID NOS: 121 ; SOFTWARE: PatentIn version 3.0 ; SEQ ID NO 26 ; LENGTH: 7 ; TYPE: PRT ; ORGANISM: Murinae gen. sp. US-09-214-095D-26</p>
<p>US-08-672-345C-26 ; NAME: White, John P. ; REGISTRATION NUMBER: 28,678 ; REFERENCE/DOCKET NUMBER: 0575/51400 ; TELECOMMUNICATION INFORMATION: ; APPLICANT: Landry Donald, W. ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY ; NUMBER OF SEQUENCES: 108 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Cooper and Dunham LLP ; STREET: 1185 Avenue of the Americas ; CITY: New York ; STATE: New York ; COUNTRY: USA ; ZIP: 10036 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS. ; SOFTWARE: PatentIn Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/672,345C ; FILING DATE: 24-JUN-1996 ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION: ; NAME: White, John P. ; REGISTRATION NUMBER: 28,678 ; REFERENCE/DOCKET NUMBER: 0575/51400 ; TELECOMMUNICATION INFORMATION: ; TELEPHONE: 212-278-0400 ; TELEFAX: 212-391-0525 ; INFORMATION FOR SEQ ID NO: 26: ; SEQUENCE CHARACTERISTICS: ; LENGTH: 7 amino acids ; TYPE: amino acid ; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: peptide ; US-08-672-345C-26</p>	<p>Query Match 100.0%; Score 31; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 1.9e+05; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <p>QY 1 LMSTRAS 7 Db 1 LMSTRAS 7</p> <p>RESULT 3 US-08-672-345C-29 ; Sequence 29, Application US/08672345C ; Patent No. 5948658 ; GENERAL INFORMATION: ; APPLICANT: Landry Donald, W. ; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY ; NUMBER OF SEQUENCES: 108 ; CORRESPONDENCE ADDRESS: ; ADDRESSEE: Cooper and Dunham LLP ; STREET: 1185 Avenue of the Americas ; CITY: New York ; STATE: New York ; COUNTRY: USA ; ZIP: 10036 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible ; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.30 ; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/672,345C ; FILING DATE: 24-JUN-1996 ; CLASSIFICATION: 435 ; ATTORNEY/AGENT INFORMATION:</p>

QY 1 LMSTRAS 7
|||||
Db 1 LMSTRAS 7

RESULT 6

US-09-214-095D-29
; Sequence 29, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-29

Query Match 100.0%; Score 31; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||
Db 1 LMSTRAS 7

RESULT 7

US-08-672-345C-20
; Sequence 20, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: /08/672,345C
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-20

Query Match 90.3%; Score 28; DB 2; Length 7;

Best Local Similarity 85.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||
Db 1 LMSTRSS 7

RESULT 8

US-09-214-095D-20
; Sequence 20, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 20
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-20

Query Match 90.3%; Score 28; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
|||||
Db 1 LMSTRSS 7

RESULT 9

US-08-672-345C-80
; Sequence 80, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-80

US-08-672-345C-80

Query Match 87.1%; Score 27; DB 2; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRXS 7

RESULT 10

US-09-214-095D-80
; Sequence 80, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen.sp.
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (6) (6)
; OTHER INFORMATION: X at position 6 represents any amino acid
US-09-214-095D-80

Query Match 87.1%; Score 27; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 1 LMSTRXS 7

RESULT 11

US-08-685-808-9
; Sequence 9, Application US/08685808
; Patent No. 6048715
; GENERAL INFORMATION:
; APPLICANT: HAYNES, CHARLES A., et al
; TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
; ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP
; STREET: 260 Sheridan Ave., Ste. 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 24-JULY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/505,860
; FILING DATE: 24-JULY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750

; REFERENCE/DOCKET NUMBER: CBTD.017.01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: no
US-08-685-808-9

Query Match 61.3%; Score 19; DB 3; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTR 5
Db 1 MSTR 4

RESULT 12

US-08-505-860C-9
; Sequence 9, Application US/08505860C
; Patent No. 6174700
; GENERAL INFORMATION:
; APPLICANT: HAYNES, CHARLES A., et al
; TITLE OF INVENTION: SEPARATION AND CONCENTRATION SYSTEMS BASED
; ON SOLUBLE OLIGOSACCHARIDE BINDING DOMAINS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP
; STREET: 260 Sheridan Ave., Ste. 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/505,860C
; FILING DATE: 24-JULY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rae-Venter, Barbara
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CBTD.017.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: no
US-08-505-860C-9

Query Match 61.3%; Score 19; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 MSTR 5
Db 1 MSTR 4

RESULT 13

US-08-353-400-31
; Sequence 31, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-31

Query Match 58.1%; Score 18; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 STRAS 7
Db 3 STRTS 7

RESULT 14
US-08-264-093-25
; Sequence 25, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rigout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-25

Query Match 54.8%; Score 17; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 MSTRAS 7
Db 2 LSYRAS 7

RESULT 15
US-08-467-420A-11
; Sequence 11, Application US/08467420A
; Patent No. 5683892
; GENERAL INFORMATION:
; APPLICANT: Ames, Robert S.
; APPLICANT: Appelbaum, Edward R.
; APPLICANT: Chaiken, Irwin M.
; APPLICANT: Cook, Richard M.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Holmes, Stephen D.
; APPLICANT: McMillan, Lynette J.
; APPLICANT: Theisen, Timothy W.
; TITLE OF INVENTION: Recombinant IL5 Antagonists Useful in
; TITLE OF INVENTION: Treatment of IL5 Mediated Disorders
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corp./Corporate
; ADDRESSEE: Intellectual Property
; STREET: P. O. Box 1539-UW2220
; CITY: King of Prussia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,420A
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/363131
; FILING DATE: 23-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610 270-5024
; TELEFAX: 610 270-5090
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-467-420A-11

Query Match 54.8%; Score 17; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.9e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 STRAS 7
 |||||
 Db 3 STRES 7

Search completed: April 22, 2003, 13:25:06
 Job time : 29 secs

GenCore version 5.1.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:28:56 ; Search time 14 Seconds
(without alignments)
61.801 Million cell updates/sec

Title: US-09-674-716b-7
Perfect score: 48
Sequence: 1 QQLVEYPPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 789

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	43.8	9	S66635	alpha-2-macroglobu
2	19	39.6	5	E60274	major protein anti
3	16	33.3	3	A43391	TRH-like tripeptid
4	14	29.2	4	A32039	tyrosine-melanocyt
5	14	29.2	4	PT0240	Ig heavy chain CRD
6	14	29.2	5	PQ0009	angiotensin-conver
7	14	29.2	6	JN0861	peptidyl-dipeptida
8	14	29.2	7	A61324	dermorphin - Ronde
9	14	29.2	7	S36662	dermorphin (Lys-7)
10	14	29.2	7	S21230	dermorphin (Trp-4,
11	14	29.2	7	S46620	aggreccan - bovine
12	14	29.2	8	S66646	cardioacceleratory
13	14	29.2	9	A61620	locustamytropin I
14	14	29.2	9	B49712	ATP-binding protei
15	13	27.1	5	JS0319	subesophageal gang
16	13	27.1	6	A61049	halo-toxin - pseud
17	13	27.1	6	I51317	bHLH transcription
18	13	27.1	7	E33932	Ig mu chain D regi
19	13	27.1	7	PX0008	glucuronosyltransf
20	13	27.1	7	I56695	hypothetical L2 pr
21	13	27.1	8	S16324	hypothetical prote
22	13	27.1	9	S15850	vitamin D3 26-mono
23	13	27.1	9	A61358	bradykinin-like pe
24	13	27.1	9	A61057	Thr-6 bradykinin -
25	13	27.1	9	A26744	bradykinin-like pe
26	13	27.1	9	A61363	bradykinin - commo
27	13	27.1	9	A60579	bradykinin-like pe
28	13	27.1	9	A26363	cardioactive pepti
29	13	27.1	9	S39766	cardioactive pepti

30	13	27.1	9	2	S27233	cardioactive pepti
31	13	27.1	9	2	S65433	bradykinin - horn
32	13	27.1	9	2	PT0080	60K Ca binding pro
33	13	27.1	9	2	PT0285	Ig heavy chain CRD
34	13	27.1	9	2	S10784	enamelin I - bovin
35	13	27.1	9	2	I46023	growth hormone rec
36	13	27.1	9	2	S39767	cardioactive pepti
37	13	27.1	9	2	A43065	hydroxyproline-3-b
38	12	25.0	5	2	B37325	pap fibrial regul
39	12	25.0	5	3	JT0870	phytosulfokine alp
40	12	25.0	7	2	S25266	piile protein - Esc
41	12	25.0	7	2	A38081	amine oxidase (cop
42	12	25.0	8	2	PL0184	capsid protein VP-
43	12	25.0	8	2	D47393	neuropeptide calla
44	12	25.0	8	2	E47393	neuropeptide calla
45	12	25.0	8	2	B45800	serum albumin - do

ALIGNMENTS

RESULT 1

S66635
alpha-2-macroglobulin isoform 1 - bovine (fragment)
C;Species: Bos primigenius indicus (zebu cattle)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S66635
R;Dolmer, K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottr
FEBS Lett. 372, 93-95, 1995
A;Title: Crystallisation and preliminary X-ray analysis of the receptor-binding domain o
A;Reference number: S66634; MUID:96032553; PMID:7556651
A;Accession: S66635
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <DOL>

Query Match 43.8%; Score 21; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 EYFP 8
|||
Db 3 EYFP 6

RESULT 2

E60274
major protein antigen MPT63 - Mycobacterium tuberculosis (fragment)
C;Species: Mycobacterium tuberculosis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: E60274
R;Negai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A;Title: Isolation and partial characterization of major protein antigens in the culture
A;Reference number: A60274; MUID:91099989; PMID:1898899
A;Accession: E60274
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-5 <NAG>

Query Match 39.6%; Score 19; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 YPPT 9
|||
Db 2 YPIT 5

RESULT 3

A43391
TRH-like tripeptide - alfalfa
C;Species: Medicago sativa (alfalfa)

C>Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: A43391

R/Lackey, D.B.

J. Biol. Chem. 267, 17508-17511, 1992

A/Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-
A/Reference number: A43391; MUID:92388092; PMID:1517203

A/Accession: A43391

A/Molecule type: protein

A/Residues: 1-3 <LAC>

C/Keywords: amidated carboxyl end; pyroglutamic acid

F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F/3/Modified site: amidated carboxyl end (Pro) #status experimental

Query Match 33.3%; Score 16; DB 3; Length 3;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 YP 7

DB 1 QVP 3

RESULT 4

A32039

tyrosine-melanocyte-stimulating hormone release-inhibiting factor 1 - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 18-Aug-2000

C/Accession: A32039

R/Horvath, A.; Kastin, A.J.

J. Biol. Chem. 264, 2175-2179, 1989

A/Title: Isolation of tyrosine-melanocyte-stimulating hormone release-inhibiting factor

A/Reference number: A32039; MUID:89123285; PMID:2563371

A/Accession: A32039

A/Molecule type: protein

A/Residues: 1-4 <HOR>

A/Experimental source: brain

C/Superfamily: unassigned animal peptides

C/Keywords: amidated carboxyl end

F/4/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match

Best Local Similarity 29.2%; Score 14; DB 2; Length 4;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7

DB 1 YP 2

RESULT 5

PT0240

Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0240

R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0240

A/Molecule type: DNA

A/Residues: 1-4 <YAM>

A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 29.2%; Score 14; DB 2; Length 4;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7

DB 1 YP 2

RESULT 6

PQ0009

angiotensin-converting enzyme inhibitor (FLP-2) - common fig

N/Alternate names: ficus latex peptide 2

C/Species: Ficus carica (common fig)

C/Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995

C/Accession: PQ0009

R/Maruyama, S.; Miyoshi, S.; Tanaka, H.

Agric. Biol. Chem. 53, 2763-2767, 1989

A/Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.

A/Reference number: PQ0008

A/Accession: PQ0009

A/Molecule type: protein

A/Residues: 1-5 <MAR>

A/Experimental source: latex

C/Keywords: angiotensin-converting enzyme inhibitor

Query Match

Best Local Similarity 29.2%; Score 14; DB 2; Length 5;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7

DB 2 YP 3

RESULT 7

JN0861

peptidyl-dipeptidase A inhibitory peptide C111 - striped bonito

C/Species: Sarda orientalis (striped bonito)

C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999

C/Accession: JN0861

R/Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.

Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993

A/Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe

A/Reference number: JN0859; MUID:94080036; PMID:7764272

A/Accession: JN0861

A/Molecule type: protein

A/Residues: 1-6 <MAT>

A/Experimental source: liver

C/Comment: The carboxyl end is essential for the protein's expression of angiotensin I-c

C/Superfamily: bradykinin-potentiating peptide

C/Keywords: angiotensin-converting enzyme inhibitor

Query Match

Best Local Similarity 29.2%; Score 14; DB 2; Length 6;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7

DB 3 YP 4

RESULT 8

A61324

dermorphin - Rohde's leaf frog

C/Species: Phyllomedusa rohdei (Rohde's leaf frog)

C/Date: 17-Jul-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999

C/Accession: A61324

R/Montecucchi, P.C.; De Castiglione, R.; Erspamer, V.

Int. J. Pept. Protein Res. 17, 316-321, 1981

A/Title: Identification of dermorphin and Hyp(6)-dermorphin in skin extracts of the Bra

A/Reference number: A61324; MUID:82029915; PMID:7287302

A/Accession: A61324

A/Molecule type: protein

A/Residues: 1-7 <MON>

C/Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

C/Keywords: amidated carboxyl end; D-amino acid; hydroxyproline; neuropeptide; skin

F/2/Modified site: D-alanine (Ala) #status experimental

F/6/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental

F/7/Modified site: amidated carboxyl end (Ser) #status experimental

Query Match 29.2%; Score 14; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7
 ||
 Db 5 YP 6

RESULT 9
 S36662
 dermorphin (lvs-7) [validated] - two-colored leaf frog
 C:Species: Phyllomedusa bicolor (two-colored leaf frog)
 C>Date: 10-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 18-Aug-2000
 C:Accession: S36662
 R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
 FEBS Lett. 302, 151-154, 1992
 A:Title: Identification and characterization of two dermorphins from skin extracts of th
 A:Reference number: S21152; MUID:92339502; PMID:1633846
 A:Accession: S36662
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <MIG>
 C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 29.2%; Score 14; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7
 ||
 Db 5 YP 6

RESULT 10
 S21230
 dermorphin (Tnp-4, Asn-7) [validated] - two-colored leaf frog (fragment)
 C:Species: Phyllomedusa bicolor (two-colored leaf frog)
 C>Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 18-Aug-2000
 C:Accession: S21230
 R:Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.
 FEBS Lett. 302, 151-154, 1992
 A:Title: Identification and characterization of two dermorphins from skin extracts of th
 A:Reference number: S21152; MUID:92339502; PMID:1633846
 A:Accession: S21230
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-7 <MIG>
 C:Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 29.2%; Score 14; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7
 ||
 Db 5 YP 6

RESULT 11
 S42620
 aggrecan - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1998 #text_change 24-Jul-1998
 C:Accession: S42620
 R:Vogel, K.G.; Sandy, J.D.; Pogany, G.; Robbins, J.R.
 Matrix Biol. 14, 171-179, 1994
 A:Title: Aggrecan in bovine tendon.
 A:Reference number: S42620; MUID:94340214; PMID:7520336
 A:Accession: S42620
 A:Molecule type: protein
 A:Residues: 1-7 <VOG>
 A:Experimental source: flexor tendon

C:Keywords: cartilage

Query Match 29.2%; Score 14; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7
 ||
 Db 1 YP 2

RESULT 12
 S66646
 cardioacceleratory protein 2b - tobacco hornworm
 C:Species: Manduca sexta (tobacco hornworm)
 C>Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C:Accession: S66646
 R:Huesmann, G.R.; Cheung, C.C.; Loi, P.K.; Lee, T.D.; Swiderek, K.M.; Tublitz, N.J.
 FEBS Lett. 371, 311-314, 1995
 A:Title: Amino acid sequence of CAP(2b), an insect cardioacceleratory peptide from the t
 A:Reference number: S66646; MUID:96013159; PMID:7556618
 A:Accession: S66646
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-8 <HUE>

Query Match 29.2%; Score 14; DB 2; Length 8;
 Best Local Similarity 33.3%; Pred. No. 2.8e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 QLYEYP 7
 : : :
 Db 1 ELYAFP 6

RESULT 13
 A61620
 locustamytropin III - migratory locust
 C:Species: Locusta migratoria (migratory locust)
 C>Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 11-Jul-1997
 C:Accession: A61620
 R:Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; Kochansky, J.P.; De Loof, A.
 Insect Biochem. Mol. Biol. 22, 447-452, 1992
 A:Title: Isolation, identification and synthesis of locustamytropin III and IV, two add
 A:Reference number: A61620
 A:Accession: A61620
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <SCH>
 C:Keywords: amidated carboxyl end; neuropeptide
 F:9/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 29.2%; Score 14; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 EYPF 8
 : : :
 Db 2 QQPF 5

RESULT 14
 B49712
 ATP-binding protein p46 - dog (fragment)
 C:Species: Canis lupus familiaris (dog)
 C>Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 07-May-1999
 C:Accession: B49712
 R:Nigam, S.K.; Goldberg, A.L.; Ho, S.; Rohde, M.F.; Bush, K.T.; Sherman, M.Y.
 J. Biol. Chem. 269, 1744-1749, 1994
 A:Title: A set of endoplasmic reticulum proteins possessing properties of molecular chap
 A:Reference number: A49712; MUID:94124514; PMID:8294423
 A:Accession: B49712
 A:Status: preliminary

A;Molecule type: protein
A;Residues: 1-9 <NIG>
C;Keywords: ATP; endoplasmic reticulum; molecular chaperone

Query Match 29.2%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7
Db 5 YP 6

RESULT 15

JS0319
subesophageal ganglion pentapeptide - house cricket
C;Species: Acheta domesticus (house cricket)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: JS0319
R;Wicker, C.; Wicker, C.
Comp. Biochem. Physiol. C 88, 185-187, 1987
A;Title: Isolation and structure of a peptide isolated from the subesophageal ganglion
A;Reference number: JS0319
A;Accession: JS0319
A;Molecule type: protein
A;Residues: 1-5 <NIG>

Query Match 27.1%; Score 13; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PF 8
Db 4 PF 5

Search completed: April 22, 2003, 13:31:56
Job time : 14 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:25:11 ; Search time 24 Seconds
(without alignments)
15.554 Million cell updates/sec

Title: US-09-674-716B-7
Perfect score: 48
Sequence: 1 QQLVEYPT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 231

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	15	31.2	8	ANG2 BOTJA
2	15	31.2	8	UPAA HUMAN
3	15	31.2	9	FLA2 TREHY
4	14	29.2	8	ALI7 CARMA
5	14	29.2	9	ALI1 CARMA
6	14	29.2	9	LMT3 LOCMI
7	14	29.2	9	UPA3 HUMAN
8	14	29.2	9	UPA7 HUMAN
9	13	27.1	5	SUGA ACHDO
10	13	27.1	7	FAR1 HELTI
11	13	27.1	7	UN06 PINPS
12	13	27.1	8	PPK2 PERAM
13	13	27.1	8	PPK3 PERAM
14	13	27.1	9	CCAP CARMA
15	13	27.1	9	UPA2 HUMAN
16	12	25.0	5	ALI4 CARMA
17	12	25.0	5	PSK DAUCA
18	12	25.0	6	ASP2 LACSN
19	12	25.0	7	ALI2 CARMA
20	12	25.0	7	ALI3 CARMA
21	12	25.0	7	ALI4 CARMA
22	12	25.0	7	ALI5 CARMA
23	12	25.0	7	ALI7 CYDPO
24	12	25.0	7	FAR2 ASCSU
25	12	25.0	8	ALI2 CARMA
26	12	25.0	8	ALI5 CARMA
27	12	25.0	8	ALI8 CARMA
28	12	25.0	8	ALI3 CYDPO
29	12	25.0	8	ALI4 CALVO
30	12	25.0	8	ALI4 CYDPO
31	12	25.0	8	ALI5 CALVO
32	12	25.0	8	ALI5 CYDPO
33	12	25.0	8	ALI7 CARMA

P81811 carcinus ma
P81812 carcinus ma
P22396 locusta mig
P81813 carcinus ma
P80977 thunnus obe
P04277 homo sapien
P82072 litoria rub
P01151 sus scrofa
P82071 litoria rub
P82073 litoria rub
P25418 libellula a
P14595 tabanus atr

34 12 25.0 8 1 ALL8 CARMA
35 12 25.0 8 1 ALL9 CARMA
36 12 25.0 8 1 LMT2 LOCMI
37 12 25.0 9 1 ALI0 CARMA
38 12 25.0 9 1 COXE THUOB
39 12 25.0 9 1 NEUX HUMAN
40 11.5 24.0 5 1 RE31 LITRU
41 11 22.9 3 1 THYL PIG
42 11 22.9 5 1 RE21 LITRU
43 11 22.9 5 1 RE32 LITRU
44 11 22.9 8 1 AKH LIBAU
45 11 22.9 8 1 AKH TABAT

ALIGNMENTS

RESULT 1
ANG2 BOTJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 15-DEC-1998 (Rel. 37, last annotation update)
DE Angiotensin-like peptide II (Fragment)
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgheresi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
plasma of the snake Bothrops jararaca."
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
DR PROSITE; PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON TER 8
SQ SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;

Query Match 31.2%; Score 15; DB 1; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.le+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 YPF 8
: : :
DB 6 HPF 8

RESULT 2
UPAA HUMAN STANDARD; PRT; 8 AA.
AC P30096;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, last sequence update)
DT 16-OCT-2001 (Rel. 40, last annotation update)
DE Unknown protein from 2D-page of plasma (Spot 36) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=93092937; PubMed=1459097;
RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;

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RT "plasma protein map: an update by microsequencing.";
RL Electrophoresis 13:707-714(1992).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 7, ITS MW IS: 12 kDa.
DR SWISS-2DPAGE; P30096; HUMAN.
FT NON TER 1
FT VARIANT 5
FT 5 F -> P.
FT 8 /FTID=VAR_000004.
FT NON TER 8
FT SEQUENCE 8 AA; 909 MW; 86677B59D1A72042 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.1e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LVEYFP 7
DB 3 LTFYFP 7

RESULT 3
ID FLA2_TREHY STANDARD; PRT; 9 AA.
AC P80159;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Flagellar filament outer layer protein flaa2 (35 kDa sheath protein)
DE (Fragment).
DN FLAA2.
OS Treponema hyodysenteriae (Serpulina hyodysenteriae).
OC Bacteria; Spirochaetales; Brachyspiraceae; Brachyspira.
OX NCBI_TaxID=159;
RN [1]
RP SEQUENCE.
RC MEDLINE=93139764; PubMed=1487733;
RX Koopman M.B.H., Baats E., van Vorstenbosch C.J.A.H.V.,
RA van der Zeijst B.A.M., Kusters J.G.;
RT "The periplasmic flagella of Serpulina (Treponema) hyodysenteriae are
RT composed of two sheath proteins and three core proteins.";
RL J. Gen. Microbiol. 138:2697-2706(1992).
CC -!- SUBUNIT: COMPONENT OF THE OUTER LAYER OF THE FLAGELLA.
CC -!- FUNCTION: THE FLAGELLUM CONSISTS OF AN OUTER LAYER COMPOSED OF TWO
CC SHEATH PROTEINS, FLAA1 (44 kDa) AND FLAA2 (35 kDa) AROUND A CORE
CC THAT CONTAINS THREE PROTEINS FLAB1 (37 kDa), FLAB2 (34 kDa) AND
CC FLAB3 (32 kDa).
CC -!- SUBCELLULAR LOCATION: Periplasmic flagellum.
KW Flagella; Periplasmic.
FT UNSURE 2
FT UNSURE 8
FT NON TER 9
FT SEQUENCE 9 AA; 1129 MW; 855A19C68B4772D1 CRC64;

Query Match 31.2%; Score 15; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.1e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QLVEYFP 8
DB 1 ETVPYMF 7

RESULT 4
ID AL17_CARMA STANDARD; PRT; 8 AA.
AC P81820;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas 17.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;

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OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 8
FT SEQUENCE 8 AA; 858 MW; C82879D5A846D865 CRC64;

Query Match 29.2%; Score 14; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 EYFP 8
DB 3 QYSF 6

RESULT 5
ID AL11_CARMA STANDARD; PRT; 9 AA.
AC P81814;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 11.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98121193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thorpe A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Amidation; Multigene family.
FT MOD RES 9
FT SEQUENCE 9 AA; 927 MW; 832D79DCB46D861 CRC64;

Query Match 29.2%; Score 14; DB 1; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 EYFP 8
DB 4 QYAF 7

RESULT 6
ID LMT3_LOCM1 STANDARD; PRT; 9 AA.
AC P41489;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Locustamytropin 3 (LOM-MT-3).
OS Locusta migratoria (Migratory locust).

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OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridoidea; Acridoidea; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Brain;
 RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., Kochansky J.P.,
 RA de Loof A.;
 RT "Isolation, identification and synthesis of locustamyotropin III and
 RT IV, two additional neuropeptides of Locusta migratoria: members of the
 RT locustamyotropin peptide family.";
 RL Insect Biochem. Mol. Biol. 22:447-452(1992).
 CC -|- MYOTROPIC ACTIVITY.
 CC -|- (MYOTROPIC ACTIVITY).
 CC -|- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; 1.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 9
 FT SEQUENCE 9 AA; 1140 MW; DSAE172C9D776C6 CRC64;
 SQ

Query Match 29.2%; Score 14; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 EYPF 8
 : ||
 Db 2 QOPF 5

RESULT 7

UPA3_HUMAN
 ID UPA3_HUMAN STANDARD; PRT; 9 AA.
 AC P30089;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 11) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochrassner D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RT Electrophoresis 13:707-714(1992).
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 4.6, ITS MW IS: 46 kDa.
 DR SWISS-2DPAGE; P30089; HUMAN.
 FT NON_TER 1
 FT NON_TER 9
 FT SEQUENCE 9 AA; 1056 MW; 26F2B1BAF769C737 CRC64;
 SQ

Query Match 29.2%; Score 14; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 YPFT 9
 : ||
 Db 4 FPXT 7

RESULT 8

UPA7_HUMAN
 ID UPA7_HUMAN STANDARD; PRT; 9 AA.
 AC P30093;
 DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of plasma (Spot 18) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=93092937; PubMed=1459097;
 RA Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
 RA Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
 RA Hochrassner D.F.;
 RT "Plasma protein map: an update by microsequencing.";
 RT Electrophoresis 13:707-714(1992).
 CC -|- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.05, ITS MW IS: 37 kDa.
 DR SWISS-2DPAGE; P30093; HUMAN.
 FT NON_TER 1
 FT NON_TER 5
 FT NON_TER 9
 FT SEQUENCE 9 AA; 1042 MW; 5C14477AEB0772C7 CRC64;
 SQ

Query Match 29.2%; Score 14; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 EYPF 8
 : ||
 Db 5 EXPY 8

RESULT 9

SUGA_ACHDO
 ID SUGA_ACHDO STANDARD; PRT; 5 AA.
 AC P19991;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Suboesophageal ganglion pentapeptide.
 OS Acheta domesticus (House cricket).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Ensifera;
 OC Gryllidae; Gryllinae; Acheta.
 OX NCBI_TaxID=6997;
 RN [1]
 RP SEQUENCE.
 RA Wicker C., Wicker C.;
 RT "Isolation and structure of a peptide isolated from the
 RT suboesophageal ganglion of Acheta domesticus (Orthoptera).";
 RL Comp. Biochem. Physiol. 88C:185-187(1987).
 CC -|- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
 CC GANGLIA.
 DR PIR; JS0319; JS0319.
 DR SEQUENCE 5 AA; 476 MW; 69D76DDDDDB00000 CRC64;
 SQ

Query Match 27.1%; Score 13; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 PF 8
 : ||
 Db 4 PF 5

RESULT 10

FARI_HEITI
 ID FARI_HEITI STANDARD; PRT; 7 AA.
 AC P41871;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE FMRamide-like neuropeptide GDFFLRP-amide.
 OS Helisoma trivolvis (Snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Basommatophora;
 OC Planorbidae; Helisoma.
 OX NCBI_TaxID=27815;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Kidney;
 RX MEDLINE=94286417; PubMed=7912428;
 RA Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
 RT "FMRamide-related peptides from the kidney of the snail, Helisoma
 RL trivolvis";
 RL Peptides 15:31-36(1994).
 CC -!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
 CC -!- THE KIDNEY, MANTLE AND SKIN.
 CC -!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
 CC -!- SIMILARITY: BELONGS TO THE FMRP (FMRPAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD RES 7
 SQ SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;

Query Match 27.1%; Score 13; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PF 8
 DB 3 PF 4

RESULT 11
 UN06 PINPS STANDARD; PRT; 7 AA.
 AC P81675;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE Unknown protein from 2D-page of needles (N141) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 OX NCBI_TaxID=71647;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Needle;
 RX MEDLINE=99274088; PubMed=10344291;
 RA Costa P., Pionneau C., Bauw G., Dubos C., Fahrman N., Kremer A.,
 RA Frigerio J.-M., Plomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 RT proteins";
 RL Electrophoresis 20:1098-1108(1999).
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC -!- PROTEIN IS: 6.6, ITS MW IS: 25 kDa.
 FT NON TER 1 1
 FT NON TER 7 7
 SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 27.1%; Score 13; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PF 8
 DB 6 PF 7

RESULT 12
 PPK2 PERAM STANDARD; PRT; 8 AA.
 AC P82632;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-2 (Pea-PK-2) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Corpora cardiaca;
 RX MEDLINE=97353923; PubMed=9210163;
 RA Predel R., Kellner R., Kaufmann R., Penzlin H., Gaede G.;
 RT "Isolation and structural elucidation of two pyrokinins from the
 RT retrocerebral complex of the American cockroach";
 RL Peptides 18:473-478(1997).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.
 CC -!- MASS SPECTROMETRY: MW=883; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 DR InterPro; IPR001484; Pyrokinin.
 DR PROSITE; PS00539; PYROKININ; FALSE_NEG.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD_RES 8
 FT MOD_RES 8
 SQ SEQUENCE 8 AA; 884 MW; C834176DD9D77775 CRC64;

Query Match 27.1%; Score 13; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 PF 8
 DB 3 PF 4

RESULT 13
 PPK3 PERAM STANDARD; PRT; 8 AA.
 AC P82618;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pyrokinin-3 (Pea-PK-3) (FXPRL-amide).
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Retrocerebral complex;
 RX MEDLINE=99212469; PubMed=10196736;
 RA Predel R., Kellner R., Nachman R.J., Holman G.M., Rapus J., Gaede G.;
 RT "Differential distribution of pyrokinin-isoforms in cerebral and
 RT abdominal neurohemal organs of the American cockroach";
 RL Insect Biochem. Mol. Biol. 29:139-144(1999).
 RN [2]
 RP TISSUE SPECIFICITY.
 RX MEDLINE=20189894; PubMed=10723010;
 RA Predel R., Eckert M.;
 RT "Tagma-specific distribution of FXPRLamides in the nervous system of
 RT the American cockroach";
 RL J. Comp. Neurol. 419:352-363(2000).
 CC -!- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
 CC (MYOTROPIC ACTIVITY).
 CC -!- TISSUE SPECIFICITY: CORPORA CARDIACA.

CC -1- MASS SPECTROMETRY: MW=996.5; METHOD=WALDI.
 CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
 KW Neuropeptide; Amidation; Pyrokinin.
 FT MOD RES 8 8
 SQ SEQUENCE 8 AA; 997 MW; 0B34177409D772C7 CRC64;

Query Match 27.1%; Score 13; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. NO. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PF 8
 ||
 Db 3 PF 4

RESULT 14

CCAP_CARMA STANDARD; PRT; 9 AA.

AC P38556;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Cardiac peptide (CCAP).
 OS Carcinus maenas (Common shore crab) (Green crab),
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm),
 OS Tenebrio molitor (Yellow mealworm), and
 OS Spodoptera eridania (Southern armyworm).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea;
 OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
 OC Brachyura; Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759, 7130, 7067, 37547;
 RN [1]

SEQUENCE.

RC SPECIES=C.maenas; TISSUE=Pericardial organs;
 RA Stangier J., Hilbich C., Beyreuther K., Keller R.;
 RT "Unusual cardioactive peptide (CCAP) from pericardial organs of the
 RT shore crab Carcinus maenas.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:575-579 (1987).
 RN [2]

SEQUENCE.

RC SPECIES=M.sexata;
 RC MEDLINE=93050243; PubMed=1426284;
 RA Cheung C.C., Loi P.K., Sylwester A.W., Lee T.D., Tublitz N.J.;
 RT "Primary structure of a cardioactive neuropeptide from the tobacco
 RT hawkmoth, Manduca sexta.";
 RL FEBS Lett. 313:165-168 (1992).
 RN [3]

SEQUENCE.

RC SPECIES=T.molitor, and S.eridania; TISSUE=Head;
 RA MEDLINE=94176032; PubMed=8129851;
 RA Furuya K., Liao S., Reynolds S.E., Ota R.B., Hackett M.,
 RA Schooley D.A.;
 RT "Isolation and identification of a cardioactive peptide from Tenebrio
 RT molitor and Spodoptera eridania.";
 RL Biol. Chem. Hoppe-Seyler 374:1065-1074 (1993).
 CC -1- FUNCTION: THE EFFECT OF CCAP IS BOTH INO- AND CHROMOTROPIC.
 CC -1- TISSUE SPECIFICITY: STORED IN PERICARDIAL ORGANS AND RELEASED
 CC INTO THE HEMOLYMPH.

PIR; A26363; A26363.

PIR; S27233; S27233.

Neuropeptide; Amidation.

DISULFID 3 9

FT MOD RES 9 9

SQ SEQUENCE 9 AA; 959 MW; C5A861A9CDD44EB9 CRC64;

Query Match 27.1%; Score 13; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. NO. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 PF 8
 ||
 Db 1 PF 2

RESULT 15

UHA2_HUMAN STANDARD; PRT; 9 AA.

AC P40929;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of heart (Spot 5603) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=95203287; PubMed=7895732;
 RA Corbett J.M., Wheeler C.H., Baker C.S., Yacoub M.H., Dunn M.J.;
 RT "The human myocardial two-dimensional gel protein database: update
 RT 1994.";
 RL Electrophoresis 15:1459-1465 (1994).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.0, ITS MW IS: 55.3 kDa.
 FT NON TER 9 9
 SQ SEQUENCE 9 AA; 1104 MW; 8874B1B5B01B2CA CRC64;

Query Match

Best Local Similarity 27.1%; Score 13; DB 1; Length 9;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVEY 6

Db 3 VLEY 6

Search completed: April 22, 2003, 13:31:00

Job time : 24 secs

GenCore version 5.1.4 p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:27:31 / Search time 28 seconds
(without alignments)
66.229 Million cell updates/sec

Title: US-09-674-716B-7
Perfect score: 48
Sequence: 1 QQLVEYPFT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 686

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	35.4	8	2	Q49534 mycoplasma
2	17	35.4	9	8	Q8WFT4
3	16	33.3	8	8	Q9MSX1
4	16	33.3	9	6	Q9TRU7
5	15	31.2	8	4	Q15898
6	15	31.2	9	4	Q14277
7	15	31.2	9	4	Q96T78
8	15	31.2	9	12	Q65711
9	14	29.2	8	2	Q93454
10	14	29.2	8	3	P82858
11	14	29.2	8	7	Q95213
12	14	29.2	8	15	Q98YK9
13	14	29.2	9	4	Q9UC36
14	14	29.2	9	8	Q9MVU2
15	14	29.2	9	8	Q9TJ85
16	14	29.2	9	8	Q9TLD0

17	14	29.2	9	8	Q9MVU1	Q9mvu1 caloglossa
18	14	29.2	9	8	Q9TJ87	Q9tj87 caloglossa
19	14	29.2	9	8	Q95BY3	Q95by3 caloglossa
20	14	29.2	9	8	Q8W7T9	Q8w7t9 bostrychia
21	14	29.2	9	8	Q9T388	Q9t388 caloglossa
22	14	29.2	9	8	Q9T387	Q9t387 bostrychia
23	14	29.2	9	8	Q78337	Q78337 caloglossa
24	14	29.2	9	8	Q9T389	Q9t389 caloglossa
25	14	29.2	9	10	Q81962	Q81962 caloglossa
26	14	29.2	9	10	Q81964	Q81964 caloglossa
27	14	29.2	9	10	Q81966	Q81966 caloglossa
28	14	29.2	9	10	Q81968	Q81968 caloglossa
29	14	29.2	9	10	Q9S8J8	Q9s8j8 oryza sativ
30	14	29.2	9	10	Q82778	Q82778 caloglossa
31	14	29.2	9	11	Q9QWT0	Q9qwt0 mus musculu
32	13	27.1	7	8	Q98866	Q98866 spinacia ol
33	13	27.1	8	3	P87225	P87225 saccharomyc
34	13	27.1	8	4	Q9UJ50	Q9uj50 homo sapien
35	13	27.1	8	4	Q9P0K3	Q9p0k3 homo sapien
36	13	27.1	8	8	Q8WGC9	Q8wgc9 upogebia af
37	13	27.1	8	12	Q83332	Q83332 murine hepa
38	13	27.1	9	2	Q9R735	Q9r735 streptomyce
39	13	27.1	9	4	Q9UMF3	Q9umf3 homo sapien
40	13	27.1	9	6	Q28121	Q28121 bos taurus
41	13	27.1	9	13	Q9PRJ4	Q9prj4 lepisosteus
42	13	27.1	9	13	P83060	P83060 bombina ori
43	13	27.1	9	13	P83059	P83059 bombina ori
44	13	27.1	9	13	P83058	P83058 bombina var
45	13	27.1	9	13	P83057	P83057 bombina var

ALIGNMENTS

RESULT 1

Q49534 ID Q49534 PRELIMINARY; PRT; 8 AA.
AC Q49534;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P120 (Fragment).
GN P120.
OS Mycoplasma hominis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_taxid=2098;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V2785;
RA Nyvold C., Birkelund S., Christiansen G.;
RT "The Mycoplasma hominis P120 membrane protein gene contains a 659 base pair hypervariable domain."
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U22025; AAA67455.1; -.
FT NON TER 1
SQ SEQUENCE 8 AA; 869 MW; 914457605B02C05D CRC64;

Query Match 35.4%; Score 17; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVEYP 7
Db ||| 6
2 IVEIP 6

RESULT 2

Q8WFT4 ID Q8WFT4 PRELIMINARY; PRT; 9 AA.
AC Q8WFT4;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

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DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Echinozoa; Echinozoa; Echinozoa; Echinozoa;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DCA3;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DCA3;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012858; AAL33832.2; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1115 MW; EDF8DB1B173B46CA CRC64;

Query Match 35.4%; Score 17; DB 8; Length 9;
Best Local Similarity 57.1%; Pred. No. 6.7e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
DB 3 QYLEEQP 9

RESULT 3
ID QMSX1 PRELIMINARY; PRT; 8 AA.
AC QMSX1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Paba (Fragment).
GN PSBA.
OS Jurinea humilis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Cardueae; Jurinea.
OX NCBI_TaxID=41594;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Hanlon P.C., Briesse D.T.;
RT "Evidence for hierarchical and non-hierarchical evolution in the
RT Carduinae thistles.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF129846; AAF78138.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 788 MW; 457451B5A76DDB10 CRC64;

Query Match 33.3%; Score 16; DB 8; Length 8;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VEYPPT 9
DB 1 LEAPST 6

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome oxidase subunit II (Fragment).
GN COII.
OS Diadema antillarum.
OG Mitochondrion.
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
OC Echinozoa; Echinozoa; Echinozoa; Echinozoa; Echinozoa;
OC Diadema.
OX NCBI_TaxID=105358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DCA3;
RX MEDLINE=21323357; PubMed=11430656;
RA Lessios H.A., Kessing B.D., Pearse J.S.;
RT "Population structure and speciation in tropical seas: global
RT phylogeography of the sea urchin Diadema.";
RL Evolution 55:955-975(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=DCA3;
RX MEDLINE=21561594; PubMed=11703875;
RA Lessios H.A., Garrido M.J., Kessing B.D.;
RT "Demographic history of Diadema antillarum, a keystone herbivore on
RT Caribbean reefs.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 268:2347-2353(2001).
DR EMBL; AY012858; AAL33832.2; -.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 9 AA; 1115 MW; EDF8DB1B173B46CA CRC64;

Query Match 35.4%; Score 17; DB 8; Length 9;
Best Local Similarity 57.1%; Pred. No. 6.7e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYP 7
DB 3 QYLEEQP 9

RESULT 3
ID QMSX1 PRELIMINARY; PRT; 8 AA.
AC QMSX1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE Paba (Fragment).
GN PSBA.
OS Jurinea humilis.
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Asterales; Asteraceae; Cardueae; Jurinea.
OX NCBI_TaxID=41594;
RN [1]
RP SEQUENCE FROM N.A.
RA O'Hanlon P.C., Briesse D.T.;
RT "Evidence for hierarchical and non-hierarchical evolution in the
RT Carduinae thistles.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF129846; AAF78138.1; -.
KW Chloroplast.
FT NON_TER 1
SQ SEQUENCE 8 AA; 788 MW; 457451B5A76DDB10 CRC64;

Query Match 33.3%; Score 16; DB 8; Length 8;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VEYPPT 9
DB 1 LEAPST 6

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```

RESULT 4
Q9TRU7
ID Q9TRU7 PRELIMINARY; PRT; 9 AA.
AC Q9TRU7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE GAP-3, GTPase-activating protein (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE
RX MEDLINE=92112868; PubMed=1309786;
RA Nice E.C., Fabri L., Hammacher A., Holden J., Simpson R.J.,
RA Burgess A.W.;
RT "The purification of a Rap1 GTPase-activating protein from bovine
RT brain cytosol.";
RL J. Biol. Chem. 267:1546-1553(1992).
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1063 MW; 89EDA77B47604B5A CRC64;

Query Match 33.3%; Score 16; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VEYP 7
DB 4 IYP 7

RESULT 5
Q15898
ID Q15898 PRELIMINARY; PRT; 8 AA.
AC Q15898;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE (clone XP6A11B) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32078; AAA73888.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 938 MW; 34A415B0477B45BB CRC64;

Query Match 31.2%; Score 15; DB 4; Length 8;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 YPFT 9
DB 3 YPIS 6

RESULT 6
Q14277
ID Q14277 PRELIMINARY; PRT; 9 AA.

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AC Q14277;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE RET protein short form (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94071887; PubMed=7902707;
 RA Ceccherini I., Boccardi R., Luo Y., Pasini B., Hofstra R.,
 RA Takahashi M., Romeo G.;
 RT "Exon structure and flanking intronic sequences of the human RET
 RT proto-oncogene.";
 RL Biochem. Biophys. Res. Commun. 196:1288-1295(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94366753; PubMed=8084609;
 RA Ceccherini I., Hofstra R., Yin L., Stulp R., Barone V., Stelwagen T.,
 RA Boccardi R., Nijveen H., Bolino A., Seri M., Ronchetto P., Pasini B.,
 RA Bozzano M., Buys C., Romeo G.;
 RT "DNA polymorphisms and conditions for SSCP analysis of the 20 exons of
 RT the ret proto-oncogene.";
 RL Oncogene 9:3025-3029(1994).
 DR EMBL; U11532; AAC50102.1; -.
 FT NON_TER 1
 SQ SEQUENCE 9 AA; 1134 MW; 034E11A9CDD1F5B0 CRC64;
 Query Match 31.2%; Score 15; DB 4; Length 9;
 Best Local Similarity 33.3%; Pred. No. 6.7e+05;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 4 VEYPT 9
 Db : :
 2 ISHAFT 7
 RESULT 7
 Q96T78 PRELIMINARY; PRT; 9 AA.
 AC Q96T78;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Contactin-associated protein 2 (Fragment).
 GN CNTNAP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21250995; PubMed=11352571;
 RA Nakabayashi K., Scherer S.W.;
 RT "The human contactin-associated protein 2 (CNTNAP2) spans over 2 Mb of
 RT DNA at chromosome 7q35.";
 RL Genomics 73:108-112(2001).
 DR EMBL; AF318295; AAK49906.1; -.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1080 MW; 9139A2D5A77B51EA CRC64;
 Query Match 31.2%; Score 15; DB 4; Length 9;
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 LVEYP 7
 Db : :
 1 LDHYP 5

RESULT 8
 Q65711 PRELIMINARY; PRT; 9 AA.
 AC Q65711;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE ORF3 (Fragment).
 OS Berne virus (BEV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Torovirus.
 OX NCBI_TaxID=11156;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90080137; PubMed=2293666;
 RA Snijder E.J., Horzinek M.C., Spaan W.J.M.;
 RT "A 3'-coterminally nested set of independently transcribed mRNAs is
 RT generated during Berne virus replication.";
 RL J. Virol. 64:331-338(1990).
 DR EMBL; M33502; AAA42817.1; -.
 FT NON_TER 9
 SQ SEQUENCE 9 AA; 1234 MW; D8E736B5451AB19 CRC64;
 Query Match 31.2%; Score 15; DB 12; Length 9;
 Best Local Similarity 66.7%; Pred. No. 6.7e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 YPF 8
 Db : :
 7 WPF 9
 RESULT 9
 Q934S4 PRELIMINARY; PRT; 8 AA.
 AC Q934S4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MerD protein (Fragment).
 GN MERD.
 OS Thiobacillus ferrooxidans.
 OC Bacteria; Proteobacteria; gamma subdivision; Acidithiobacillus.
 OX NCBI_TaxID=920;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=G66; TRANSPOSON=TN5037; Bass I.A., Gorlenko A.M., Yurieva O.V.,
 RA Kalyaeva E.S., Kholodii G.Y.,
 RA Nikiforov V.G.;
 RT "Tn5037, a Tn21-like mercury resistance transposon from Thiobacillus
 RT ferrooxidans.";
 RL Russ. J. Genet. 37:972-975(2001).
 DR EMBL; AJ251743; CAC69252.1; -.
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 937 MW; ED15A2D77B5DD446 CRC64;
 Query Match 29.2%; Score 14; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 YP 7
 Db : :
 4 YP 5
 RESULT 10
 P82858 PRELIMINARY; PRT; 8 AA.
 AC P82858;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Uricase (EC 1.7.3.3) (Urate oxidase) (Fragment).

```

OS Puccinia recondita f. sp. triestii.
OC Eukaryota; Fungi; Basidiomycota; Urediniomycetes; Urediniomycetidae;
OC Uredinales; Pucciniaceae; Puccinia.
OX NCBI_TaxID=142679;
RN [1]
RP SEQUENCE, FUNCTION, AND DEVELOPMENTAL STAGE.
RC TISSUE=SPORE;
RA Aguilar M., Montalbini P., Pineda M.;
RL Submitted (NOV-2000) to the SWISS-PROT data bank.
CC -1- FUNCTION: INVOLVED IN HOST-PARASITE RELATIONSHIP BETWEEN PLANTS
CC AND FUNGI.
CC -1- CATALYTIC ACTIVITY: URATE + O(2) + H(2)O = 5-HYDROXYISOURATE +
CC H(2)O(2) (5-HYDROXYISOURATE DECOMPOSE TO FORM ALLANTOIN).
CC -1- SUBCELLULAR LOCATION: PEROXISOMAL (BY SIMILARITY).
CC -1- DEVELOPMENTAL STAGE: GERMINATION.
CC -1- SIMILARITY: BELONGS TO THE URICASE FAMILY.
DR InterPro: IPR002042; Uricase.
DR PROSITE: PS00366; URICASE; PARTIAL..
KW Oxidoreductase; Purine metabolism; Peroxisome.
FT NON_TER 8
SQ SEQUENCE 8 AA; 777 MW; 98CLADD735B9D76D CRC64;

Query Match 29.2%; Score 14; DB 3; Length 8;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 PFT 9
DB 2 PFS 4

RESULT 11
Q95213
ID Q95213 PRELIMINARY; PRT; 8 AA.
AC Q95213;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Germline DH (DH) gene (Fragment).
GN DH.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagonomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P-I/RGM;
RA Mage R.G., Chen H.-T., Alexander C.B., Chen F.F.;
RT "Rabbit DQ52 and DH Gene Rearrangements in Early B-cell Development.";
RL Mol. Immunol. 0:0-0(1996).
DR EMBL; U62585; AAB18735.1; -.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 845 MW; 5CA861B5A858677B CRC64;

Query Match 29.2%; Score 14; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YP 7
DB 1 YP 2

RESULT 12
Q98VK9
ID Q98VK9 PRELIMINARY; PRT; 8 AA.
AC Q98VK9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Truncated pol protein (Fragment).
GN POL.

```

```

OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=991614;
RA Schmidt B., Walter H., Moschik G., Paatz C., Werwein M., Schwingel E.,
RA Korn K.;
RT "Recovery of HIV-1 pol gene sequences by direct sequencing of
RT amplification products derived from plasma samples.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF347458; AAK32535.1; -.
FT NON_TER 1
SQ SEQUENCE 8 AA; 845 MW; 72CDDDB1DD736CAB8 CRC64;

Query Match 29.2%; Score 14; DB 15; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 OLVE 5
DB 3 QLAE 6

RESULT 13
Q9UC36
ID Q9UC36 PRELIMINARY; PRT; 9 AA.
AC Q9UC36;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 28 Kda heat shock protein homolog fragment 1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=92218434; PubMed=1560006;
RA Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
RT "Copurification of small heat shock protein with alpha B crystallin
RT from human skeletal muscle.";
RL J. Biol. Chem. 267:7718-7725(1992).
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F77B43 CRC64;

Query Match 29.2%; Score 14; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YP 7
DB 3 YP 4

RESULT 14
Q9MVU2
ID Q9MVU2 PRELIMINARY; PRT; 9 AA.
AC Q9MVU2; Q9MVU3; Q9MVU4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit
DE (Fragment).
GN RBCL.
OS Caloglossa intermedia.
OC Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
OC Caloglossa.
OX NCBI_TaxID=100879;
RN [1]
RP SEQUENCE FROM N.A.

```



```

RC STRAIN-SOUTH CAROLINA USA, NEW JERSEY USA, AND GEORGIA USA;
RA Kamiya M., West J.A., Zuccarello G.C., Kawai H.;
RT "Caloglossa intermedia sp. nov. (Delesseriaceae, Rhodophyta),
RT morphologically intermediate between C. lepieurii and C. monosticha,
RT from the western Atlantic coast.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB030266; BAA90253.1; -
DR EMBL; AB030265; BAA90251.1; -
DR EMBL; AB030264; BAA90249.1; -
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 29.2%; Score 14; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VEYP 7
DB 2 VETP 5

RESULT 15
Q9TJ85 PRELIMINARY; PRT; 9 AA.
AC Q9TJ85;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Ribulose 1,5-bisphosphate carboxylase/oxygenase large subunit
DE (Fragment).
GN RBCL.
OS Caloglossa stipitata.
OG Chloroplast.
OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
OC Caloglossa.
OX NCBI_TaxID=88391;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Kamiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawai H.;
RT "Reproductive and genetic distinction between broad and narrow
RT entities of Caloglossa continua (Delesseriaceae, Rhodophyta).";
RL Phycologia 38:356-367(1999).
DR EMBL; AB023384; BAA88918.1; -
KW Chloroplast.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 977 MW; CA1A4DC1B771AB02 CRC64;

Query Match 29.2%; Score 14; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VEYP 7
DB 2 VETP 5

```

Search completed: April 22, 2003, 13:31:37
Job time : 30 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:24:36 ; Search time 73 Seconds
(without alignments)
16.428 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYPT 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 130868

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /SID82/gcgdata/geneseq/geneseq-embl/AA2000.DAT.*
22: /SID82/gcgdata/geneseq/geneseq-embl/AA2001.DAT.*
23: /SID82/gcgdata/geneseq/geneseq-embl/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	21 AAY32256	Light chain CDR L3
2	44	91.7	9	19 AAW39823	Light chain CDR3 o
3	36	75.0	9	19 AAW39817	Light chain CDR3 o
4	34	70.8	9	21 AAY92171	Murine 13H10 light
5	33	68.8	9	14 AAR30450	C242:11 MAb kappa
6	31	64.6	9	21 AAY97234	Complementary dete
7	31	64.6	9	22 AAE13142	Humanised antibody
8	31	64.6	9	22 AAB82708	VEGF antagonist an
9	31	64.6	9	22 AAB82896	Anti-human CD154 a
10	31	64.6	9	22 AAG63993	Complementarity de

11	31	64.6	9	23 AAU74411	Light chain comple
12	30	62.5	9	19 AAW59175	Mouse PAF receptor
13	30	62.5	9	19 AAW39820	Light chain CDR3 o
14	30	62.5	9	19 AAW39826	Light chain CDR3 o
15	28	58.3	9	18 AAW24776	Human immunoglobul
16	28	58.3	9	19 AAW73171	CDR3 of light chai
17	28	58.3	9	19 AAW80146	Light chain CDR3 p
18	28	58.3	9	19 AAW62016	Light chain variab
19	28	58.3	9	20 AAY40428	Amino acid sequenc
20	28	58.3	9	20 AAY28392	Peptide fragment f
21	28	58.3	9	21 AAY82342	Humanised anti-CD1
22	28	58.3	9	22 AAB83165	Mouse ganglioside
23	27	56.2	8	14 AAR35879	Hepatitis C virus
24	27	56.2	8	14 AAR35880	Hepatitis C virus
25	27	56.2	8	14 AAR35878	Hepatitis C virus
26	27	56.2	9	18 AAW23435	CDR-3 of rW12 ligh
27	27	56.2	9	19 AAW39877	Light chain CDR3 o
28	27	56.2	9	20 AAW89158	Humanised antibody
29	27	56.2	9	21 AAY95235	Humanised antibody
30	27	56.2	9	22 AAB60407	Erbb2-reactive VL
31	27	56.2	9	22 AAB61592	Humanised Fab vers
32	26	54.2	7	12 AAB13525	Analgescic heptapep
33	26	54.2	7	16 AAR82702	Blood triglyceride
34	26	54.2	7	17 AAR97351	Peptide fragment o
35	26	54.2	7	18 AAW30321	Haemorphin peptide
36	26	54.2	7	18 AAW01800	Heptaepetide which
37	26	54.2	7	20 AAY42565	Oligopeptide compo
38	26	54.2	7	22 AAU79894	Anti-stress agent
39	26	54.2	7	23 AAU98728	Peptide inhibitor
40	26	54.2	8	17 AAR97350	Peptide fragment o
41	26	54.2	8	18 AAW30320	Haemorphin peptide
42	26	54.2	9	17 AAR97349	Peptide fragment o
43	26	54.2	9	18 AAW30319	Haemorphin peptide
44	26	54.2	9	19 AAW71857	Human anti-tissue
45	26	54.2	9	20 AAY06698	Ab2 variable light

ALIGNMENTS

RESULT 1
AAY32256
ID AAY32256 standard; Peptide; 9 AA.

XX AC AAY32256;
XX DT 15-FEB-2000 (first entry)
XX DE Light chain CDR L3 of mouse anti-CD23 MAb C11.
XX KW CD23; FCERII; IGE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy.

OS Mus musculus.

XX PN WO958679-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB01434.

XX PR 09-MAY-1998; 98GB-0009839.

XX PA (GLAX) GLAXO GROUP LTD.

XX XX

PI Bonnefoy JMP, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 DR WPI; 2000-053101/04.
 DR N-PSDB; AAZ34741.
 XX
 PT Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis -
 XX
 PS Claim 1; Page 40; 81pp; English.
 XX
 CC This sequence represents complementarity determining region 3
 CC (CDR L3) of the light chain of murine anti-CD23 (PCERII) monoclonal
 CC antibody C11 (see also AAY32262). The invention provides altered
 CC antibodies, such as chimeric or humanised antibodies, which comprise
 CC sufficient of the amino acid sequences of C11 light and heavy chain
 CC CDRs (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies
 CC are used to block soluble CD23 formation for treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (claimed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.
 XX
 SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||
 Db 1 QQLVEYPFT 9

RESULT 2
 AAW39823
 ID AAW39823 standard; peptide; 9 AA.
 AC AAW39823;
 XX
 DT 16-JUN-1998 (first entry)
 XX
 DE Light chain CDR3 of catalytic antibody 2A10.
 XX
 KW Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.
 XX
 PN WO9749800-A1.
 XX
 PD 31-DEC-1997.
 XX
 PF 25-JUN-1997; 97WO-US10965.
 XX
 PR 25-JUN-1996; 96US-0672345.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX
 DR WPI; 1998-077166/07.
 XX
 PT New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required

PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX
 PS Claim 15; Page 82; 147pp; English.
 XX
 CC AAW39821-23 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 2A10, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 2A10 antibody was
 CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoester transition state analogue. Antibody 2A10 has a per minute Kcat
 CC of 0.011. The antibodies reduce the concentration of cocaine in a
 CC subject, and are used particularly for the treatment of an overdose. They
 CC are also used for treating addiction (by reducing the in vivo
 CC concentration that can be achieved).
 XX
 SQ Sequence 9 AA;

Query Match 91.7%; Score 44; DB 19; Length 9;
 Best Local Similarity 88.9%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 |||||
 Db 1 QQFVEYPFT 9

RESULT 3
 AAW39817
 ID AAW39817 standard; peptide; 9 AA.
 XX
 AC AAW39817;
 XX

DT 16-JUN-1998 (first entry)
 XX
 DE Light chain CDR3 of catalytic antibody 3B9.

XX Variable domain; lambda light chain; catalytic antibody; degradation;
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
 KW overdose; addiction.
 XX
 OS Mus sp.

XX WO9749800-A1.
 XX
 PD 31-DEC-1997.
 XX

PF 25-JUN-1997; 97WO-US10965.
 XX
 PR 25-JUN-1996; 96US-0672345.

XX (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Landry DW;
 XX

DR WPI; 1998-077166/07.

XX New catalytic antibodies able to decompose cocaine, single-chain
 PT analogues - used to treat cocaine overdose and addiction, required
 PT in far smaller doses than antibodies that antagonise cocaine by
 PT simply binding
 XX

PS Claim 11; Page 81; 147pp; English.

XX AAW39815-17 represent the sequences of the light chain complementarity
 CC determining regions (CDRs) of the catalytic antibody 3B9, which is able
 CC to degrade cocaine. A series of cocaine transition state analogues
 CC (TSAs) were prepared and used to immunise mice for production of
 CC hybridomas. Catalytic antibodies were identified by their capacity to
 CC release 3H-benzoic acid from 3H-phenyl cocaine. The 3B9 antibody was

CC identified using TSA1, which is an immunogenic conjugate of a phosphate
 CC monoeaster transition state analogue. Antibody 3B9 has a per minute Kcat
 CC of 0.11. The antibodies reduce the concentration of cocaine in a subject,
 CC and are used particularly for the treatment of an overdose. They are also
 CC used for treating addiction (by reducing the in vivo concentration that
 CC can be achieved).

XX Sequence 9 AA;

Query Match 75.0%; Score 36; DB 19; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QLVVEYPPT 9

Db 1 QHFVDYPT 9

RESULT 4

AAV92171

ID AAY92171 standard; Peptide; 9 AA.

XX

AC AAY92171;

DT 01-AUG-2000 (first entry)

DE Murine 13H10 light chain variable region CDR 3.

XX Light chain; variable region; complementarity determining region; CDR 3;
 KW anti-Tie2 kinase receptor; monoclonal antibody; 1598; angiogenetic;
 KW vascular-general; proliferative; antischismic; cerebroprotective;
 KW cardiac; agonist; antibody inhibition.

XX Mus musculus.

OS WO200018804-A1.

FN 06-APR-2000.

XX 28-SEP-1999; 99WO-US22428.

XX 28-SEP-1998; 98US-0102098.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Holmes SD, Erickson-miller CL, Winkler JD;

PI WPI; 2000-293114/25.

XX Tie2 receptor agonist antibodies useful for promoting angiogenesis in

PT patients suffering from strokes and myocardial infarctions

PS Claim 20; Page 46; 50pp; English.

XX AAY92169-71 are light chain CDR (complementarity determining regions)
 CC from a novel murine anti-Tie2 kinase receptor agonist monoclonal
 CC antibody 13H10. Tie2 is a single-transmembrane, tyrosine kinase receptor
 CC ('Tie' stands for tyrosine kinase receptor with immunoglobulin and
 CC endothelial growth factor (EGF) homology domain(s)). Anti-Tie2
 CC antibodies may be administered to enhance angiogenesis in mammals
 CC suffering from ischemic disease, myocardial infarction or cerebral stroke
 CC or other vascular diseases such as diabetes. It may also be used to
 CC enhance endothelial cell survival and to promote haematopoietic or
 CC megakaryocyte cell proliferation (claimed).

XX Sequence 9 AA;

Query Match 70.8%; Score 34; DB 21; Length 9;

Best Local Similarity 75.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QLVVEYPPT 9

Db 2 QLVVEYPPT 9

RESULT 5

AAAR30450

ID AAR30450 standard; peptide; 9 AA.

XX

AC AAR30450;

XX 06-MAY-1993 (first entry)

DE C242:11 MAb kappa chain CDR3.

XX Kappa; chain; heavy; complementarity determining region; CDR; MAb;
 KW monoclonal antibody; C242:11; murine; IgG; hybridoma; cell line;
 KW spleen; human; colonic; adenocarcinoma; myeloma; Sp2/0; antigen;
 KW endocytosis.

OS Synthetic.

XX EF521842-A.

XX 07-JAN-1993.

XX 03-JUL-1992; 92EP-0850166.

XX 03-JUL-1991; 91SE-0002074.

XX (KABI) KABI PHARMACIA AB.

XX Holmgren J, Lind P, Lindholm L;

PI WPI; 1993-002345/01.

XX Monoclonal antibody reacting with CA-242 antigen - obtd. by

PT culturing hybridoma cell line C242:11 or mutants, useful for

PS diagnosis and therapy of pancreatic or colorectal cancers

XX Claim 5; Page 11; 15pp; English.

XX The sequences given in AAR30448-50 represent the kappa chain and
 CC AAR30451-53 the heavy chain complementarity determining regions (CDR)
 CC of a monoclonal antibody (MAb), C242:II. C242:II is a monoclonal
 CC murine Ab of IgG class produced when culturing in an appropriate
 CC medium a hybridoma cell line obtained by fusing spleen cells from a
 CC mouse, which has been immunised with a human colonic adenocarcinoma
 CC cell line, with the murine myeloma cell line Sp2/0. C242:II when
 CC bound to a cell surface antigen is capable of being endocytosed or
 CC internalised into cells.

XX Sequence 9 AA;

Query Match 68.8%; Score 33; DB 14; Length 9;

Best Local Similarity 75.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QLVVEYPPT 9

Db 2 QLVVEYPPT 9

RESULT 6

AAAY97234

ID AAY97234 standard; Protein; 9 AA.

XX

AC AAY97234;

XX 19-DEC-2000 (first entry)

DE Complementary determining region (CDRL3) of anti-SI (KDR) antibody.

XX Immunoglobulin; antibody; complementary determining region; CDR;

KW VEGF; vascular endothelial growth factor; KDR;
 KW kinase insert domain containing receptor; multivalent; monovalent;
 KW humanised antibody; chimeric antibody; tumour; diabody; triabody;
 KW glioblastoma multiforme; hemangioblastoma; AIDS;
 KW central nervous system neoplasms; AIDS associated Karposi's sarcoma;
 KW acquired immune deficiency syndrome; AIDS; human.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200044777-A1.
 XX
 PD 03-AUG-2000.
 XX
 PF 28-JAN-2000; 2000WO-US02180.
 XX
 PR 29-JAN-1999; 99US-0117726.
 PR 29-JAN-1999; 99US-0240736.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 PI Zhu Z, Witte L;
 XX
 DR WPI; 2000-505966/45.
 DR N-PSDB; AAA53766.
 XX
 PT Novel immunoglobulin molecules binding kinase insert domain-containing
 PT receptor with the same affinity as vascular endothelial growth factor,
 PT used to reduce tumour growth
 XX
 PS Claim 3; Page 50; 55pp; English.
 XX
 CC New immunoglobulin molecules are described that bind kinase insert
 CC domain-containing receptor (KDR) with a comparable affinity to human
 CC vascular endothelial growth factor (VEGF). The antibodies neutralise
 CC KDR activation. The immunoglobulin may be a multivalent single
 CC chain antibody, a monovalent single chain antibody, a diabody, a
 CC triabody, a humanised antibody or a chimerised antibody.
 CC The immunoglobulin molecules bind specifically to an
 CC extracellular domain of the KDR receptor with the same affinity as
 CC VEGF. Overexpression of the KDR receptor with the same affinity as
 CC human tumour cell lines including glioblastoma multiforme,
 CC hemangioblastoma, central nervous system neoplasms and AIDS
 CC associated Karposi's sarcoma. The antibodies therefore have
 CC applications in treating these conditions. This sequence encodes a
 CC preferred heavy chain complementary determining region of the
 CC immunoglobulins of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 64.6%; Score 31; DB 21; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 QQLVEYPPT 9
 |||||
 Db 1 QQRSSYPPT 9
 |||||
 RESULT 7
 AAEL13142
 ID AAEL13142 standard; peptide; 9 AA.
 XX
 AC AAEL13142;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Humanised antibody murine light chain hypervariable region (VL) CDR3.
 XX
 KW Vascular endothelial growth factor receptor; VEGFR; antagonist; tumour;
 KW cytostatic; light chain hypervariable region; VL; myelocytic leukaemia;
 KW lymphocytic; erythrocytic; monocytic; multiple myeloma; lymphoid cell;
 KW Hodgkin's disease; complementarity determining region-3; CDR-3; mouse.

XX Mus sp.
 OS
 XX WO200174296-A2.
 PN
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US10504.
 XX
 PR 31-MAR-2000; 2000US-0540770.
 XX
 PA (IMCL-) IMCLONE SYSTEMS INC.
 PA (CORR) CORNELL RES FOUND INC.
 XX
 XX Witte L, Rafii S;
 XX
 DR WPI; 2001-662942/76.
 DR N-PSDB; AAD21668.
 XX
 PT Inhibiting growth of non-solid tumor cells useful to treat bone marrow
 PT tumors such as leukemias or multiple myeloma comprises treatment with
 PT an antagonist of a vascular endothelial growth factor receptor -
 XX
 PS Claim 8; Page 15; 68pp; English.
 XX
 CC The invention relates to a method for inhibiting the growth of non-solid
 CC tumour cells that are stimulated by a ligand of vascular endothelial
 CC growth factor receptor (VEGFR) in mammals particularly humans. The method
 CC involves treating the mammals with humanised VEGFR monoclonal antibodies
 CC (antagonists). Humanised monoclonal antibody comprises humanised mouse
 CC variable region joined to human constant region, where the humanised
 CC mouse variable region contains mouse complementarity determining region
 CC (CDR) grafted into human variable region. The method is useful for
 CC treating leukemias such as acute or chronic myelocytic leukaemia, acute
 CC or chronic lymphocytic leukaemia, erythrocytic or monocytic leukaemia,
 CC multiple myelomas and lymphoid cells, particularly those related to
 CC non-Hodgkin's and Hodgkin's disease. The present sequence is humanised
 CC antibody murine light chain hypervariable region (VL) CDR-3 used in the
 CC exemplification of the invention.
 XX
 SQ Sequence 9 AA;
 Query Match 64.6%; Score 31; DB 22; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 QQLVEYPPT 9
 |||||
 Db 1 QQRSSYPPT 9
 |||||
 RESULT 8
 AAB82708
 ID AAB82708 standard; Peptide; 9 AA.
 XX
 AC AAB82708;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE VEGF antagonist antibody IMC-1C11 VL CDR-3.
 XX
 KW IMC-1C11; chimeric antibody; mouse; human; antagonist; VEGF;
 KW vascular endothelial growth factor; angiogenesis; antiangiogenic;
 KW antitumour; neoplasm; collagen-vascular disease; autoimmune disease;
 KW tumour; breast carcinoma; lung carcinoma; prostate carcinoma;
 KW colon carcinoma; ovarian carcinoma; neuroblastoma;
 KW glioblastoma multiforme; melanoma; therapy; light chain; CDR;
 KW complementarity determining region.
 XX
 OS Chimeric - Mus sp.
 OS Chimeric - Homo sapiens.
 XX
 PN WO200154723-A1.

XX PD 02-AUG-2001.
 XX PF 29-JAN-2001; 2001WO-US02839.
 XX PR 28-JAN-2000; 2000US-0178791.
 XX PR 31-MAR-2000; 2000US-0539692.
 XX PA (SUNN-) SUNNYBROOK HEALTH SCI CENT.
 XX PA (IMCL-) IMCLONE SYSTEMS INC.
 XX PI Kerbel R;
 XX PI WPI; 2001-514531/56.
 XX DR
 XX PT Treating or controlling an angiogenic dependent condition (e.g. a
 PT neoplasm, collagen-vascular or autoimmune disease) in mammal by
 PT administering a combination of an antiangiogenic molecule and a
 PT chemotherapeutic agent
 XX PS Disclosure; Page 37; 42pp; English.
 XX CC The present sequence is that of complementarity determining region
 CC 3 of the light chain variable region (see also AAB82702) of
 CC IMC-1C11, a mouse-human chimeric antibody that has vascular
 CC endothelial growth factor (VEGF) antagonist activity. The antibody,
 CC or a fragment of it, can be used as an anti-angiogenic molecule,
 CC together with a chemotherapeutic agent, for the treatment of an
 CC angiogenic dependent condition in a mammal, especially a human.
 CC The invention relates generally to a method of treating or
 CC controlling an angiogenic dependent condition by administering an
 CC anti-angiogenic molecule and a chemotherapeutic agent, to produce a
 CC regression or arrest of the condition while minimising or
 CC preventing significant toxicity of the chemotherapeutic agent.
 CC The anti-angiogenic molecule inhibits or blocks the action of a
 CC vascular endothelium survival factor such as VEGF or its receptor,
 CC and is especially IMC-1C11. Conditions that can be treated include
 CC a neoplasm, a collagen-vascular disease or an autoimmune disease,
 CC especially a solid tumour, including breast carcinoma, lung
 CC carcinoma, prostate carcinoma, colon carcinoma, prostate carcinoma,
 CC ovarian carcinoma, neuroblastoma, central nervous system tumour,
 CC neuroblastoma, glioblastoma multiforme or melanoma (all claimed).
 XX SQ Sequence 9 AA;
 Query Match 64.6%; Score 31; DB 22; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 QQLVEYPFT 9
 DB 1 QQRSSYPFT 9
 RESULT 9
 AAB82896
 ID AAB82896 standard; Peptide; 9 AA.
 AC AAB82896;
 XX DT 26-NOV-2001 (first entry)
 XX DE Anti-human CD154 antibody ABI793 light chain variable region CDR3.
 XX KW CD154; gp39; CD40-L; antibody; ABI793; transplant rejection;
 KW autoimmune disease; inflammation; atherosclerosis;
 KW Alzheimer's disease; antiinflammatory; antiarteriosclerotic;
 KW immunosuppressive; therapy; complementarity determining region;
 XX CDR3.
 XX OS Mus musculus.
 XX PN WO200168860-A1.

XX PD 20-SEP-2001.
 XX PF 14-MAR-2001; 2001WO-EP02875.
 XX PR 16-MAR-2000; 2000GB-0006398.
 XX PA (NOVS) NOVARTIS AG.
 XX PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX PI Di Padova FE, Schuler W;
 XX PI WPI; 2001-590062/66.
 XX DR
 XX PT CD154 binding molecule, in particular antibody to human CD154 for use
 PT in treatment, prevention of autoimmune, inflammatory diseases,
 PT atherosclerosis, Alzheimer's disease and prevention of transplant
 PT rejection
 XX PS Claim 2; Page 23; 37pp; English.
 XX CC The present sequence is that of complementarity determining region
 CC 3 (CDR3) of the light chain variable region (VL, see also AAB82890)
 CC of mouse anti-human CD154 monoclonal antibody ABI793. The invention
 CC provides a CD154 binding molecule, in particular an antibody to
 CC human CD154, in which the VH region has the CDR1, CDR2 and CDR3 of
 CC ABI793 VH and the VL region has the CDR1, CDR2 and CDR3 of ABI793
 CC VL. The CD154 binding molecule is especially a human antibody in
 CC which the VH and VL domains are essentially those of ABI793, with
 CC constant regions from human heavy and light chains. The antibodies
 CC are used to inhibit an immune response mediated by CD154-positive
 CC cell interactions with CD40-positive cells, in the treatment and/or
 CC prevention of diseases, disorders or conditions where CD154
 CC modulation and/or interference with or inhibition of the CD154:CD40
 CC interactions is therapeutically beneficial, prevention of
 CC macrophage-associated inflammatory processes and in the treatment of
 CC diseases where suppression of antibody responses to antigens is
 CC desirable (claimed). The CD154 binding molecules are useful for
 CC prevention of cell, tissue or organ graft rejection, in the prevention
 CC and treatment of autoimmune or inflammatory diseases, atherosclerosis
 CC or Alzheimer's disease, and also for inhibiting B cell proliferation
 CC and differentiation, T cell responses, induction or modulation of T
 CC or B cell tolerance or inhibition of the growth of tumour cells
 CC expressing CD154 antigen. Such conditions include autoimmune and
 CC non-autoimmune disorders, in particular, Addison's disease, Celiac
 CC sprue, glomerulonephritis, Grave's disease, Hashimoto's thyroiditis,
 CC haemolytic disease of the newborn, keratitis, multiple sclerosis,
 CC polymyositis, psoriasis, rheumatic fever, rheumatoid arthritis,
 CC sarcoidosis, syphilis, tuberculosis, ulcerative colitis,
 CC HIV infection, leukaemia or lymphoma.
 XX SQ Sequence 9 AA;
 Query Match 64.6%; Score 31; DB 22; Length 9;
 Best Local Similarity 66.7%; Pred. No. 7.8e+05;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 QQLVEYPFT 9
 DB 1 QQYNSYPFT 9
 RESULT 10
 AAG63993
 ID AAG63993 standard; peptide; 9 AA.
 XX AC AAG63993;
 XX DT 26-NOV-2001 (first entry)
 XX DE Complementarity determining region of light chain of antibody 2C4.
 XX KW Monoclonal antibody 2C4; sialoadhesin factor-2; SAF-2; allergic rhinitis;

KW	allergy; asthma, anemia; eczema; lymphoma; systemic mastocytosis;
KW	leukemia; eosinophil.
XX	
OS	Mus sp.
XX	
PN	WO200166126-A1.
XX	
PD	13-SEP-2001.
XX	
PF	05-MAR-2001; 2001WO-US07193.
XX	
PR	07-MAR-2000; 2000US-0187595.
XX	
PA	(SMIK) SMITHKLINE BEECHAM CORP.
PA	(SMIK) SMITHKLINE BEECHAM PLC.
PA	(UYJO) UNIV JOHNS HOPKINS.
XX	
PI	Abrahamson JA, Bochner B, Erickson-Miller CL, Kikly KK;
PI	Schleimer R;
XX	
DR	WPI; 2001-570749/64.
XX	
PT	Novel monoclonal antibody specific for human sialoadhesin factor-2 for
PT	diagnosis, prevention, treatment of allergy, asthma, eczema or diseases
PT	such as lymphoma, leukemia or systemic mastocytosis, in a mammal
XX	
PS	Claim 10; Page 34; 35pp; English.
XX	
CC	AAG63991-93 represent the complementarity determining regions (CDRs)
CC	of the light chain variable region of murine monoclonal antibody 2C4.
CC	This antibody binds to human sialoadhesin factor-2 (SAF-2). The
CC	antibody is useful for treating or preventing allergic rhinitis,
CC	allergies, asthma, anemia, eczema or diseases such as lymphoma,
CC	leukemia or systemic mastocytosis in a mammal. It is also useful for
CC	detecting the presence of a cell, especially eosinophil in a sample,
CC	by detecting binding of the antibody to SAF-2. The antibody can be
CC	coupled to toxins, antiproliferative drugs or radionuclides to
CC	kill cells in areas of excessive SAF-2 expression.
XX	
SQ	Sequence 9 AA;
	Query Match 64.6%; Score 31; DB 22; Length 9;
	Best Local Similarity 66.7%; Pred. No. 7.8e+05;
	Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps
QY	1 QQLVEYVPFT 9
DB	1 QQRSSVPFT 9
RESULT 11	
AAU74411	
ID	AAU74411 standard; peptide; 9 AA.
AC	
AC	AAU74411;
DT	
DT	26-MAR-2002 (first entry)
XX	
DE	Light chain complementarity determining region L3 (CDRL3).
DE	
KW	Complementarity determining region; CDR; CDRL3; antigen; cytostatic;
KW	angiogenesis inhibitor; vascular endothelial growth factor receptor;
KW	VEGF; tumour; leukaemia; antibody; cell proliferation inhibitor;
KW	antibody light chain variable domain.
OS	
OS	Mus sp.
XX	
PN	WO200190192-A2.
XX	
PD	29-NOV-2001.
XX	
PD	24-MAR-2001; 2001WO-US16924.
XX	


```

Db      1 QHFEDYPFT 9

RESULT 15
AAW24776
ID AAW24776 standard; peptide; 9 AA.
XX
AC AAW24776;
XX
DT 03-DEC-1997 (first entry)
XX
DE Human immunoglobulin light chain CDR3 region peptide.
XX
KW Ig; affinity constant; human; antigen; hybridoma; B cell; transgene;
KW transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
KW transplant rejection.
XX
OS Homo sapiens.
XX
PN WO9713852-A1.
XX
PD 17-APR-1997.
XX
PF 10-OCT-1996; 96WO-US16433.
XX
PR 10-OCT-1995; 95US-0544404.
XX
PA (GENP-) GENPHARM INT INC.
XX
PI Kay RM, Lonberg N;
XX
DR WPI; 1997-235888/21.
XX
PT Novel anti-CD4 antibody produced by transgenic mice - used in the
PT treatment of auto-immune disease etc.
XX
PS Claim 60; Page 287; 396pp; English.
XX
CC A novel composition has been developed which comprises an immunoglobulin
CC (Ig) having an affinity constant (Ka) of at least 2 multiply
CC 1000000000 M-1 for binding to a predetermined human antigen. The
CC present sequence represents a human light chain CDR3 region peptide
CC which forms part of an immunoglobulin comprising a VKL15 segment,
CC a JK2 segment, and the present light chain CDR3 region. The
CC anti-CD4 antibodies may be used in therapeutic and diagnostic
CC applications, especially for the treatment of human diseases. These
CC antibodies reduce activity of CD4 cells and reduce undesirable
CC autoimmune reactions, inflammatory response and transplant rejection.
CC Transgenic animals are capable of producing heterologous antibodies
CC of multiple isotypes by undergoing isotype switching. These animals
CC produce a first Ig type that is necessary for antigen-stimulated B-cell
CC maturation and can switch to encode and produce one or more subsequent
CC heterologous isotypes.
XX
SQ Sequence 9 AA;

Query Match 58.3%; Score 28; DB 18; Length 9;
Best Local Similarity 55.6%; Pred. No. 7.8e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 1 QQYDSYPFT 9

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Job time : 74 secs

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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:31:41 ; Search time 41 Seconds
(without alignments)
17,589 Million cell updates/sec

Title: US-09-674-716B-7

Perfect score: 48

Sequence: 1 QQLVEYPPT 9

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Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 29135

Minimum DB seq length: 0

Maximum DB seq length: 9

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pdp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pdp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pdp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pdp.*
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- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pdp.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pdp.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	31	64.6	9	10	US-09-976-787-6
2	31	64.6	9	10	US-09-865-198-6
3	30	62.5	9	10	US-09-828-708-51
4	27	56.2	9	9	US-10-091-236-16
5	27	56.2	9	9	US-10-032-482-14
6	27	56.2	9	9	US-10-091-313-6
7	27	56.2	9	9	US-09-155-106-6
8	27	56.2	9	9	US-10-091-268-6
9	26	54.2	9	9	US-09-293-854-7
10	26	54.2	9	9	US-09-996-288-16
11	26	54.2	9	9	US-09-977-797A-62
12	26	54.2	9	9	US-09-977-797A-66
13	26	54.2	9	10	US-09-808-037-17
14	26	54.2	9	10	US-09-808-037-19
15	25	52.1	4	9	US-09-994-078-2
16	25	52.1	9	9	US-09-771-415-5
17	25	52.1	9	9	US-09-771-415-14
18	25	52.1	9	9	US-09-771-415-15
19	25	52.1	9	9	US-09-771-415-16

20	52.1	9	9	US-09-996-288-6	Sequence 6, Appli
21	52.1	9	9	US-09-996-288-61	Sequence 61, Appl
22	52.1	9	9	US-10-144-644-47	Sequence 47, Appl
23	52.1	9	9	US-10-144-644-48	Sequence 48, Appl
24	52.1	9	10	US-09-796-848A-7	Sequence 7, Appli
25	52.1	9	10	US-09-796-848A-23	Sequence 23, Appl
26	52.1	9	9	US-09-782-672-53	Sequence 53, Appl
27	52.1	9	9	US-09-782-672-53	Sequence 12, Appl
28	52.1	9	9	US-10-144-644-12	Sequence 12, Appl
29	52.1	9	10	US-09-910-059-28	Sequence 28, Appl
30	47.9	9	9	US-10-161-145-20	Sequence 20, Appl
31	47.9	9	10	US-09-808-037-18	Sequence 18, Appl
32	47.9	9	10	US-09-809-739-4	Sequence 4, Appli
33	47.9	9	10	US-09-974-449-50	Sequence 50, Appl
34	45.8	9	9	US-09-423-800-61	Sequence 61, Appl
35	45.8	9	9	US-09-875-221A-6	Sequence 6, Appli
36	45.8	9	9	US-10-015-535-4	Sequence 4, Appli
37	45.8	9	9	US-09-269-921-5	Sequence 5, Appli
38	45.8	9	9	US-10-182-018-61	Sequence 61, Appl
39	45.8	9	10	US-09-286-240-19	Sequence 19, Appl
40	45.8	9	10	US-09-954-166-13	Sequence 13, Appl
41	45.8	9	10	US-09-949-559-6	Sequence 6, Appli
42	45.8	9	10	US-09-434-955-1	Sequence 1, Appli
43	43.8	7	10	US-09-870-472-13	Sequence 13, Appl
44	43.8	8	9	US-10-046-801-32	Sequence 32, Appl
45	43.8	9	9	US-09-900-590-88	Sequence 88, Appl
		9	9	US-09-782-672-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-976-787-6
; Sequence 6, Application US/09976787
; Patent No. US20020064528A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; APPLICANT: Witte, Larry
; TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
; FILE REFERENCE: 11245/46505
; CURRENT APPLICATION NUMBER: US/09/976,787
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 09/493,539
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/117,726
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: WordPerfect 8.0 for Windows
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-976-787-6

Query Match 64.6%; Score 31; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.7e+05;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
DB 1 QQRSSYPPT 9

RESULT 2
US-09-865-198-6
; Sequence 6, Application US/09865198
; Patent No. US20020103345A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Zhenping
; TITLE OF INVENTION: Bispecific Immunoglobulin-Like Antigen Binding Proteins and Methc
; TITLE OF INVENTION: Production
; FILE REFERENCE: 11245/47102
; CURRENT APPLICATION NUMBER: US/09/865,198

; CURRENT FILING DATE: 2001-05-24
 ; PRIOR APPLICATION NUMBER: US 60/206,749
 ; PRIOR FILING DATE: 2000-03-24
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: WordPerfect 8.0 for Windows
 ; SEQ ID NO 6
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Mouse
 US-09-865-198-6

Query Match 64.6%; Score 31; DB 10; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.7e+05;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 Db 1 QQRSSYPFT 9

RESULT 3

US-09-828-708-51
 ; Sequence 51, Application US/09828708
 ; Patent No. US20020146753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ditzel, H.
 ; APPLICANT: Burton, D.
 ; APPLICANT: Schaller, M.
 ; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
 ; FILE REFERENCE: 1361,005US1
 ; CURRENT APPLICATION NUMBER: US/09/828,708
 ; CURRENT FILING DATE: 2001-09-24
 ; NUMBER OF SEQ ID NOS: 123
 ; SOFTWARE: FastSeq for Windows Version 4.70
 ; SEQ ID NO 51
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-828-708-51

Query Match 62.5%; Score 30; DB 10; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.7e+05;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 Db 1 QQLNSYPLT 9

RESULT 4

US-10-091-236-16
 ; Sequence 16, Application US/10091236
 ; Patent No. US20020168360A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DINGIVAN, CHRISTINE A.
 ; TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING INFLAMMATORY OR AUTOIMMUNE
 ; TITLE OF INVENTION: DISORDERS BY ADMINISTERING INTEGRIN ALPHA-V-BETA-3 ANTAGONISTS
 ; FILE REFERENCE: 10271-053-999
 ; CURRENT APPLICATION NUMBER: US/10/091,236
 ; CURRENT FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: US 60/273,098
 ; PRIOR FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: US 60/316,321
 ; PRIOR FILING DATE: 2001-08-31
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-10-091-236-16

Query Match 56.2%; Score 27; DB 9; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.7e+05;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QQLVEYPFT 9
 Db 2 QFTHYPFT 9

RESULT 5

US-10-032-482-14
 ; Sequence 14, Application US/10032482
 ; Publication No. US20020197270A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cohen, Irun
 ; APPLICANT: ROTTER, Varda
 ; APPLICANT: Wolkowicz, Roland
 ; APPLICANT: Ruiz, Pedro
 ; APPLICANT: EREZ-ALON, Neta
 ; APPLICANT: HERKEL, Johannes
 ; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS FOR INDUCTION OF ANTI-TUMOR
 ; FILE REFERENCE: COHEN42
 ; CURRENT APPLICATION NUMBER: US/10/032,482
 ; CURRENT FILING DATE: 2002-01-02
 ; PRIOR APPLICATION NUMBER: US/09/445,602
 ; PRIOR FILING DATE: 2001-01-24
 ; PRIOR APPLICATION NUMBER: PCT/IL98/00266
 ; PRIOR FILING DATE: 1999-12-09
 ; PRIOR APPLICATION NUMBER: IL 121041
 ; PRIOR FILING DATE: 1997-06-09
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 14
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-10-032-482-14

Query Match 56.2%; Score 27; DB 9; Length 9;
 Best Local Similarity 55.6%; Pred. No. 2.7e+05;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
 Db 1 QQRSSFPFT 9

RESULT 6

US-10-091-313-6
 ; Sequence 6, Application US/10091313
 ; Publication No. US20030044406A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DINGIVAN, CHRISTINE
 ; TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING INFLAMMATORY OR AUTOIMMUNE
 ; TITLE OF INVENTION: DISORDERS BY ADMINISTERING CD2 ANTAGONISTS IN COMBINATION WITH G
 ; FILE REFERENCE: 10271-063
 ; CURRENT APPLICATION NUMBER: US/10/091,313
 ; CURRENT FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: US 60/273,098
 ; PRIOR FILING DATE: 2001-03-02
 ; PRIOR APPLICATION NUMBER: US 60/346,918
 ; PRIOR FILING DATE: 2001-10-19
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Mus sp.
 US-10-091-313-6

Query Match 56.2%; Score 27; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QLVYEPFT 9
DB 2 QFTHYPT 9

RESULT 7
US-09-155-106-6
; Sequence 6, Application US/09155106
; Publication No. US20030054003A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOMABRYONIC
; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
; NUMBER OF SEQUENCES: 45
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/09/155.106
; PRIOR APPLICATION NUMBER:
; APPLICATION DATA:
; FILING DATE: PCT/US97/04696
; APPLICATION NUMBER: 19-MAR-1997
; FILING DATE: US 60/013,708
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-6

Query Match 56.2%; Score 27; DB 9; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 EYPFT 9
DB 5 EYPFT 9

RESULT 8
US-10-091-268-6
; Sequence 6, Application US/10091268
; Publication No. US20030068320A1
; GENERAL INFORMATION:
; APPLICANT: DINGIVAN, CHRISTINE A
; TITLE OF INVENTION: METHODS OF ADMINISTERING/DOSING CD2 ANTAGONISTS FOR THE PREVENTION
; TITLE OF INVENTION: AND TREATMENT OF AUTOIMMUNE DISORDERS OR INFLAMMATORY DISORDERS
; FILE REFERENCE: 10271-054-999
; CURRENT APPLICATION NUMBER: US/10/091,268
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/273,098
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: US 60/346,918
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-091-268-6

Query Match 56.2%; Score 27; DB 9; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 QLVYEPFT 9
DB 2 QFTHYPT 9

RESULT 9
US-09-293-854-7
; Sequence 7, Application US/09293854
; Patent No. US20020168357A1
; GENERAL INFORMATION:
; APPLICANT: Wong, Hing C.
; Jiao, Jin-an
; Esperanza, Nieves
; Lawrence, Luepschen
; TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
; TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,854
; FILING DATE: 16-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/814,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Corless, Peter F
; REGISTRATION NUMBER: 33,860
; REFERENCE/DOCKET NUMBER: 46943
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-293-854-7

Query Match 54.2%; Score 26; DB 9; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.7e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVYEPFT 9
DB 1 QQVYSPEFT 9

RESULT 10
US-09-996-288-16

; Sequence 16, Application US/09996288
; Patent No. US2002017126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-16

Query Match 54.2%; Score 26; DB 9; Length 9;
Best Local Similarity 62.5%; Pred. No. 2.7e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QLVVEYPFT 9
| | | | |
Db 2 QFSGYPFT 9

RESULT 11

US-09-977-797A-62
; Sequence 62, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-62

Query Match 54.2%; Score 26; DB 9; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.7e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
| | | | |
Db 1 QQYSRYPLT 9

RESULT 12

US-09-977-797A-66
; Sequence 66, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-66

Query Match 54.2%; Score 26; DB 9; Length 9;
Best Local Similarity 55.6%; Pred. No. 2.7e+05;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
| | | | |
Db 1 QQYSRYPLT 9

RESULT 13

US-09-808-037-17
; Sequence 17, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: HANAN, Eilat
; APPLICANT: SOLOMON, Beka
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON=2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: US 60/152,417
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-808-037-17

Query Match 54.2%; Score 26; DB 10; Length 9;
Best Local Similarity 62.5%; Pred. No. 2.7e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QLVVEYPFT 9
| | | | |
Db 2 QRSSYPT 9

RESULT 14

US-09-808-037-19
; Sequence 19, Application US/09808037
; Patent No. US20020052311A1
; GENERAL INFORMATION:
; APPLICANT: SOLOMON, Beka
; APPLICANT: HANAN, Eilat
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
; TITLE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
; FILE REFERENCE: SOLOMON=2D
; CURRENT APPLICATION NUMBER: US/09/808,037
; CURRENT FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 09/629,971
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 09/473,653

; PRIOR FILING DATE: 1999-12-29
 ; PRIOR APPLICATION NUMBER: US 60/152,417
 ; PRIOR FILING DATE: 1999-09-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 19
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic peptide
 US-09-808-037-19

Query Match 54.2%; Score 26; DB 10; Length 9;
 Best Local Similarity 62.5%; Pred. No. 2.7e+05;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 QLVYEPFT 9
 Db 2 QRSSYPFT 9

RESULT 15
 US-09-994-078-2
 ; Sequence 2, Application US/09994078
 ; Publication No. US20030032774A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BROWN, WILLIAM
 ; APPLICANT: DIMAIO, JOHN
 ; APPLICANT: SCHILLER, PETER
 ; APPLICANT: MARTEL, RENE
 ; APPLICANT: MARTEL, FRANCIS
 ; APPLICANT: MARTEL, DIANE
 ; APPLICANT: MARTEL, PIERRE
 ; TITLE OF INVENTION: NOVEL OPIOID PEPTIDES FOR THE TREATMENT OF PAIN
 ; FILE REFERENCE: WAS/81823/282437
 ; CURRENT APPLICATION NUMBER: US/09/994,078
 ; CURRENT FILING DATE: 2001-11-26
 ; PRIOR APPLICATION NUMBER: 09/159,518
 ; PRIOR FILING DATE: 1998-09-24
 ; PRIOR APPLICATION NUMBER: 08/392,918
 ; PRIOR FILING DATE: 1995-03-03
 ; PRIOR APPLICATION NUMBER: 08/718,585
 ; PRIOR FILING DATE: 1996-10-02
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: Peptide
 US-09-994-078-2

Query Match 52.1%; Score 25; DB 9; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.7e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 YPFT 9
 Db 1 YPFT 4

Search completed: April 22, 2003, 13:39:11
 Job time : 42 secs

GenCore version 5.1.4.p5 4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:29:16 Search time 14 Seconds
(without alignments)
18.915 Million cell updates/sec

Title: US-09-674-716B-7
Perfect score: 48
Sequence: 1 QQLVEYPT 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 66399

Minimum DB seq length: 0
Maximum DB seq length: 9

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA.*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	91.7	9	2	US-08-672-345C-27
2	44	91.7	9	2	US-09-214-095D-27
3	36	75.0	9	4	US-08-672-345C-21
4	36	75.0	9	4	US-09-214-095D-21
5	34	70.8	9	4	US-09-406-532-20
6	33	68.8	9	1	US-08-438-123-3
7	32	66.7	9	1	US-08-264-093-26
8	30	62.5	9	2	US-08-672-345C-24
9	30	62.5	9	2	US-08-672-345C-30
10	30	62.5	9	4	US-09-214-095D-30
11	30	62.5	9	4	US-09-214-095D-30
12	28	58.3	9	2	US-08-116-778E-11
13	28	58.3	9	2	US-08-438-562-11
14	28	58.3	9	2	US-08-483-528B-99
15	28	58.3	9	3	US-08-974-899-15
16	28	58.3	9	4	US-09-042-353-368
17	28	58.3	9	4	US-08-758-417A-216
18	28	58.3	9	4	US-09-393-385B-110
19	27	56.2	8	4	US-08-444-818-362
20	27	56.2	8	4	US-08-444-818-363
21	27	56.2	8	4	US-08-444-818-364
22	27	56.2	8	4	US-08-672-345C-81
23	27	56.2	9	4	US-09-214-095D-81
24	27	56.2	9	4	US-09-170-769A-24
25	26	54.2	7	2	US-08-627-173-7
26	26	54.2	7	2	US-08-535-882A-7
27	26	54.2	7	3	US-08-981-384-1

28	26	54.2	7	3	US-09-005-546-7	Sequence 7, Appli
29	26	54.2	8	2	US-08-627-173-6	Sequence 6, Appli
30	26	54.2	8	2	US-08-535-882A-6	Sequence 6, Appli
31	26	54.2	8	3	US-09-005-546-6	Sequence 6, Appli
32	26	54.2	9	2	US-08-627-173-5	Sequence 5, Appli
33	26	54.2	9	2	US-08-535-882A-5	Sequence 5, Appli
34	26	54.2	9	2	US-08-814-806-7	Sequence 7, Appli
35	26	54.2	9	3	US-09-005-546-5	Sequence 5, Appli
36	26	54.2	9	4	US-08-918-148-24	Sequence 24, Appli
37	25	52.1	8	2	US-08-350-260A-521	Sequence 521, App
38	25	52.1	8	2	US-08-350-260A-521	Sequence 524, App
39	25	52.1	9	1	US-08-467-420A-47	Sequence 47, Appli
40	25	52.1	9	1	US-08-467-420A-48	Sequence 48, Appli
41	25	52.1	9	1	US-08-470-110A-47	Sequence 48, Appli
42	25	52.1	9	1	US-08-470-110A-48	Sequence 48, Appli
43	25	52.1	9	1	US-08-667-769A-47	Sequence 47, Appli
44	25	52.1	9	1	US-08-667-769A-48	Sequence 48, Appli
45	25	52.1	9	2	US-08-940-371-47	Sequence 47, Appli

ALIGNMENTS

RESULT 1
US-08-672-345C-27
Sequence 27, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-27

Query Match 91.7%; Score 44; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. NO. 1.9e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QQLVEYPT 9
DB 1 QQLVEYPT 9
RESULT 2

```

US-09-214-095D-27
; Sequence 27, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-27

Query Match          91.7%; Score 44; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 1 QQFVDYPT 9

RESULT 3
US-08-672-345C-21
; Sequence 21, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-21

Query Match          75.0%; Score 36; DB 2; Length 9;
Best Local Similarity 66.9%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 1 QQFVDYPT 9

US-09-214-095D-21
; Sequence 21, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-21

Query Match          75.0%; Score 36; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
DB 1 QQFVDYPT 9

RESULT 5
US-09-406-532-20
; Sequence 20, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(9)
; OTHER INFORMATION: light chain CDR 3
US-09-406-532-20

Query Match          70.8%; Score 34; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVEYPFT 9
DB 2 QRLVEYPT 9

RESULT 6
US-08-438-123-3
; Sequence 3, Application US/08438123
; Patent No. 5552293
; GENERAL INFORMATION:
; APPLICANT: Lindholm et al
; TITLE OF INVENTION: TUMOR ANTIGEN SPECIFIC ANTIBODY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

```

ADDRESSEE: Lowe, Price, Leblanc & Becker
STREET: Suite 300, 99 Canal Center Plaza
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: DOS Text File
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,123
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/906,350
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: J.G. Mullins
REGISTRATION NUMBER: 33073
REFERENCE/DOCKET NUMBER: 149-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 684 1111
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Polypeptide
US-08-438-123-3

Query Match 68.8%; Score 33; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPT 9
| : |||||
Db 2 QHLEVPPT 9

RESULT 7
US-08-264-093-26
Sequence 26, Application US/08264093
Patent No. 5639863
GENERAL INFORMATION:
APPLICANT: Michael D. Dan
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
TITLE OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ridout & Maybee
STREET: 2300 Richmond-Adelaide Centre
STREET: 101 Richmond Street West
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5H 2J7
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS-DOS 6.00
SOFTWARE: ASCII Editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,093
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA: No. 5639863 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Lake, James R.
REGISTRATION NUMBER: 31081

REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 868-1482
TELEFAX: (416) 362-0823
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: not applicable
TOPOLOGY: linear
US-08-264-093-26

Query Match 66.7%; Score 32; DB 1; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.9e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QLVVEYPT 9
| : |||||
Db 2 QRIEFPPT 9

RESULT 8
US-08-672-345C-24
Sequence 24, Application US/08672345C
Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-24

Query Match 62.5%; Score 30; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.9e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPT 9
| : |||||
Db 1 QHVEDYPT 9

RESULT 9
US-08-672-345C-30
Sequence 30, Application US/08672345C

Patent No. 5948658
GENERAL INFORMATION:
APPLICANT: Landry, Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-30

Query Match 62.5%; Score 30; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.9e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QQLVEYPT 9
Db 1 QHFEDYPT 9

RESULT 10
US-09-214-095D-24
Sequence 24, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
SEQ ID NO 24
LENGTH: 9
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-214-095D-24

Query Match 62.5%; Score 30; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.9e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QQLVEYPT 9
Db 1 QHFEDYPT 9

RESULT 11
US-09-214-095D-30
Sequence 30, Application US/09214095D
Patent No. 6280987
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
SEQ ID NO 30
LENGTH: 9
TYPE: PRT
ORGANISM: Murinae gen. sp.
US-09-214-095D-30

Query Match 62.5%; Score 30; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.9e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 QQLVEYPT 9
Db 1 QHFEDYPT 9

RESULT 12
US-08-116-778E-11
Sequence 11, Application US/08116778E
Patent No. 5830470
GENERAL INFORMATION:
APPLICANT: NAKAMURA, KAZUYASU
APPLICANT: KOIKE, MASAMICHI
APPLICANT: SHITARA, KENYA
APPLICANT: HANAI, NOBUO
APPLICANT: KUWANA, YOSHIHISA
APPLICANT: HASEGAWA, MAMORU
TITLE OF INVENTION: HUMANIZED ANTIBODIES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHVE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VIRGINIA
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/116,778E
FILING DATE: 07-SEP-93
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 249-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)816-4000
TELEFAX: (703)816-4100
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-116-778E-11

Query Match 58.3%; Score 28; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.9e+05;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
|||
Db 1 QQRSSVPYT 9

RESULT 13

US-08-438-562-11
; Sequence 11, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO
; APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,562
; FILING DATE: 10-MAY-95
; CLASSIFICATION: 424

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/116,778
; FILING DATE: 07-SEP-93
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.

REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 249-76
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100

INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-438-562-11

Query Match 58.3%; Score 28; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.9e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
|||
Db 1 QQRSSVPYT 9

RESULT 14

US-08-483-528B-99
; Sequence 99, Application US/08483528B
; Patent No. 5939532
; GENERAL INFORMATION:
; APPLICANT: NAKAMURA, KAZUYASU
; APPLICANT: KOIKE, MASAMICHI
; APPLICANT: SHITARA, KENYA
; APPLICANT: HANAI, NOBUO

APPLICANT: KUWANA, YOSHIHISA
; APPLICANT: HASEGAWA, MAMORU
; TITLE OF INVENTION: HUMANIZED ANTIBODIES
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHVE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,528B
; FILING DATE: 07-JUN-95
; CLASSIFICATION: 536

TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)816-4000
; TELEFAX: (703)816-4100
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-483-528B-99

Query Match 58.3%; Score 28; DB 2; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.9e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
|||
Db 1 QQRSSVPYT 9

RESULT 15

US-08-974-899-15
; Sequence 15, Application US/08974899
; Patent No. 6037454
; GENERAL INFORMATION:

APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,899
; FILING DATE:

CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: 60/031971
; APPLICATION NUMBER: 60/031971
; FILING DATE: 11/27/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1014R1
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-1994
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 15:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-974-899-15

Query Match 58.3%; Score 28; DB 3; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QQLVVEYPFT 9
 Db 1 QQHNEYPLT 9

Search completed: April 22, 2003, 13:32:17
 Job time : 15 secs

GenCore version 5.1.4 p5-4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:38:27 ; Search time 43 Seconds
(without alignments)
11.178 Million cell updates/sec

Title: US-09-674-716B-9
Perfect score: 33
Sequence: 1 GYWS 5
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 206

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	60.6	5	2 JH0253	gut pentapeptide -
2	16	48.5	5	2 A32516	cholecystokinin-5
3	13	39.4	4	2 S09478	globulin IV alpha
4	13	39.4	5	2 P70308	Ig heavy chain CRD
5	11	33.3	3	3 F37196	bradykinin-potenti
6	11	33.3	4	2 A34626	RPCB-related neuro
7	11	33.3	4	2 B53284	T-cell receptor be
8	11	33.3	4	2 P70661	T-cell receptor be
9	11	33.3	5	2 A60803	neuropeptide - sea
10	11	33.3	5	2 G37196	bradykinin-potenti
11	11	33.3	5	2 P70281	Ig heavy chain CRD
12	11	33.3	5	2 P70729	T-cell receptor be
13	11	33.3	5	2 P70580	T-cell receptor be
14	9	27.3	3	3 I50412	gene p20K protein
15	9	27.3	4	2 A32480	achatin-I - giant
16	9	27.3	5	2 S70154	pap fibrial regul
17	9	27.3	5	2 B37325	pap fibrial regul
18	9	27.3	5	2 A40469	hypoanthine phosph
19	9	27.3	5	2 A37114	hypoanthine phosph
20	9	27.3	5	2 B61445	Leu-enkephalin - b
21	9	27.3	5	2 A61445	Met-enkephalin - b
22	9	27.3	5	2 B61168	cocoonase (EC 3.4.
23	8	24.2	3	3 GRHU	growth-modulating
24	8	24.2	4	2 P60140	carbon-monoxide de
25	8	24.2	4	2 I38888	COI intron 16 prot
26	8	24.2	5	2 P70278	Ig heavy chain CRD
27	8	24.2	5	2 S69237	surface protein te
28	7	21.2	3	3 A22565	R-phycoerythrin al
29	7	21.2	3	3 A43391	TRH-like tripeptid

30	7	21.2	3	3 S68328	blood cell protein
31	7	21.2	4	2 A32039	tyrosine-melanocyt
32	7	21.2	4	2 A37832	phenol 2-monooxyge
33	7	21.2	4	2 I61883	protamine P1 - ora
34	7	21.2	4	2 P70240	Ig mu chain V regi
35	7	21.2	4	2 S43959	Ig mu chain V regi
36	7	21.2	4	2 I37013	protamine P1 - Cer
37	7	21.2	4	2 I84439	protamine P1 - sav
38	7	21.2	5	1 HOROHA	proctolin - Americ
39	7	21.2	5	2 I39964	ribosomal protein
40	7	21.2	5	2 I39966	ribosomal protein
41	7	21.2	5	2 I39965	major protein anti
42	7	21.2	5	2 E60274	R-phycoerythrin ga
43	7	21.2	5	2 F22565	angiotensin-conver
44	7	21.2	5	2 PQ0009	photosystem I 10.4
45	7	21.2	5	2 PQ0689	

ALIGNMENTS

RESULT 1

JH0253
gut pentapeptide - Japanese eel
C;Species: Anguilla japonica (Japanese eel)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 11-Apr-1995
C;Accession: JH0253
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.
Biochem. Biophys. Res. Commun. 180, 828-832, 1991
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.
A;Reference number: JH0253; MUID:92062113; PMID:1953755
A;Accession: JH0253
A;Molecule type: protein
A;Residues: 1-5 <UNS>
A;Experimental source: gut
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric, and of the circular muscle of the gastro-intestinal junction.

Query Match 60.6%; Score 20; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYW 3
Db 1 GFW 3

RESULT 2

A32516
cholecystokinin-5 - dog
N;Alternate names: CCK-5
C;Species: Canis lupus familiaris (dog)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Aug-2000
C;Accession: A32516
R;Shively, J.; Reeve Jr., J.R.; Eysselein, V.E.; Ben-Avram, C.; Vigna, S.R.; Walsh, J.H.
Am. J. Physiol. 252, G272-G275, 1987
A;Title: CCK-5: sequence analysis of a small cholecystokinin from canine brain and intest
A;Reference number: A32516; MUID:87153671; PMID:3826354
A;Accession: A32516
A;Molecule type: protein
A;Residues: 1-5 <SHI>
C;Comment: This peptide corresponds to the five carboxyl-terminal residues of cholecysto
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide
F;5/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 48.5%; Score 16; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 WM 4
Db 2 WM 3

RESULT 3
S09478
Globulin IV alpha subunit gamma chain, seed - cucurbit (fragment)
N/Alternate names: 11S globulin alpha subunit gamma chain
C/Species: Cucurbita sp. (cucurbit)
C/Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 08-Nov-1996
C/Accession: S09478
R/Ohmliya, M.; Hara, I.; Matsubara, H.
Plant Cell Physiol. 21, 157-167, 1990
A/Title: Pumpkin (Cucurbita sp.) seed globulin IV. Terminal sequences of the acidic and
A/Reference number: S09066
A/Accession: S09478
A/Molecule type: protein
A/Residues: 1-4 <OH>

Query Match 39.4%; Score 13; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2
||
Db 3 GY 4

RESULT 4
PT0308
Ig heavy chain CRD3 region (clone 6-88) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0308
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovers, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0308
A/Molecule type: DNA
A/Residues: 1-5 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 39.4%; Score 13; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 WMS 5
||
Db 2 WES 4

RESULT 5
F37196
bradykinin-potentiating peptide 6 - island jaxaraca
C/Species: Bothrops insularis (island jaxaraca)
C/Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C/Accession: F37196
R/Cintrá, A.C.O.; Vieira, C.A.; Giglio, J.M.
J. Protein Chem. 9, 221-227, 1990
A/Title: Primary structure and biological activity of bradykinin potentiating peptides f
A/Reference number: A37196; MUID:90351557; PMID:2386615
A/Accession: F37196
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-3 <CIN>
C/Keywords: pyroglutamic acid
P;/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 11; DB 3; Length 3;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3,

Db 3 W 3

RESULT 6
A34626
RPCH-related neuropeptide - ferruginous spindle
C/Species: Fuscus ferrugineus (ferruginous spindle)
C/Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C/Accession: A34626
R/Kuroki, Y.; Kanda, T.; Kubota, I.; Fujisawa, Y.; Ikeda, T.; Miura, A.; Minamitake, Y.;
Biochem. Biophys. Res. Commun. 167, 273-279, 1990
A/Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A/Reference number: A34626; MUID:90179762; PMID:2310394
A/Accession: A34626
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-4 <KUR>
C/Keywords: neuropeptide

Query Match 33.3%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
||
Db 4 W 4

RESULT 7
B53284
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C/Accession: B53284
R/Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A/Title: Evolutionarily conserved organization and sequences of germline diversity and
A/Reference number: A53284; MUID:91342695; PMID:1678859
A/Accession: B53284
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-4 <HAB>
A/Cross-references: GB:S60737; NID:9233916; PIDN:AAB19518.1; PID:G233918
A/Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIP:60738)
C/Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
||
Db 2 W 2

RESULT 8
PT0661
T-cell receptor beta chain V-D-J region (121-1BV) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PT0661
R/Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A/Reference number: PT0509; MUID:91277601; PMID:1711558
A/Accession: PT0661
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-4 <FEE>
A/Experimental source: day 4 postnatal thymus, strain BALB/c
C/Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
|
DB 3 W 3

RESULT 9
A60803
neuropeptide - sea anemone (*Anthopleura elegantissima*)
C:Species: *Anthopleura elegantissima*
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: A60803
R:Graff, D.; Grimmelikhuijzen, C.J.P.
Brain Res. 442, 354-358, 1988
A:Title: Isolation of <Glu-Ser-Lu-Arg-Trip-NH-2, a novel neuropeptide from sea anemones.
A:Reference number: A60803; MUID:88222764; PMID:2897223
A:Accession: A60803
A:Molecule type: protein
A:Residues: 1-5 <GHA>
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:5/Modified site: amidated carboxyl end (Trp) #status experimental

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
|
DB 5 W 5

RESULT 10
G37196
bradykinin-potentiating peptide 7 - island jararaca
C:Species: *Bothrops insularis* (Island jararaca)
C>Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 05-Aug-1994
C:Accession: G37196
R:Cintrà, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A:Title: Primary structure and biological activity of bradykinin potentiating peptides 6
A:Reference number: A37196; MUID:90351557; PMID:2386615
A:Accession: G37196
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-5 <CIN>
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
|
DB 3 W 3

RESULT 11
PT0281
Ig heavy chain CRD3 region (clone 4-91C) - human (fragment)
C:Species: *Homo sapiens* (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0281
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0281
A:Molecule type: DNA

A:Residues: 1-5 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
|
DB 4 W 4

RESULT 12
PT0729
T-cell receptor beta chain V-D-J region (120-1J) - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0640; PT0685; PT0729
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0640
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: newborn thymus, strain BALB/c, clone 120-1J
A:Accession: PT0685
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE2>
A:Experimental source: day 18 fetal thymus, strain BALB/c, clone 154-1C
A:Accession: PT0729
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-5 <FE3>
A:Experimental source: newborn thymus, strain BALB/c, clone 135-1AG
C:Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
|
DB 5 W 5

RESULT 13
PT0580
T-cell receptor beta chain V-D-J region (159-2B) - mouse (fragment)
C:Species: *Mus musculus* (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0580
R:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601; PMID:1711558
A:Accession: PT0580
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-5 <FEE>
A:Experimental source: day 19 fetal thymus, strain BALB/c
C:Keywords: T-cell receptor

Query Match 33.3%; Score 11; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 W 3
|
DB 4 W 4

RESULT 14

I50412
 gene p20K protein - chicken (fragment)
 C;Species: Gallus gallus (Chicken)
 C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
 C;Accession: I50412
 R;Mao, P. L.; Beauchemin, M.; Bedard, P. A.
 J. Biol. Chem. 268, 8131-8139, 1993
 A;Title: Quiescence-dependent activation of the p20K promoter in growth-arrested chicken
 A;Reference number: A46643; MUID:93216790; PMID:8463325
 A;Accession: I50412
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-3 <MAO>
 A;Cross-references: GB:L02537; NID:G212616; PID:G212617
 C;Genetics:
 A;Gene: p20K

Query Match 27.3%; Score 9; DB 3; Length 3;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 MS 5
 ||
 Db 1 MS 2

RESULT 15

A32480
 achatin-I - giant African snail
 N;Contains: achatin-II
 C;Species: Achatina fulica (giant African snail)
 C;Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 17-Mar-1999
 C;Accession: A32480
 R;Kamatani, Y.; Minakata, H.; Kenny, P. T. M.; Iwashita, T.; Watanabe, K.; Funase, K.; Sur
 Biochem. Biophys. Res. Commun. 160, 1015-1020, 1989
 A;Title: Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica feru
 A;Reference number: A32480; MUID:89273551; PMID:2597281
 A;Accession: A32480
 A;Molecule type: protein
 A;Residues: 1-4 <KAM>
 A;Note: stereochemistry of the active form confirmed by chemical synthesis
 R;Ishida, T.; In, Y.; Inoue, M.; Yasuda-Kamatani, Y.; Minakata, H.; Iwashita, T.; Nomoto
 FEBS Lett. 307, 253-256, 1992
 A;Title: Effect of the D-Phe(2) residue on molecular conformation of an endogenous neuro
 (H-Gly-Phe-Ala-Asp-OH).
 A;Reference number: A44691; MUID:92354723; PMID:1644179
 A;Contents: annotation; X-ray crystallography, 0.85 angstroms
 A;Note: achatin-II has L-phenylalanine
 C;Keywords: D-amino acid
 P;2/Modified site: D-phenylalanine (Phe) #status experimental

Query Match 27.3%; Score 9; DB 2; Length 4;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2
 ||
 Db 1 GF 2

Search completed: April 22, 2003, 13:42:27
 Job time : 44 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:32:21 ; Search time 11 Seconds
(without alignments)
18.853 Million cell updates/sec

Title: US-09-674-716B-9

Perfect score: 33
Sequence: 1 GYWS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 38

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	45.5	4	1 OCP3 OCTMI	P58649 octopus min
2	15	45.5	5	1 UF01 MOUSE	P38639 mus musculus
3	11	33.3	5	1 BPP7 BOTIN	P30425 bothrops in
4	10	30.3	5	1 PAP2 PARMA	P81864 pardachirus
5	10	30.3	5	1 RE32 LITRU	P82073 litoria rub
6	9	27.3	4	1 ACHI ACHFU	P35904 achatina fu
7	9	27.3	4	1 OCP1 OCTMI	P58648 octopus min
8	8	24.2	3	1 GRW1 HUMAN	P01157 homo sapien
9	8	24.2	4	1 DCML PSECH	P19916 pseudomonas
10	7	21.2	4	1 FAR3 HIRME	P42562 hirudo medi
11	7	21.2	4	1 FAR4 HIRME	P42563 hirudo medi
12	7	21.2	4	1 FYRI ANTEL	P58706 anthopleura
13	7	21.2	5	1 AL14 CARMA	P81817 carcinus ma
14	7	21.2	5	1 PAPP ANTR	P41853 artiposthi
15	7	21.2	5	1 PRCT PERAM	P04373 periplaneta
16	7	21.2	5	1 PSK DAUCA	P58261 daucus caro
17	6	18.2	4	1 DCMS PSECH	P19918 pseudomonas
18	6	18.2	4	1 E0S1 HUMAN	P02731 homo sapien
19	6	18.2	4	1 PMRF MACNI	P01162 macrocallis
20	6	18.2	5	1 B10A CITER	P13071 citrobacter
21	6	18.2	5	1 B10B CITER	P12997 citrobacter
22	6	18.2	5	1 TPIS CANFA	P54714 canis famil
23	6	18.2	5	1 UXA4 CHLTR	P38005 chlamydia t
24	5	15.2	4	1 E103 LITRU	P82099 litoria rub
25	4	12.1	4	1 FFKA ANTEL	P58705 anthopleura
26	4	12.1	4	1 RM01 YEAST	P36515 saccharomyc
27	4	12.1	5	1 RE11 LITRU	P82070 litoria rub
28	4	12.1	5	1 RE21 LITRU	P82071 litoria rub
29	4	12.1	5	1 RE31 LITRU	P82072 litoria rub
30	4	12.1	5	1 UC22 MAIZE	P80628 zea mays (m
31	3	9.1	4	1 FLRF HIRME	P42561 hirudo medi
32	3	9.1	4	1 FLRN ANTEL	P58707 anthopleura
33	3	9.1	5	1 E104 LITRU	P82100 litoria rub

34 3 9.1 5 1 SUGA ACHDO P19991 acheta dome
35 2 6.1 3 1 THYL PIG P01151 sus scrofa
36 1 3.0 3 1 LUXE VIBFI P24272 vibrio fisc
37 1 3.0 4 1 TUFT HUMAN P01858 homo sapien
38 1 3.0 5 1 TRM3_ECOLI P13973 escherichia

ALIGNMENTS

RESULT 1
OCP3 OCTMI
ID OCP3 OCTMI STANDARD; PRT; 4 AA.
AC P58649;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-3/Ocp-4.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor.";
RL Peptides 21:623-630(2000).
CC -!- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-4 is a 1000 time less
CC active than Ocp-3.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- PTM: Ocp-4 has D-Ser instead of L-Ser.
CC -!- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI.
KW Hormone; D-amino acid.
FT MOD RES 2 2 D-SERINE (IN OCP-4).
SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 45.5%; Score 15; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 GYW 3
| | |
DB 1 GSW 3

RESULT 2
UF01 MOUSE
ID UF01 MOUSE STANDARD; PRT; 5 AA.
AC P38639;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Unknown protein from 2D-page of fibroblasts (P19) (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TISSUE=Fibroblast;
RX MEDLINE=95009907; PubMed=7523108;
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT "Separation and sequencing of familial and novel murine proteins
RT using preparative two-dimensional gel electrophoresis.";
RL Electrophoresis 15:735-745(1994).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.6, ITS MW IS: 19 kDa.
FT NON TER 5 5
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

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Query Match      45.5%; Score 15; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GYW 3
Db 3 GRW 5

RESULT 3
BPP7_BOTIN
ID BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Queimada jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidogaulia; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90351557; PubMed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom.";
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: THIS PEPTIDE BOTH INHIBITS THE ACTIVITY OF THE
CC ANGIOTENSIN-CONVERTING ENZYME AND ENHANCES THE ACTION OF
CC BRADYKININ BY INHIBITING THE KINASES THAT INACTIVATE IT.
CC IT ACTS AS AN INDIRECT HYPOTENSIVE AGENT.
DR PIR; G37196; G37196.
KW Hypotensive agent; Venom.
FT MOD RES 1
SQ SEQUENCE 5 AA; 629 MW; 776DC37326B00000 CRC64;

Query Match      33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 W 3
Db 3 W 3

RESULT 4
PAP2_PARMA
ID PAP2_PARMA STANDARD; PRT; 5 AA.
AC P81864;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pardaxin II (PXII) (Fragment).
OS Pardachirus marmoratus (Red sea mosses sole).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleurocteniformes;
OC Soleiidae; Soleidae; Pardachirus.
OX NCBI_TaxID=31087;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=87057369; PubMed=3782138;
RA Lazarovici P., Primor N., Loew L.M.;
RT "Purification and pore-forming activity of two hydrophobic
RT polypeptides from the secretion of the Red sea mosses sole (Pardachirus
RT marmoratus).";
RJ J. Biol. Chem. 261:16704-16713(1986).

CC -1- FUNCTION: EXHIBITS UNUSUAL SHARK REPELLENT AND SURFACTANT
CC PROPERTIES. FORMS VOLTAGE-DEPENDENT, ION-PERMEABLE CHANNELS
CC IN MEMBRANES. AT HIGH CONCENTRATION CAUSES CELL MEMBRANE LYSIS.
CC -1- SUBUNIT: MONOMER. IN AQUEOUS SOLUTION EXISTS AS A TETRAMER.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PARDAXIN FAMILY.
KW Toxin.
FT NON_TER 5
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match      30.3%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.1e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3
Db 1 GFF 3

RESULT 5
RE32_LITRU
ID RE32_LITRU STANDARD; PRT; 5 AA.
AC P82073;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Rubellidin 3.2.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Litoria electrica. Comparison with the skin peptides from Litoria
RT rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- FUNCTION: SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR ANTIBIOTIC
CC ACTIVITY.
CC -1- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
KW Amphibian skin.
SQ SEQUENCE 5 AA; 570 MW; 71A9C9C82A000000 CRC64;

Query Match      30.3%; Score 10; DB 1; Length 5;
Best Local Similarity 33.3%; Pred. No. 1.1e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYW 3
Db 2 GFF 4

RESULT 6
ACH1_ACHFU
ID ACH1_ACHFU STANDARD; PRT; 4 AA.
AC P35904;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Achatina-I.
OS Achatina fulica (Giant African snail).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
OC Achatinacea; Achatinidae; Achatina.
OX NCBI_TaxID=6530;
RN [1]
RP SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.
RX STRAIN=Perussac; TISSUE=Ganglion;
RX MEDLINE=89273551; PubMed=2597281;
RA Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K.,
RA Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P.,

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RA Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.;
RT "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina
RT fulica Ferussac containing a D-amino acid residue";
RL Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
RN [2]
RP CHARACTERIZATION.
RC STRAIN=Ferussac; TISSUE=Heart atrium;
RX MEDLINE=91264856; PubMed=1675568;
RA Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
RA Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
RT "Purification of achatin-I from the atria of the African giant snail,
RT Achatina fulica, and its possible function";
RL Biochem. Biophys. Res. Commun. 177:847-853(1991).
RN [3]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=93014529; PubMed=1399265;
RA Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H.,
RA Ishida T., Nomoto K.;
RT "Crystal structure and molecular conformation of achatin-I
RT (H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
RT D-amino acid residue";
RL Int. J. Pept. Protein Res. 39:258-264(1992).
CC -I- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
CC AND PRODUCES A SPIKE BROADENING OF THE IDENTIFIED HEART EXCITATORY
CC NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
CC HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
DR PIR; A32480; A32480.
KW Hormone; D-amino acid.
FT MOD RES 2 2 D-PHENYLALANINE.
SQ SEQUENCE 4 AA; 408 MW; 6AADD9C810000000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2
|:
DB 1 GF 2

RESULT 7
OCPI_OCTMI STANDARD; PRT; 4 AA.
AC P58648;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cardioactive peptides Ocp-1/Ocp-2.
OS Octopus minor (Octopus).
OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Octopoda;
OC Incirrata; Octopodidae; Octopus.
OX NCBI_TaxID=89766;
RN [1]
RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.
RC TISSUE=Brain;
RX MEDLINE=20336815; PubMed=10876044;
RA Iwakoshi E., Hisada M., Minakata H.;
RT "Cardioactive peptides isolated from the brain of a Japanese octopus,
RT Octopus minor";
RL Peptides 21:623-630(2000).
CC -I- FUNCTION: Cardioactive; has both positive chronotropic and
CC inotropic effects on the heart. Ocp-2 is a 1000 time less
CC active than Ocp-1.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- PTM: Ocp-2 has L-Phe instead of D-Phe.
CC -I- MASS SPECTROMETRY: MW=395.2; METHOD=WALDI.
KW Hormone; D-amino acid.
FT MOD RES 2 2 D-PHENYLALANINE.
SQ SEQUENCE 4 AA; 394 MW; 6AA879C810000000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2
|:
DB 1 GF 2

RESULT 8
GRWM_HUMAN STANDARD; PRT; 3 AA.
ID GRWM_HUMAN
AC P01157;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE Growth-modulating peptide.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=77162369; PubMed=858356;
RA Schlesinger D.H., Pickart L., Thaler M.M.;
RT "Growth-modulating serum tripeptide is glycyl-histidyl-lysine";
RL Experientia 33:324-325(1977).
CC -I- MISCELLANEOUS: THIS SERUM TRIPEPTIDE HAS BEEN FOUND TO STIMULATE
CC GROWTH OF SOME CELL TYPES AND TO INHIBIT OTHER TYPES IN VITRO.
DR PIR; A01421; GKHU.
SQ SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 3;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2
|:
DB 1 GH 2

RESULT 9
DCML_PSECH STANDARD; PRT; 4 AA.
AC P19916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase large chain (EC 1.2.99.2) (CO
DE dehydrogenase subunit L) (CO-DH L) (Fragment).
GN CUTL.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group.
OX NCBI_TaxID=290;
RN [1]
RP SEQUENCE.
RX MEDLINE=90055678; PubMed=2818128;
RA Kraut M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydrotrophic bacteria";
RL Arch. Microbiol. 152:335-341(1989).
CC -I- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
CC dioxide.
CC -I- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
CC acceptor.
CC -I- COFACTOR: Molybdenum (molybdopterin).
CC -I- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
CC SMALL.
DR PIR; PLO140; PLO140.
KW Oxidoreductase; Molybdenum.
FT NON TER 4 4
SQ SEQUENCE 4 AA; 441 MW; 7761E876F0000000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 4;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GY 2

DB 2 GH 3

RESULT 10

FAR3_HIRME

ID FAR3_HIRME STANDARD; PRT; 4 AA.

AC P42562;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE FMRFamide-like neuropeptide YMRP-amide.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

OX NCBI_TaxID=6421;

RN [1]

RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933;

RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of RFamide neuropeptides in the medicinal leech.;"

RL Peptides 12:897-908(1991).

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 4

SQ SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;

Query Match

Best Local Similarity 21.2%; Score 7; DB 1; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2

DB 1 Y 1

RESULT 11

FAR4_HIRME

ID FAR4_HIRME STANDARD; PRT; 4 AA.

AC P42563;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE FMRFamide-like neuropeptide YMRP-amide.

OS Hirudo medicinalis (Medicinal leech).

OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;

OC Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.

OX NCBI_TaxID=6421;

RN [1]

RP SEQUENCE.

RX MEDLINE=92195954; PubMed=1686933;

RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

RT "Identification of RFamide neuropeptides in the medicinal leech.;"

RL Peptides 12:897-908(1991).

CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)

CC FAMILY.

KW Neuropeptide; Amidation.

FT MOD_RES 4

SQ SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;

Query Match

Best Local Similarity 21.2%; Score 7; DB 1; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2

DB 1 Y 1

RESULT 12

FYRI_ANTEL

ID FYRI_ANTEL STANDARD; PRT; 4 AA.

AC P58706;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DE Antho-Riamide I [Contains: Antho-Riamide II].

OS Anthopleura elegansissima (Sea anemone).

OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;

OC Nynanthaeae; Actiniidae; Anthopleura.

OX NCBI_TaxID=6110;

RN [1]

RP SEQUENCE.

RX MEDLINE=92270459; PubMed=1821096;

RA Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.;

RT "Isolation of two novel neuropeptides from sea anemones: the unusual,

biologically active L-3-phenylacetyl-tyr-Arg-Ile-NH2 and its

des-phenylacetyl fragment Tyr-Arg-Ile-NH2.;"

RL Peptides 12:1165-1173(1991).

RN [2]

RP FUNCTION.

RX MEDLINE=93391436; PubMed=8397415;

RA McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.;

RT "The expansion behaviour of sea anemones may be coordinated by two

inhibitory neuropeptides, Antho-Kamide and Antho-Riamide.;"

Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).

CC -!- FUNCTION: Inhibits spontaneous contractions in several muscle

groups. May be involved in the expansion phase of feeding

behaviour in sea anemones.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Neuron-specific.

DR InterPro; IPR01023; Hsp70.

KW Neuropeptide; Amidation.

FT CHAIN 1 4

FT MOD_RES 2 4

FT MOD_RES 1 1

FT MOD_RES 4 4

SQ SEQUENCE 4 AA; 598 MW; 60441B59A0000000 CRC64;

Query Match

Best Local Similarity 21.2%; Score 7; DB 1; Length 4;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2

DB 2 Y 2

RESULT 13

ALI4_CARMA

ID ALI4_CARMA STANDARD; PRT; 5 AA.

AC P81817;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DE Carcinus maenas (Common shore crab) (Green crab).

OS Carcinus maenas (Common shore crab) (Green crab).

OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;

OC Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;

OC Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.

OX NCBI_TaxID=6759;

RN [1]

RP SEQUENCE.

RX MEDLINE=98121193; PubMed=9461295;

RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.;

RT "Isolation and identification of multiple neuropeptides of the

allatostatin superfamily in the shore crab Carcinus maenas.;"

Eur. J. Biochem. 250:727-734(1997).

CC -!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD RES 5 5 AMIDATION (POTENTIAL).
 SQ SEQUENCE 5 AA; 586 MW; 672879D5AB300000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2

Db 1 Y 1

RESULT 14

FARP_ARTTR STANDARD; PRT; 5 AA.

ID FARP_ARTTR STANDARD; PRT; 5 AA.
 AC P41853;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide RYRFP-amide.
 OS Artiposatha triangulata.
 OC Eukaryota; Metazoa; Platyhelminthes; Turbellaria; Seriata; Tricladida;
 OC Terricola; Geoplanidae; Arthurdendyus.
 OX NCBI_TaxID=132421;
 RN [1]

RP SEQUENCE, AND SYNTHESIS.
 RX MEDLINE=94211927; PubMed=7909164;
 RA Maule A.G., Shaw C., Halton D.W., Curry W.J., Thim L.;
 RT "RYRFPamide: a turbellarian FMRFamide-related peptide (FARP).";
 RL Regul. Pept. 50:37-43(1994).

CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY
 KW Neuropeptide; Amidation.
 FT MOD RES 5 5 AMIDATION.
 SQ SEQUENCE 5 AA; 754 MW; 69D4004B46000000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2

Db 2 Y 2

RESULT 15

PRCT_PERAM STANDARD; PRT; 5 AA.

ID PRCT_PERAM STANDARD; PRT; 5 AA.
 AC P01373;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE Proctolin.
 OS Periplaneta americana (American cockroach),
 OS Limulus polyphemus (Atlantic horseshoe crab), and
 OS Carcinus maenas (Common shore crab) (Green crab).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blattodea; Blattidae; Periplaneta.
 OX NCBI_TaxID=6978, 6850, 6759;
 RN [1]

RP SEQUENCE.

RC SPECIES=P.americana;
 RX MEDLINE=76074708; PubMed=576;
 RA Starratt A.N., Brown B.E.;

RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
 in insects."
 RL Life Sci. 17:1253-1256(1975).
 RN [2]

RP BIOLOGICAL SOURCE.
 RC SPECIES=P.americana;

RX MEDLINE=81225865; PubMed=6113690;
 RA O'Shea M., Adams M.E.;
 RT "Pentapeptide (proctolin) associated with an identified neuron."
 RL Science 213:567-569(1981).
 RN [3]
 RP SEQUENCE.
 RC SPECIES=L.polyphemus;
 RX MEDLINE=90287800; PubMed=2356151;
 RA Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
 RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
 RA Shabanowitz J.;
 RT "Identification of proctolin in the central nervous system of the
 RT horseshoe crab, Limulus polyphemus."
 RL Peptides 11:205-211(1990).
 RN [4]
 RP SEQUENCE.
 RC SPECIES=C.maenas;
 RX MEDLINE=86232789; PubMed=2872661;
 RA Stangier J., Dirksen H., Keller R.;
 RT "Identification and immunocytochemical localization of proctolin in
 RT pericardial organs of the shore crab, Carcinus maenas."
 RL Peptides 7:67-72(1986).
 CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
 CC MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
 CC THE CRAB PERICARDIAL ORGANS.
 DR* PIR; A01644; HORCHA.
 DR PIR; A60411; A60411.
 KW Neuropeptide.

SQ SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;

Query Match 21.2%; Score 7; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2

Db 2 Y 2

Search completed: April 22, 2003, 13:40:08

Job time: 11 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:37:57 ; Search time 82 Seconds
(without alignments)
12.564 Million cell updates/sec

Title: US-09-674-716b-9
Perfect score: 33
Sequence: 1 GYWS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 4

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacterioph.*
17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6	18.2	5	10 Q99007	Q99007 hordeum vul
2	5	15.2	5	2 P83073	P83073 bacillus ce
3	3	9.1	5	13 P83308	P83308 gallus gall
4	2	6.1	4	11 Q08433	Q08433 rattus norv

ALIGNMENTS

RESULT 1
Q99007
ID Q99007 PRELIMINARY; PRT; 5 AA.
AC Q99007
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE Alpha-amylase (EC 3.2.1.1) (Fragment).
GN AMYL.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]_TaxID=4513;
RP SEQUENCE FROM N.A.
RC STRAIN=HIMALAYA; TISSUE=ALEURONE LAYER;
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic acid and abscisic acid in protoplasts prepared from mature barley aleurone layers";
RL Plant Mol. Biol. 16:713-721(1991).
CC -|- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -|- COPACTOR: BINDS A CALCIUM ION REQUIRED FOR ITS ACTIVITY.
CC -|- MISCELLANEOUS: THERE ARE AT LEAST 4 TYPES OF ALPHA-AMYLASE IN BARLEY.
DR EMBL; X54643; CAA38455.1; -.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Seed; Germination;
KW Calcium; Multigene family.
FT NON_TER 5
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 18.2%; Score 6; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 MS 5
Db 1 MA 2

RESULT 2

P83073
ID P83073 PRELIMINARY; PRT; 5 AA.
AC P83073
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE 88 kDa protein (Fragment).
OS Bacillus cereus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=1396;
RN [1]_TaxID=1396;
RP SEQUENCE
RC STRAIN=NCIMB 11796;
RA Browne N., Dowds B.C.A.;
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
FT NON_TER 5
SQ SEQUENCE 5 AA; 623 MW; 6B01AAA336F00000 CRC64;

Query Match 15.2%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 M 4
Db 1 M 1

RESULT 3

P83308
ID P83308 PRELIMINARY; PRT; 5 AA.
AC P83308
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE FMRFamide-like neuropeptide (LPLRF-amide).

OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;

RN [1]
 RP SEQUENCE AND SYNTHESIS.
 RC TISSUE=BRAIN;

RX PubMed=6137771;

RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
 RT "A novel active pentapeptide from chicken brain identified by
 RT antibodies to FMRamide";
 RL Nature 305:328-330(1983).

CC -|- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.

CC -|- SIMILARITY: BELONGS TO THE FARP (FMRPAMIDE RELATED PEPTIDE)
 CC FAMILY.

KW Neuropeptide.

SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match 9.1%; Score 3; DB 13; Length 5;

Best Local Similarity 0.0%; Pred.No. 6.7e+05;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 Y 2

Db 5 F 5

RESULT 4

Q08433

ID Q08433 PRELIMINARY; PRT; 4 AA.

AC Q08433;

DT 01-NOV-1996 (TRENBLrel. 01, Created)

DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)

DT 01-JAN-1999 (TRENBLrel. 09, Last annotation update)

DE UDP-glucuronosyltransferase, microsomal (EC 2.4.1.17) (UDPGT)

DE (Fragment).

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GUNN;

EX MEDLINE=91282758; PubMed=1840486;

RA Sato H., Aono S., Kashiwamata S., Koizumi O.;

RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the

RT hyperbilirubinemic Gunn rat.";

RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).

CC -|- FUNCTION: UDPGT IS OF MAJOR IMPORTANCE IN THE CONJUGATION AND

CC SUBSEQUENT ELIMINATION OF POTENTIALLY TOXIC XENOBIOTICS AND

CC ENDOGENOUS COMPOUNDS.

CC -|- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR

CC BETA-D-GLUCURONOSIDE.

CC -|- SUBCELLULAR LOCATION: MICROSOME.

DR EMBL; S38636; AAB19259.1; -.

KW Transferase; Glycosyltransferase; Microsome; Multigene family.

FT NON_TER 1 1

FT NON_TER 4 4

SQ SEQUENCE 4 AA; 473 MW; 633732C420000000 CRC64;

Query Match

Best Local Similarity 6.1%; Score 2; DB 11; Length 4;

Matches 0; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 M 4

Db 3 L 3

Search completed: April 22, 2003, 13:41:37

Job time : 82 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:32:01 ; Search time 33 Seconds
(without alignments)
20.189 Million cell updates/sec

Title: US-09-674-716B-9
Perfect score: 33
Sequence: 1 GYMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 24944

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq 101002.*
1: /SID82/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
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21: /SID82/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID82/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID82/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	100.0	5	21	Light chain CDR H1
2	29	87.9	5	15	Murine anti-human
3	27	81.8	5	17	Humanised monoclon
4	27	81.8	5	20	Tumour antigen ant
5	27	81.8	5	22	Anti-TANGO 268 scf
6	27	81.8	5	23	Human FAPalpha spe
7	27	81.8	5	23	Anti-(MCP)-1 antib
8	25	75.8	5	16	MAB 55.1 heavy cha
9	24	72.7	4	23	Murine MC-1 antibo
10	24	72.7	5	16	ScFv(FWP51) CDR1H.

11	24	72.7	5	18	AAW23429	CDR-1 of rW12 heavy
12	24	72.7	5	20	AAW93474	mak TPC8 hypervari
13	24	72.7	5	22	AB62861	Anti-SAF-1 antibody
14	24	72.7	5	23	AB07357	22A5 IGM heavy cha
15	23	69.7	5	16	ABW74929	H-CDR-1 of anti-id
16	23	69.7	5	16	AAW74931	H-CDR-1 of anti-id
17	23	69.7	5	18	AAW24546	CDR #1 of r101-2 h
18	23	69.7	5	19	AAW83024	Anti-Fas MAB HFE7A
19	23	69.7	5	19	AAW62192	Mouse anti-HM1.24
20	23	69.7	5	19	AAW57588	Chimeric H chain V
21	23	69.7	5	19	AAW44181	Monoclonal antibody
22	23	69.7	5	20	AAV02550	Artificial CDR(1)
23	23	69.7	5	20	AAV05045	Tumour antigen ant
24	23	69.7	5	20	AAW83632	Mouse humanised an
25	23	69.7	5	21	AAW19754	Erythropoietin rec
26	23	69.7	5	21	AAW14741	Mouse anti-Fas ant
27	23	69.7	5	21	AAW12174	Human CDR1 for IL-
28	23	69.7	5	21	AAW90891	Murine anti-Fas an
29	23	69.7	5	21	AAW92158	Murine 15B8 heavy
30	23	69.7	5	21	AAW80139	Chimeric anti-CD25
31	23	69.7	5	21	AAW77518	Antibody L chain V
32	23	69.7	5	22	AAO14422	CD25 binding prote
33	23	69.7	5	22	AAW67116	Amino acid sequenc
34	23	69.7	5	22	AAW63398	Amino acid sequenc
35	23	69.7	5	22	AAW64780	Anti-PTHrP Ab VH C
36	23	69.7	5	22	AAW76894	Human PTHrP mouse
37	23	69.7	5	22	AAW76913	Human PTHrP mouse
38	23	69.7	5	22	AAW76932	Human PTHrP mouse
39	23	69.7	5	22	AAW61281	Anti-TANGO 268 scf
40	23	69.7	5	23	ABW95192	Human joint diseas
41	23	69.7	5	23	ABW74860	Humanised anti-Fas
42	23	69.7	5	23	ABW74906	Humanised anti-Fas
43	23	69.7	5	23	AAU11183	Mouse antibody Act
44	22	66.7	5	22	AAU05472	Synthetic pentapep
45	21	63.6	5	18	AAW19405	Tissue factor pept

ALIGNMENTS

RESULT 1
AAV32257
ID AAV32257 standard; Peptide; 5 AA.
AC AAV32257;
XX
XX
15-FEB-2000 (first entry)
DT
XX
XX
Light chain CDR H1 of mouse anti-CD23 MAb C11.
DE
XX
XX
CD23; FCERII; IgE receptor; monoclonal antibody; C11; mouse;
KW monoclonal antibody; chimeric antibody; humanised antibody;
KW complementarity determining region; CDR; autoimmune disease;
KW inflammation; arthritis; lupus erythematosus; multiple sclerosis;
KW Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;
KW urticaria; nephrotic syndrome; glomerulonephritis;
KW inflammatory bowel disease; ulcerative colitis; Crohn's disease;
KW Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;
KW graft-versus-host disease; COPD; bronchitis; diabetes;
KW B-cell malignancy; therapy.
XX
XX
Mus musculus.
OS
XX
PN WO9558679-A1.
XX
PD 18-NOV-1999.
XX
XX
PF 07-MAY-1999; 99WO-GB01434.
XX
PR 09-MAY-1998; 98GB-0009839.
XX
PA (GLAX) GLAXO GROUP LTD.
XX

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 DR N-PSDB; AA234742.
 XX
 PT Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis -
 XX
 PS Claim 1; Page 40; 81pp; English.
 XX
 CC This sequence represents complementarity determining region 1
 CC (CDR H1) of the heavy chain of murine anti-CD23 (FCERII) monoclonal
 CC antibody C11 (see also AAY32263). The invention provides altered
 CC antibodies, such as chimeric or humanised antibodies, which comprise
 CC sufficient of the amino acid sequences of C11 light and heavy chain
 CC CDRs (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies
 CC are used to block soluble CD23 formation for treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, insulinitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (clabated). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 33; DB 21; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWMS 5
 Db 1 GYWMS 5
 RESULT 2
 AAR62882
 ID AAR62882 standard; peptide; 5 AA.
 XX
 AC AAR62882;
 XX
 DT 18-JUL-1995 (first entry)
 XX
 DE Murine anti-human atherosclerotic plaque MAB Z2D3 VH CDR1.
 XX
 KW Atherosclerosis; atherosclerotic plaque; anti-hydroxysteroid antibody;
 KW murine monoclonal antibody; heavy chain variable region: CDR1;
 KW complementarity determining region; imaging; plaque ablation.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Region 1..5
 FT /label= CDR1
 XX
 PN WO9425053-A.
 XX
 PD 10-NOV-1994.
 XX
 PF 26-APR-1994; 94WO-US04641.
 XX
 PR 26-APR-1993; 93US-0053451.
 XX
 PA (SCOT-) SCOTGEN BIOPHARMACEUTICALS INC.
 XX
 PI Calenoff E, Chen FW, Dittlow CC;
 XX WPI; 1994-357904/44.
 DR

DR N-PSDB; AAQ78734.
 XX
 PT New antigen comprising hydroxy-steroid and quat. ammonium salt -
 PT and related antibodies, useful e.g. for imaging, ablating or
 PT treating atherosclerotic plaque, and detecting plaque specific
 PT antibodies
 XX
 PS Claim 199; Page 147; 289pp; English.
 XX
 CC Mice were immunised with an extract of human atherosclerotic plaque,
 CC then spleen cells were fused with SP2/O1-Ag-14 myeloma cells.
 CC Hybridomas were screened by ELISA for reactivity with the immunogen
 CC and clone Z2D3 was isolated. The Z2D3 antibody reacts specifically
 CC with atherosclerotic tissue; it recognises a non-protein antigen
 CC containing cholesterol (or similar steroid that is a substrate for
 CC cholesterol oxidase) and a tertiary ammonium salt (pref. a
 CC phosphatidylcholine or related compound that is a substrate for
 CC phospholipase C). The CDR sequences for the heavy and light chains
 CC of Z2D3 were determined; peptides comprising the CDRs are claimed,
 CC including chimeric (CDR-grafted) murine-human antibodies.
 XX
 SQ Sequence 5 AA;
 Query Match 87.9%; Score 29; DB 15; Length 5;
 Best Local Similarity 80.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GYWMS 5
 Db 1 GYWMS 5
 RESULT 3
 AAR97316
 ID AAR97316 standard; peptide; 5 AA.
 XX
 AC AAR97316;
 XX
 DT 15-OCT-1996 (first entry)
 XX
 DE Humanised monoclonal antibody heavy chain CDR.
 XX
 KW Monoclonal antibody; humanised; mouse; framework region; FR; CDR;
 KW complementary determining region; anti-carcinoembryonic antigen;
 KW CEA; diagnosis; imaging; therapy; immune response.
 XX
 OS Mus musculus.
 XX
 PN WO9611013-A1.
 XX
 PD 18-APR-1996.
 XX
 PF 28-SEP-1995; 95WO-US11964.
 XX
 PR 05-OCT-1994; 94US-0318157.
 XX
 PA (IMMU-) IMMUNOMEDICS INC.
 XX
 FT Armour KL, Hansen HJ;
 XX
 DR WPI; 1996-209653/21.
 XX
 CC New humanised anti-CEA monoclonal antibody - having engrafted murine
 CC CDRs, used for diagnosis, imaging and therapy of CEA-producing
 CC cancers
 XX
 PS Claim 5; Page 38; 62pp; English.
 XX
 CC New humanised monoclonal antibodies (MABs) comprising the
 CC complementary determining regions (CDRs) of a parental murine class
 CC III anti-carcinoembryonic (CEA) MAB engrafted to the framework
 CC regions (FRs) of a heterologous antibody which can be derived from
 CC any species including human, retain the anti-CEA binding specificity

CC of the parental murine MAb but are less immunogenic in a human
 CC subject than the parental MAb. The humanised antibodies can be used
 CC in diagnosis, imaging and therapy of CEA-producing cancers and
 CC patients receiving the humanised antibodies and conjugates show
 CC improved therapeutic results, decreased immune responses and
 CC decreased immune-mediated adverse effects compared to the parent
 CC antibody. This sequence is a murine derived CDR region which
 CC corresponds to CDR 1 in the heavy chain of the humanised MAb. See
 CC AAR97313-97333.

SQ Sequence 5 AA;
 Query Match 81.8%; Score 27; DB 17; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
 Db |||||
 2 YWMS 5

RESULT 4
 ID AAY05038 standard; peptide; 5 AA.
 AC AAY05038;
 DT 16-JUN-1999 (first entry)
 DE Tumour antigen antibody heavy chain CDR1 clone F15.
 KW Tumour antigen; antibody; CDR; complementarity determining region;
 KW binding molecule identification; tumour-specific binding polypeptide;
 KW cancer therapy; heavy chain.
 OS Homo sapiens.
 XX WO9906834-A2.
 PN 11-FEB-1999.
 PD 04-AUG-1998; 98WO-US16280.
 PF 04-AUG-1997; 97US-0905825.
 PR 04-AUG-1997; 97US-1112222.
 XX (IXSY-) IXSYS INC.
 PA Huse WD, Watkins JD, Wu H;
 PI WPI; 1999-153951/13.
 DR N-PSDB; AAX28215.
 XX Identifying binding molecules for ligands, particularly tumour
 PT antigens - by selectively immobilising a population of binding
 PT molecules to a solid support and screening for binding to two or
 PT more ligands
 XX Claim 15; Page 60; 80pp; English.
 PS This sequence represents a heavy chain complementarity determining
 XX region (CDR) from a tumour antigen specific antibody.
 CC The invention relates to a method for identifying a binding molecule
 CC having selective affinity for a ligand comprising: (a) selectively
 CC immobilising a diverse population of binding molecules to a solid
 CC support; (b) simultaneously contacting the diverse population immobilised
 CC on the solid support with 2 or more ligands; and (c) determining at least
 CC one binding molecule which selectively binds to one or more of the
 CC ligands. The method allows for the rapid and efficient methods for the
 CC identification of binding molecules which exhibit selective affinity for
 CC one or more ligands of interest. They are used particularly for
 CC identifying tumour-specific binding polypeptides which can be used as
 CC targeting agents for cancer therapy that minimises impact on non-tumour

CC tissues.
 XX Sequence 5 AA;
 SQ Query Match 81.8%; Score 27; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
 Db |||||
 2 YWMS 5

RESULT 5
 ID AAB61293 standard; Peptide; 5 AA.
 AC AAB61293;
 DT 04-APR-2001 (first entry)
 DE Anti-TANGO 268 scFv CDR, SEQ ID NO: 61.
 XX Human; antibody; scFv; CDR; complementarity determining region;
 KW TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KW platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KW cancer.
 XX Homo sapiens.
 OS WO200100810-A1.
 PN 04-JAN-2001.
 PD 30-JUN-2000; 2000WO-US18152.
 PF 30-JUN-1999; 99US-0345468.
 PR 06-DEC-1999; 99US-0454824.
 PR 14-FEB-2000; 2000US-0503387.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA Busfield SJ, Villelall J, Jandrot-Perrus M, Vainchenker W, Gill DS;
 PI Qian MD, Kingsbury G;
 DR WPI; 2001-080877/09.
 XX New genes encoding human platelet-expressed collagen receptor,
 PT glycoprotein VI, and its modulators, useful for preventing, treating
 PT and diagnosing hemorrhagic disorders, thrombotic diseases and
 PT immunological disorders -
 XX Claim 31; Page 102; 227pp; English.
 PS The present sequence is given in a specification relating to an isolated
 CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
 CC and polypeptides and their modulators, e.g. antisense nucleic acids,
 CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders
 CC (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
 CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 CC infarction), immunological diseases (e.g. platelet disorder) and
 CC embryonic liver disorders. Preferably they are used to prevent acute
 CC cardiac ischaemia following angioplasty and metastatic cancers,
 CC especially of the colon and liver.
 XX

SQ Sequence 5 AA;

Query Match 81.8%; Score 27; DB 22; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
 ||||
 Db 2 YWMS 5

RESULT 6

AA017609

ID AA017609 standard; Peptide; 5 AA.

XX AC AA017609;

XX AC AA017609;

DT 08-AUG-2002 (first entry)

XX Human FAPalpha specific VL region from VH50 CDR1 peptide.

XX Human: FAPalpha; fibroblast activating protein alpha; antibody; Ab;
 gene therapy; cancer; wound healing; inflammation; cytostatic.

XX Homo sapiens.

XX WO200168708-A2.

XX 20-SEP-2001.

XX 16-MAR-2001; 2001WO-EP04716.

XX 17-MAR-2000; 2000DE-1013286.

XX 11-SEP-2000; 2000GB-0022216.

XX (BOEH) BOEHRINGER INGELHEIM PHARMA KG.

XX Park J, Garin-Chesa P, Pfizenmaier K, Moosmayer D, Mersmann M;
 Schmidt A;

XX WPI; 2002-041180/05.

XX N-PSDB; AAL46554.

XX New human humanized antibody that specifically binds to fibroblasts
 activating protein alpha, useful for treating cancer or tumor, and for
 imaging tumors associated with activated stromal fibroblasts, e.g. lung
 or breast cancer

XX Disclosure; Fig 6C; 109pp; English.

XX The present invention relates to a human or humanised antibody (Ab) which
 specifically binds to fibroblast activating protein alpha (FAPalpha). The
 antibodies are useful for preparing a composition for the treatment of
 cancer, and for imaging tumours associated with activated stromal
 fibroblasts, such as colorectal cancer, non-small-cell lung cancer,
 breast cancer, head and neck cancer, ovarian cancer, lung cancer, bladder
 cancer, pancreatic cancer and metastatic brain cancer, and diseases
 associated with the same, such as inflammation and wound healing. The
 present sequence is a peptide described in the exemplification of the
 invention.

SQ Sequence 5 AA;

Query Match 81.8%; Score 27; DB 23; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
 ||||
 Db 2 YWMS 5

RESULT 7

AAU75739

ID AAU75739 standard; Peptide; 5 AA.

XX AC AAU75739;

XX DT 08-MAY-2002 (first entry)

XX Anti-(MCP)-1 antibody heavy chain protein hypervariable region CDR1.

XX Human; antibody; MCP; monocyte chemoattractant; antiasthmatic;
 anti-allergic; anti-inflammatory; idiopathic thrombocytopaenia;
 immunosuppressive; cytostatic; vasotropic; antiarteriosclerotic;
 antirheumatic; antiarthritic; osteopathic; antigen-binding site;
 immunoglobulin heavy chain; monocyte migration; T cell migration;
 CC-type chemokine; etaxin; allergic rhinitis; cancer;
 hypersensitivity response; allergic contact dermatitis;
 inflammatory disease; asthma; psoriasis; COPD; osteoporosis;
 inflammatory bowel disease; multiple sclerosis; autoimmune disease;
 rheumatoid arthritis; diabetes; systemic lupus erythematosus;
 bone disease; osteoporosis; osteoarthritis; periodontal disease;
 hematological disorder; haemolytic anaemia; graft rejection;
 leucocyte infiltration; restenosis; arteriosclerosis; CDR1.

XX Homo sapiens.

XX WO200202640-A2.

XX 10-JAN-2002.

XX 29-JUN-2001; 2001WO-EP07468.

XX 30-JUN-2000; 2000GB-0016138.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Hiestand P, Hofstetter H, Payne TG, Urfer R, Di Padova FE;
 WPI; 2002-164525/21.

XX New compound that binds human monocyte chemoattractant protein-1,
 useful e.g. for treating inflammation, comprises immunoglobulin chains
 with specific hypervariable regions

XX Claim 1; Page 35; 42pp; English.

XX This invention relates to a molecule that binds MCP-1 (human monocyte
 chemoattractant protein-1). The molecule has at least one antigen
 binding site comprising at least one immunoglobulin (Ig) heavy and/or
 light chain variable domain (Vh, Vl). The antibody of the invention
 inhibits binding of MCP-1 (and also etaxin) to specific receptors, so
 preventing migration of monocytes and T cells. These are human
 antibodies with very high affinity for MCP-1, but no significant
 reaction with other human CC-type chemokines or MCP-1 from other
 species. The MCP-1 binding molecules, specifically antibodies that cross
 -react with etaxin, are used to prevent or treat MCP-1 or etaxin-
 mediated disorders, particularly those that involve migration or
 activation of monocytes and T cells, e.g. allergies (allergic rhinitis,
 hypersensitivity responses, allergic contact dermatitis), inflammatory
 diseases (asthma, psoriasis, COPD, inflammatory bowel disease,
 multiple sclerosis), autoimmune disease (rheumatoid arthritis, diabetes,
 systemic lupus erythematosus), diseases of bone and cartilage
 (osteoporosis, osteoarthritis, periodontal disease) haematological
 disorders (haemolytic anaemia, idiopathic thrombocytopaenia) graft
 rejection, cancers that include leucocyte infiltration, (re)stenosis,
 arteriosclerosis, osteoporosis and many other diseases listed in the
 specification. The present sequence represents the human anti-(MCP)
 antibody heavy chain sequence hypervariable domain peptide CDR1 of the
 invention.

XX Sequence 5 AA;

Query Match 81.8%; Score 27; DB 23; Length 5;

```

Best Local Similarity 100.0%; Pred. No. 7.8e+05; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 0;

QY 2 YWMS 5
DB 2 YWMS 5

RESULT 8
AAR76079
ID AAR76079 standard; Peptide; 5 AA.
AC AAR76079;
XX
XX
XX 21-NOV-1995 (first entry)
XX
XX MAb 55.1 heavy chain CDR1.
DE
XX
XX Antigen binding structure; complementarity determining region; CDR;
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin.
XX
XX Mus sp.
OS
XX
XX WO9515382-A.
XX
XX PD 08-JUN-1995.
XX
XX PF 29-NOV-1994; 94WO-GB02610.
XX
XX PR 03-JUN-1994; 94GB-0011089.
XX PR 03-DEC-1993; 93GB-0024819.
XX
XX (ZENE) ZENECA LTD.
XX
XX PI Blakey DC, Boot C, Copley CG, Hall SM, Paterson DS;
PI Rose MS, Wright AF;
XX
XX WPI; 1995-215262/28.
XX
XX Antigen binding structures containing CDRs recognising the CA55.1
PT antigen - produced by hybridomas and host cells, for use in the
PT diagnosis and therapy of cancer
XX
XX Claim 2; Page 96; 121pp; English.
XX
XX An antigen binding structure is based on the CDRs (given in AAR76078-
CC 84) of the heavy and light chains of MAb 55.1 (ECACC 93081901),
CC which recognises the colorectal tumor-associated antigen CA55.1.
CC It is optionally humanized and in the form F(ab')2, F(ab)'', Fab,
CC Fv, scFv or V-min, and is produced in transgenic animals or plants.
XX
XX Sequence 5 AA;

Query Match 75.8%; Score 25; DB 16; Length 5;
Best Local Similarity 75.0%; Pred. No. 7.8e+05; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0;

QY 1 GYWM 4
DB 1 GYWI 4

RESULT 9
AAE22200
ID AAE22200 standard; peptide; 4 AA.
XX
XX AAE22200;
XX
XX 25-JUL-2002 (first entry)
DT
XX

```

```

DE Murine MC-1 antibody heavy chain variable domain (VH) CDR1 peptide.
XX
XX Chemokine construct; human immunodeficiency virus 1; allergic disease;
KW skin disease; immunological disorder; autoimmune disease; psoriasis;
KW multiple sclerosis; rheumatoid arthritis; inflammatory bowel disease;
KW diabetes; skin inflammation; atopic dermatitis; inflammatory disease;
KW inflammatory renal disease; HIV-1; transplant rejection; murine; CDR1;
KW heavy chain variable domain; VH; complementarity determining region 1;
KW MC-1; antibody.
XX
XX Mus sp.
OS
XX WO200220615-A2.
XX
XX 14-MAR-2002.
PD
XX
XX 10-SEP-2001; 2001WO-EP10433.
XX
XX 08-SEP-2000; 2000EP-0119694.
XX PR 05-SEP-2001; 2001US-0948004.
XX
XX (MICR-) MICROMET AG.
XX
XX Mack M, Schloendorff D, Spring M;
XX WPI; 2002-362240/39.
XX
XX Use of an antibody and/or chemokine construct that binds to a chemokine
PT receptor, for eliminating cells latently infected with primate
PT immunodeficiency virus, or treating, preventing and alleviating immune
PT disorders -
XX
XX Disclosure; Page 116; 117pp; English.
XX
XX The invention relates to the use of an antibody and/or chemokine
CC construct that binds a chemokine receptor for preparing a pharmaceutical
CC composition for eliminating cells latently infected with a primate
CC immunodeficiency virus (e.g. human immunodeficiency virus (HIV-1)). They
CC are used in gene therapy and as vaccines. The antibody and/or chemokine
CC construct is also used for preparing a pharmaceutical composition for
CC treating, preventing and/or alleviating immunological disorders
CC including autoimmune diseases (e.g. multiple sclerosis, type I diabetes
CC and rheumatoid arthritis), allergic diseases, skin diseases (e.g. skin
CC inflammation, atopic dermatitis and psoriasis), inflammatory diseases
CC such as inflammatory joint diseases (chronic arthritis), inflammatory
CC renal diseases and inflammatory bowel diseases and graft versus host
CC and transplant rejections. The present sequence is murine MC-1 antibody
CC heavy chain variable domain (VH) complementarity determining region 1
CC (CDR1) peptide.
XX
XX Sequence 4 AA;
XX
XX Query Match 72.7%; Score 24; DB 23; Length 4;
XX Best Local Similarity 75.0%; Pred. No. 7.8e+05;
XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
DB 1 YWMN 4

RESULT 10
AAR85499
ID AAR85499 standard; Peptide; 5 AA.
XX
XX AAR85499;
XX
XX 16-MAR-1996 (first entry)
DT
XX
XX SCFv(FWP51) CDR1H.
DE
XX
XX Single chain antibody; scFv; antibody engineering; antitumour;
KW tumour antigen binding; cytotoxic T-lymphocyte; cell targeting;

```

KW monoclonal antibody; cancer; adoptive immunotherapy;
 KW complementarity determining region; CDR.
 XX
 OS Synthetic.
 XX
 FN WO9530014-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 20-APR-1995; 95WO-EP01494.
 XX
 PR 02-MAY-1994; 94EP-0810244.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Groner B, Moritz D;
 XX
 DR WPI; 1995-393085/50.
 XX
 PT New bifunctional proteins for use in killing tumour cells - contg. a
 PT tumour antigen binding domain, a hinge region and a zeta chain
 PT derived from a T-cell antigen receptor
 XX
 PS Disclosure; Page 6; 46pp; English.
 XX
 CC Complementarity determining regions (CDRs) CDR1H, CDR2H and CDR3H
 CC (AAR85496-98) and CDR1L, CDR2L and CDR3L (AAR85502-04) are components
 CC of the heavy chain variable region and light chain variable region,
 CC respectively, of single chain antibody scFv(FWP51) (AAR85495). The CDRs
 CC are derived from mouse monoclonal antibody FWP51 (ECACC 90112118)
 CC directed to the human growth factor receptor HER2. The scFv is
 CC used as the tumour antigen binding domain of a bifunctional protein
 CC that is expressed in cytotoxic T-lymphocytes (CTLs), allowing
 CC adoptive immunotherapy of cancer.
 XX
 SQ Sequence 5 AA;
 Query Match 72.7%; Score 24; DB 16; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YWMS 5
 DB |||:
 2 YWMN 5
 RESULT 11
 AAW23429 AAW23429 standard; peptide; 5 AA.
 XX
 AC AAW23429;
 XX
 DT 23-APR-1998 (first entry)
 XX
 DE CDR-1 of rW12 heavy chain.
 XX
 KW Antibody; complementarity determining region; CDR; heavy chain; rat; CEA;
 KW rW12; anti-carcinoembryonic antigen; vaccine; immune response; cancer;
 KW therapy; idiotype region.
 XX
 OS Rattus sp.
 XX
 FN WO9734636-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 19-MAR-1997; 97WO-US04696.
 XX
 PR 20-MAR-1996; 96US-0013708.
 XX
 PA (IMMU-{ IMMUNOMEDICS INC.
 XX
 PI Hansen H, Leung S, Losman WJ;
 KW monoclonal antibody; cancer; adoptive immunotherapy;
 KW complementarity determining region; CDR.
 XX
 OS Synthetic.
 XX
 FN WO9530014-A1.
 XX
 PD 09-NOV-1995.
 XX
 PF 20-APR-1995; 95WO-EP01494.
 XX
 PR 02-MAY-1994; 94EP-0810244.
 XX
 PA (CIBA) CIBA GEIGY AG.
 XX
 PI Groner B, Moritz D;
 XX
 DR WPI; 1995-393085/50.
 XX
 PT New bifunctional proteins for use in killing tumour cells - contg. a
 PT tumour antigen binding domain, a hinge region and a zeta chain
 PT derived from a T-cell antigen receptor
 XX
 PS Disclosure; Page 6; 46pp; English.
 XX
 CC Complementarity determining regions (CDRs) CDR1H, CDR2H and CDR3H
 CC (AAR85496-98) and CDR1L, CDR2L and CDR3L (AAR85502-04) are components
 CC of the heavy chain variable region and light chain variable region,
 CC respectively, of single chain antibody scFv(FWP51) (AAR85495). The CDRs
 CC are derived from mouse monoclonal antibody FWP51 (ECACC 90112118)
 CC directed to the human growth factor receptor HER2. The scFv is
 CC used as the tumour antigen binding domain of a bifunctional protein
 CC that is expressed in cytotoxic T-lymphocytes (CTLs), allowing
 CC adoptive immunotherapy of cancer.
 XX
 SQ Sequence 5 AA;
 Query Match 72.7%; Score 24; DB 18; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 2 YWMS 5
 DB |||:
 2 YWMN 5
 RESULT 12
 AAW93474
 ID AAW93474 standard; Protein; 5 AA.
 XX
 AC AAW93474;
 XX
 DT 11-JUN-1999 (first entry)
 XX
 DE mAk TTC8 hypervariable domain heavy chain CDR1 protein fragment.
 XX
 KW Monoclonal antibody; hypervariable domain; heavy chain; CDR1; neutralise;
 KW Clostridium difficile; epitope; ligand domain; immunotherapy; disease;
 KW translocation domain; catalytic domain; humanised antibody; enterotoxin;
 KW toxin A; toxin B; pseudomembranous colitis.
 XX
 OS Synthetic.
 XX
 FN DE19739685-A1.
 XX
 PD 11-MAR-1999.
 XX
 PF 10-SEP-1997; 97DE-1039685.
 XX
 PR 10-SEP-1997; 97DE-1039685.
 XX
 PA (VEIC/) VON EICHEL-STREIBER C.
 XX
 PI Moos M, Von Eichel-Streiber C;
 XX
 DR WPI; 1999-182094/16.
 DR N-PSDB; AAX23235.
 XX
 PT Monoclonal antibodies specific for Clostridium difficile toxins -
 PT especially humanised antibodies for treating pseudomembranous
 PT colitis
 XX
 PS Claim 20; Page 8; 14pp; German.

CC This invention describes a novel monoclonal antibody that is directed
 CC against a Clostridium difficile toxin and recognises and neutralises
 CC an epitope in the ligand domain, translocation domain or catalytic
 CC domain of the toxin. Humanised antibodies are described which are
 CC expressed in plants and can be used for immunotherapy of diseases caused
 CC by Clostridium difficile enterotoxin (toxin A) or cytotoxin (toxin B),
 CC especially pseudomembranous colitis.

XX SQ Sequence 5 AA;
 Query Match 72.7%; Score 24; DB 20; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 YWMS 5
 |||:
 Db 2 YWMN 5

RESULT 13

AA62861
 ID AAB62861 standard; peptide; 5 AA.

XX AC AAB62861;

XX DT 15-MAY-2001 (first entry)

XX DE Anti-SAF-1 antibody 13G3 H chain V region CDR peptide SEQ ID 3.

XX KW Sialoadhesin factor-1; SAF-1; anti-SAF-1 monoclonal antibody; 13G3;
 KW 11G4; osteomyelitis; wound infection; sepsis; listeria monocytogene;
 KW Salmonella; Leishmania; heavy chain variable region; mouse;
 KW complementarity determining region; CDR.

XX OS Mus musculus.

XX FN WO200112646-A1.

XX PD 22-FEB-2001.

XX PF 18-AUG-2000; 2000WO-US22663.

XX PR 19-AUG-1999; 99US-0149753.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PA (SMIK) SMITHKLINE BEECHAM PLC.

XX PI Erickson-Miller CL, Holmes SD, King AG, Taylor AH;

XX DR WPI; 2001-211197/21.

XX DR N-PSDB; AAF62142.

XX PT New sialoadhesin factor-1 agonist antibody having the characteristic of
 PT monoclonal antibody 13G3 or 11G4 for treating osteomyelitis, deep
 PT seated wound infections and antibiotic resistant bacterial infections

XX PS Claim 22; Fig 1; 43pp; English.

XX CC This invention relates to sialoadhesin factor-1 (SAF-1) monoclonal
 CC antibodies 13G3 and 11G4. A neurophil-priming dose of SAF-1 agonist
 CC antibody or a pharmaceutical composition comprising the antibody is
 CC useful for treating or preventing an infectious disease state such as
 CC osteomyelitis, deep seated wound infections, sepsis, antibiotic resistant
 CC bacterial infection, viral infections and those involving intracellular
 CC pathogens and parasites such as listeria monocytogenes, salmonella and
 CC leishmania in a mammal. Nucleic acid sequences encoding the variable
 CC light chain and heavy chain peptide sequences are useful for mutagenic
 CC introduction of specific changes within the nucleic acid sequences
 CC encoding the (complementarity determining regions) CDRs or framework
 CC regions, and for incorporation of the resulting modified or fusion
 CC nucleic acid sequence into a plasmid for expression. The CDR-encoding
 CC regions comprising silent mutations are used in construction of humanized

CC antibodies or other engineered antibodies. The present sequence
 CC represents anti-SAF-1 monoclonal antibody 13G3 heavy chain variable
 CC region complementarity determining region peptide sequence.

XX SQ Sequence 5 AA;

Query Match 72.7%; Score 24; DB 22; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 YWMS 5
 |||:
 Db 2 YWMN 5

RESULT 14

ABB07357

ID ABB07357 standard; peptide; 5 AA.

XX AC ABB07357;

XX DT 09-APR-2002 (first entry)

XX DE 22A5 IGM heavy chain variable region CDR1 sequence.

XX KW Immunoglobulin; Ig; reperfusion; ischaemic injury; pathogenic; CDR;
 KW vasotrophic; antibody; 22A5; IGM; complementarity determining region.

XX OS Mus musculus.

XX PN WO200193892-A1.

XX PD 13-DEC-2001.

XX PF 08-JUN-2001; 2001WO-US18510.

XX PR 08-JUN-2000; 2000US-210272P.

XX PA (BLOO-) CENT BLOOD RES INC.

XX PI Carroll MC, Moore FD, Hechtman HB;

XX DR WPI; 2002-139643/18.

XX DR N-PSDB; ABA94514.

XX PT Treating or preventing immunoglobulin-mediated reperfusion or ischemic
 PT injury resulting from e.g. angioplasty or bypass surgery, by
 PT administering an inhibitor of pathogenic immunoglobulin and ischemic
 PT antigen interaction

XX PS Claim 54; Page 72; 77pp; English.

XX CC The invention provides a method of treating or preventing immunoglobulin-
 CC mediated reperfusion or ischemic injury in a subject. The method involves
 CC administering an inhibitor of an interaction between a pathogenic
 CC immunoglobulin, and an ischemic-specific antigen or a component of the
 CC complement pathway. The method is useful for treating or preventing
 CC immunoglobulin-mediated reperfusion or ischemic injury, in particular,
 CC injury that results following a naturally occurring episode, a surgical
 CC procedure (e.g. angioplasty, stenting procedure, atherectomy or bypass
 CC surgery), or in an injury that occurs in a cardiovascular tissue. The
 CC method is also useful for treating or preventing, in a subject, tissue
 CC damage following reperfusion caused by a pathogenic immunoglobulin, e.g.
 CC pathogenic IGMs. The present sequence represents the complementarity
 CC determining region (CDR) of a heavy chain variable region of 22A5 IGM, a
 CC pathogenic immunoglobulin.

XX SQ Sequence 5 AA;

Query Match 72.7%; Score 24; DB 23; Length 5;
 Best Local Similarity 75.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWMS 5
Db 2 YWMN 5

RESULT 15

AAR74929
ID AAR74929 standard; peptide; 5 AA.

XX AC AAR74929;
XX DT 19-JAN-1996 (first entry)

XX DE H-CDR-1 of anti-idiotypic antibody against human anticancer antibody.
XX KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
XX KW complementarity determining region.

XX OS Mus sp.

XX PN JP07101999-A.

XX PD 18-APR-1995.

XX PF 06-OCT-1993; 93JP-0272950.

XX PR 06-OCT-1993; 93JP-0272950.

XX PA (HAGI/) HAGIWARA Y.

XX DR WPI; 1995-182987/24.

XX PT Novel anti-idiotypic antibody against an human anticancer monoclonal
PT antibody - and DNA sequences encoding the antibody, useful in
PT pharmacology, medicine and biochemical fields.
XX PS Claim 1; Page 2; 28pp; Japanese.

XX CC A new anti-idiotypic antibody against a human anticancer monoclonal
CC antibody is claimed. This antibody contains in its heavy chain 3
CC complementarity determining regions CDR1 (AAR74929-R74931), CDR2
CC (AAR74932-R74935) and CDR3 (AAR74936-R74939), this is also true of the
CC light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2
CC (AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA
CC encoding it are useful in pharmacological, medical and biochemical
CC fields.

SQ Sequence 5 AA;

Query Match 69.7%; Score 23; DB 16; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YWM 4
Db 2 YWM 4

Search completed: April 22, 2003, 13:39:53
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:41:42 ; Search time 15 Seconds
(without alignments)
26.710 Million cell updates/sec

Title: US-09-674-716b-9

Perfect score: 33
Sequence: 1 GYMS 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 4813

Minimum DB seq length: 0

Maximum DB seq length: 5

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	81.8	5	US-09-977-797A-76	Sequence 76, Appl
2	27	81.8	5	US-09-832-312-61	Sequence 61, Appl
3	27	81.8	5	US-09-253-794-23	Sequence 23, Appl
4	24	72.7	5	US-09-968-561A-265	Sequence 265, App
5	24	72.7	5	US-09-155-106-1	Sequence 1, Appli
6	24	72.7	5	US-09-192-854-151	Sequence 151, App
7	23	69.7	5	US-09-423-800-62	Sequence 62, Appl
8	23	69.7	5	US-09-269-921-6	Sequence 6, Appli
9	23	69.7	5	US-09-977-797A-90	Sequence 90, Appl
10	23	69.7	5	US-10-182-018-62	Sequence 62, Appl
11	23	69.7	5	US-09-748-960-12	Sequence 12, Appl
12	23	69.7	5	US-09-832-312-49	Sequence 49, Appl
13	23	69.7	5	US-09-770-002-1	Sequence 1, Appli
14	20	60.6	5	US-09-291-417-40	Sequence 40, Appl
15	19	57.6	5	US-10-029-301-4	Sequence 4, Appli
16	18	54.5	4	US-09-750-754-14	Sequence 14, Appl
17	18	54.5	4	US-10-156-820-31	Sequence 31, Appl
18	18	54.5	5	US-09-750-754-3	Sequence 3, Appli
19	18	54.5	5	US-09-750-754-15	Sequence 15, Appl

20	18	54.5	5	12	US-10-156-820-34	Sequence 34, Appl
21	17	51.5	5	9	US-09-977-797A-88	Sequence 88, Appl
22	16	48.5	4	8	US-08-484-409-5	Sequence 5, Appli
23	16	48.5	4	9	US-09-882-781-15	Sequence 15, Appl
24	16	48.5	4	10	US-09-982-172-194	Sequence 194, App
25	16	48.5	4	10	US-09-929-924-41	Sequence 41, Appl
26	16	48.5	5	9	US-09-963-298-8	Sequence 8, Appli
27	16	48.5	5	9	US-09-291-417-38	Sequence 38, Appl
28	15	45.5	4	9	US-10-165-015-10	Sequence 10, Appl
29	15	45.5	4	10	US-09-853-918-19	Sequence 19, Appl
30	15	45.5	4	10	US-09-977-831-10	Sequence 10, Appl
31	15	45.5	5	9	US-10-105-930-67	Sequence 67, Appl
32	15	45.5	5	9	US-10-171-077-2	Sequence 2, Appli
33	15	45.5	5	9	US-09-788-006-95	Sequence 95, Appl
34	15	45.5	5	9	US-09-788-006-96	Sequence 96, Appl
35	15	45.5	5	9	US-09-788-006-97	Sequence 97, Appl
36	15	45.5	5	9	US-09-977-797A-80	Sequence 80, Appl
37	15	45.5	5	10	US-09-952-768-69	Sequence 69, Appl
38	15	45.5	5	10	US-09-952-768-70	Sequence 70, Appl
39	15	45.5	5	10	US-09-730-857-84	Sequence 84, Appl
40	14	42.4	4	9	US-09-264-516A-29	Sequence 29, Appl
41	14	42.4	4	9	US-09-758-426-58	Sequence 58, Appl
42	14	42.4	4	9	US-09-769-145-74	Sequence 74, Appl
43	14	42.4	4	9	US-09-758-198-58	Sequence 58, Appl
44	14	42.4	4	9	US-09-185-908-24	Sequence 24, Appl
45	14	42.4	4	9	US-10-119-537-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-09-977-797A-76
; Sequence 76, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR FILING DATE: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-76

Query Match 81.8%; Score 27; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy. 2 YWMS 5
Db 2 YWMS 5

RESULT 2

US-09-832-312-61
; Sequence 61, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312

;; CURRENT FILING DATE: 2001-04-09
;; PRIOR APPLICATION NUMBER: 09/610,118
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: 09/503,387
;; PRIOR FILING DATE: 2000-02-14
;; PRIOR APPLICATION NUMBER: 09/454,824
;; PRIOR FILING DATE: 1999-12-06
;; PRIOR APPLICATION NUMBER: 09/345,468
;; PRIOR FILING DATE: 1999-06-30
;; NUMBER OF SEQ ID NOS: 78
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 61
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-832-312-61

Query Match 81.8%; Score 27; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
Db 2 YWMS 5

RESULT 3

US-09-253-794-23
;; Sequence 23, Application US/09253794
;; Patent No. US20020018750A1
;; GENERAL INFORMATION:
;; APPLICANT: HANSEN, Hans J.
;; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
;; NUMBER OF SEQUENCES: 58
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/253,794
;; FILING DATE: 22-Feb-1999
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,157
;; FILING DATE: 05-OCT-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SAXE, Bernhard D.
;; REGISTRATION NUMBER: 28,665
;; REFERENCE/DOCKET NUMBER: 18733/464
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202)672-5300
;; TELEFAX: (202)672-5399
;; TELEX: 904136

;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-253-794-23

Query Match 81.8%; Score 27; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 YWMS 5
Db 2 YWMS 5

RESULT 4

US-09-968-561A-265
;; Sequence 265, Application US/09968561A
;; Patent No. US20020164642A1
;; GENERAL INFORMATION:
;; APPLICANT: Tomlinson, Ian M
;; APPLICANT: Winter, Gregory
;; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
;; FILE REFERENCE: 8039/1073B
;; CURRENT APPLICATION NUMBER: US/09/968,561A
;; CURRENT FILING DATE: 2001-10-01
;; PRIOR APPLICATION NUMBER: GB 9722131.1
;; PRIOR FILING DATE: 1997-10-20
;; PRIOR APPLICATION NUMBER: US 60/065,248
;; PRIOR FILING DATE: 1997-11-13
;; PRIOR APPLICATION NUMBER: US 60/066,729
;; PRIOR FILING DATE: 1997-11-21
;; PRIOR APPLICATION NUMBER: PCT/GB98/03135
;; PRIOR FILING DATE: 1998-10-20
;; PRIOR APPLICATION NUMBER: US 09/511,939
;; PRIOR FILING DATE: 2000-02-24
;; NUMBER OF SEQ ID NOS: 350
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 265
;; LENGTH: 5
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-968-561A-265

Query Match 72.7%; Score 24; DB 9; Length 5;
Best Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
Db 1 GYWS 5

RESULT 5

US-09-155-106-1
;; Sequence 1, Application US/09155106
;; Publication No. US20030054003A1
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: HUMANIZATION OF AN ANTI-CARCINOEMBRYONIC
;; TITLE OF INVENTION: ANTIGEN ANTI-IDIOTYPE ANTIBODY AND USE AS A TUMOR VACCINE
;; TITLE OF INVENTION: AND FOR TARGETING APPLICATIONS
;; NUMBER OF SEQUENCES: 45
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/155,106
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US97/04696
;; FILING DATE: 19-MAR-1997
;; APPLICATION NUMBER: US 60/013,708
;; FILING DATE: 20-MAR-1996
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids

;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 5 amino acids

;
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-155-106-1

Query Match 72.7%; Score 24; DB 9; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
|||
DB 2 YWMT 5

RESULT 6

US-09-132-854-151
; Sequence 151, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 151
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-151

Query Match 72.7%; Score 24; DB 10; Length 5;
Best Local Similarity 80.0%; Pred. No. 2.7e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYWS 5
|||
DB 1 GYMS 5

RESULT 7

US-09-423-800-62
; Sequence 62, Application US/09423800
; Patent No. US20020165363A1
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: TSUNENARI, TOSHIKI
; APPLICANT: ISHII, KIMIE
; TITLE OF INVENTION: CACHEXIA REMEDY
; FILE REFERENCE: 04853-0036
; CURRENT APPLICATION NUMBER: US/09/423,800
; CURRENT FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: PCT/JP98/02116
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: JP 125505/1997
; PRIOR FILING DATE: 1997-05-15
; PRIOR APPLICATION NUMBER: JP 194445/1997
; PRIOR FILING DATE: 1997-07-18
; NUMBER OF SEQ ID NOS: 87
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-423-800-62

Query Match 69.7%; Score 23; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 YWM 4
|||
DB 2 YWM 4

RESULT 8

US-09-269-921-6
; Sequence 6, Application US/09269921
; Publication No. US20030045691A1
; GENERAL INFORMATION:
; APPLICANT: Ono, Koichiro
; APPLICANT: Ohtomo, Toshihiko
; APPLICANT: Tsuchiya, Masayuki
; APPLICANT: Yoshimura, Yasuo
; APPLICANT: Koishihara, Yasuo
; TITLE OF INVENTION: RESHAPED HUMAN ANTI-HM 1.24 ANTIBODY
; FILE REFERENCE: 35029-20007.00
; CURRENT APPLICATION NUMBER: US/09/269,921
; CURRENT FILING DATE: 1999-04-01
; EARLIER APPLICATION NUMBER: PCT/JP97/03553
; EARLIER FILING DATE: 1997-10-03
; EARLIER APPLICATION NUMBER: JP 8-264756
; EARLIER FILING DATE: 1996-10-04
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 5
; TYPE: PRT
; ORGANISM: murine
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of CDR(1) of H chain V region of
; OTHER INFORMATION: mouse anti-HM 1.24 antibody
US-09-269-921-6

Query Match 69.7%; Score 23; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWM 4
|||
DB 2 YWM 4

RESULT 9

US-09-977-797A-90
; Sequence 90, Application US/09977797A
; Publication No. US20030044772A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; FILE REFERENCE: AME-06805
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-90

Query Match 69.7%; Score 23; DB 9; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5
|||
Db 2 YWIS 5

RESULT 10

US-10-182-018-62
; Sequence 62, Application US/10182018
; Publication No. US2003004911A1

; GENERAL INFORMATION:

; APPLICANT: CHUGAI SEIYAKU KABUSHIKI KAISHA

; TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES

; FILE REFERENCE: PH-1092-PCT

; CURRENT APPLICATION NUMBER: US/10/182,018

; CURRENT FILING DATE: 2002-07-24

; PRIOR APPLICATION NUMBER: JP 2000-83034

; PRIOR FILING DATE: 2000-01-25

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 62

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-182-018-62

Query Match

Best Local Similarity 69.7%; Score 23; DB 9; Length 5;

Mismatches 0; Pred. No. 2.7e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWM 4

|||

Db 2 YWM 4

RESULT 11

US-09-748-960-12

; Sequence 12, Application US/09748960

; Patent No. US20010046496A1

; GENERAL INFORMATION:

; APPLICANT: Brettman, Lee R.

; APPLICANT: Fox, Judith A.

; APPLICANT: Allison, David Edward

; TITLE OF INVENTION: Method of Administering an Antibody

; FILE REFERENCE: 1855,2007-001

; CURRENT APPLICATION NUMBER: US/09/748,960

; CURRENT FILING DATE: 2000-12-27

; PRIOR APPLICATION NUMBER: US 09/550,082

; PRIOR FILING DATE: 2000-04-14

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Mus musculus

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (1)....(5)

; OTHER INFORMATION: CDR1 of the heavy chain of antibodies Act-1 and

; OTHER INFORMATION: LDP-02

US-09-748-960-12

Query Match

Best Local Similarity 69.7%; Score 23; DB 10; Length 5;

Mismatches 0; Pred. No. 2.7e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWM 4

|||

Db 2 YWM 4

RESULT 12

US-09-832-312-49

; Sequence 49, Application US/09832312

; Patent No. US20010049829A1

; GENERAL INFORMATION:

; APPLICANT: Busfield et al.

; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF

; FILE REFERENCE: 7853-234

; CURRENT APPLICATION NUMBER: US/09/832,312

; CURRENT FILING DATE: 2001-04-09

; PRIOR APPLICATION NUMBER: 09/610,118

; PRIOR FILING DATE: 2000-06-30

; PRIOR APPLICATION NUMBER: 09/503,387

; PRIOR FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: 09/454,824

; PRIOR FILING DATE: 1999-12-06

; PRIOR APPLICATION NUMBER: 09/345,468

; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 49

; LENGTH: 5

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-832-312-49

Query Match

Best Local Similarity 69.7%; Score 23; DB 10; Length 5;

Mismatches 1; Pred. No. 2.7e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWMS 5

|||

Db 2 YWIS 5

RESULT 13

US-09-770-002-1

; Sequence 1, Application US/09770002

; Patent No. US20020110558A1

; GENERAL INFORMATION:

; APPLICANT: Peter Lloyd Amlot

; APPLICANT: Max H. Schreier

; APPLICANT: Karin Schreier

; TITLE OF INVENTION: Use of CD25 binding molecules in the

; FILE REFERENCE: 4-30583A/30967C1

; CURRENT APPLICATION NUMBER: US/09/770,002

; CURRENT FILING DATE: 2001-09-17

; PRIOR APPLICATION NUMBER: PCT/EP99/05316

; PRIOR FILING DATE: 1999-07-26

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 5

; TYPE: PRT

; ORGANISM: mus musculus

; FEATURE:

US-09-770-002-1

Query Match

Best Local Similarity 69.7%; Score 23; DB 10; Length 5;

Mismatches 0; Pred. No. 2.7e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 YWM 4

|||

Db 2 YWM 4

RESULT 14

US-09-291-417-40

; Sequence 40, Application US/09291417A

; Publication No. US20030050230A1

; GENERAL INFORMATION:

; APPLICANT: PLOWMAN, GREGORY

; APPLICANT: MARTINEZ, RICARDO

; APPLICANT: WHITE, DAVID

```

; TITLE OF INVENTION: STE20-RELATED PROTEIN KINASES
; FILE REFERENCE: 240/300
; CURRENT APPLICATION NUMBER: US/09/291,417A
; EARLIER FILING DATE: 1999-04-13
; EARLIER APPLICATION NUMBER: US 60/081,784
; EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: CCK4b
US-09-291-417-40

```

```

Query Match          60.6%; Score 20; DB 9; Length 5;
Best Local Similarity 100.0%; Pred.No. 2.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 3 WMS 5
Db 1 WMS 3

```

```

RESULT 15
US-10-029-301-4
; Sequence 4, Application US/10029301
; Publication No. US20020188107A1
; GENERAL INFORMATION:
; APPLICANT: Mynott, Tracy Lehanne
; APPLICANT: Engwerda, Christian
; APPLICANT: Peak, Keith
; TITLE OF INVENTION: Component of Stem Bromelain (as amended)
; FILE REFERENCE: 0623.0760002
; CURRENT APPLICATION NUMBER: US/10/029.301
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: US 09/382,685
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/GB98/00592
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: GB 9704252.7
; PRIOR FILING DATE: 1997-02-28
; PRIOR APPLICATION NUMBER: GB 9703850.9
; PRIOR FILING DATE: 1997-02-25
; PRIOR APPLICATION NUMBER: GB 9703827.7
; PRIOR FILING DATE: 1997-02-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Ananas comosus
US-10-029-301-4

```

```

Query Match          57.6%; Score 19; DB 9; Length 5;
Best Local Similarity 66.7%; Pred.No. 2.7e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 2 YWM 4
Db 1 YWI 3

```

Search completed: April 22, 2003, 13:47:05
Job time : 16 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:39:17 ; Search time 28 Seconds
(without alignments)
5.254 Million cell updates/sec

Title: US-09-674-716B-9
Perfect score: 33
Sequence: 1 GYVMS 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 19691

Minimum DB seq length: 0
Maximum DB seq length: 5

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	87.9	5	2	US-08-480-434-22
2	29	87.9	5	2	US-08-480-434-31
3	29	87.9	5	2	US-08-053-451B-22
4	29	87.9	5	2	US-08-053-451B-31
5	27	81.8	5	1	US-08-244-626-12
6	27	81.8	5	2	US-08-480-434-32
7	27	81.8	5	2	US-08-318-157B-23
8	27	81.8	5	2	US-08-053-451B-32
9	25	75.8	5	1	US-08-353-400-27
10	24	72.7	5	6	5185431-15
11	23	69.7	5	1	US-08-318-970B-1
12	23	69.7	5	1	US-08-318-970B-3
13	23	69.7	5	4	US-09-406-532-5
14	23	69.7	5	4	US-08-479-089A-7
15	20	60.6	4	1	US-07-869-933-21
16	20	60.6	4	2	US-09-103-663-21
17	20	60.6	5	2	US-08-476-176B-50
18	20	60.6	5	3	US-08-127-721A-50
19	20	60.6	5	3	US-08-485-246A-50
20	20	60.6	5	6	5217869-8
21	19	57.6	5	3	US-08-469-141A-64
22	19	57.6	5	4	US-07-987-264-1
23	19	57.6	5	4	US-09-382-689A-4
24	19	57.6	5	5	PCT-US95-13794-64
25	19	57.6	5	6	5217869-44
26	18	54.5	3	1	US-08-440-504A-1
27	18	54.5	3	4	US-08-433-613-1

28	18	54.5	4	1	US-08-321-625-14	Sequence 14, Appl
29	18	54.5	4	1	US-08-222-851-19	Sequence 19, Appl
30	18	54.5	4	1	US-08-469-486-39	Sequence 39, Appl
31	18	54.5	4	1	US-08-440-504A-2	Sequence 2, Appl
32	18	54.5	4	2	US-08-469-658-39	Sequence 39, Appl
33	18	54.5	4	2	US-08-671-487A-8	Sequence 8, Appl
34	18	54.5	4	2	US-08-651-179B-2	Sequence 2, Appl
35	18	54.5	4	4	US-08-433-613-2	Sequence 2, Appl
36	18	54.5	4	4	US-09-181-083-14	Sequence 14, Appl
37	18	54.5	4	4	US-09-155-613A-31	Sequence 31, Appl
38	18	54.5	4	4	US-09-441-063-1	Sequence 1, Appl
39	18	54.5	5	1	US-08-068-947-1	Sequence 1, Appl
40	18	54.5	5	1	US-08-325-509-50	Sequence 50, Appl
41	18	54.5	5	1	US-08-332-071B-1	Sequence 1, Appl
42	18	54.5	5	1	US-07-946-421-4	Sequence 4, Appl
43	18	54.5	5	1	US-08-321-625-3	Sequence 3, Appl
44	18	54.5	5	1	US-08-321-625-15	Sequence 15, Appl
45	18	54.5	5	1	US-07-789-184-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-08-480-434-22
; Sequence 22, Application US/08480434
; Patent No. 5811248
; GENERAL INFORMATION:
; APPLICANT: Charles C. Dittlow, et al.
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
; TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,434
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: N
; ANTI-SENSE: N
US-08-480-434-22

Query Match 87.9%; Score 29; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GYVMS 5
|:|

Db 1 GFWMS 5

RESULT 2

US-08-480-434-31
 ; Sequence 31, Application US/08480434
 ; Patent No. 5811248

GENERAL INFORMATION:

APPLICANT: Charles C. Dittlow, et al.
 TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
 TITLE OF INVENTION: ANTIBODIES THERETO, AND USES THEREOF
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.24
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,434
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Albert P. Halluin
 REGISTRATION NUMBER: 25,227
 REFERENCE/DOCKET NUMBER: 7606-053
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 854-3660
 TELEFAX: (415) 854-3694
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid

STRANDEDNESS: unknown
 TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: N
 ANTI-SENSE: N
 US-08-480-434-31

Query Match

Best Local Similarity 87.9%; Score 29; DB 2; Length 5;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5

|:|

Db 1 GFWMS 5

RESULT 3

US-08-053-451B-22
 ; Sequence 22, Application US/08053451B
 ; Patent No. 5955584

GENERAL INFORMATION:

APPLICANT: Chen, Francis W.
 APPLICANT: Dittlow, Charles C.
 APPLICANT: Calenoff, Emanuel
 TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
 TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF

NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

; ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/053,451B
 FILING DATE: 26-APR-1993
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.
 REGISTRATION NUMBER: 25,227
 REFERENCE/DOCKET NUMBER: 7606-033-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-3660
 TELEFAX: 415-854-3694
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid

STRANDEDNESS: unknown
 TOPOLOGY: unknown

MOLECULE TYPE: DNA
 HYPOTHETICAL: N
 ANTI-SENSE: N

US-08-053-451B-22

Query Match

Best Local Similarity 87.9%; Score 29; DB 2; Length 5;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GYWS 5

|:|

Db 1 GFWMS 5

RESULT 4

US-08-053-451B-31
 ; Sequence 31, Application US/08053451B
 ; Patent No. 5955584

GENERAL INFORMATION:

APPLICANT: Chen, Francis W.
 APPLICANT: Dittlow, Charles C.
 APPLICANT: Calenoff, Emanuel
 TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
 TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF

NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA

; ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/053,451B
 FILING DATE: 26-APR-1993
 CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Halluin, Albert P.
 REGISTRATION NUMBER: 25,227
 REFERENCE/DOCKET NUMBER: 7606-033-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-854-3660
 TELEFAX: 415-854-3694
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 31:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA
 HYPOTHETICAL: N
 ANTI-SENSE: N
 US-08-053-451B-31

Query Match 87.9%; Score 29; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 2e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;

QY 1 YWMS 5
 Db 1 GFWS 5

RESULT 5
 US-08-244-626-12
 ; Sequence 12, Application US/08244626
 ; Patent No. 5502167
 ; GENERAL INFORMATION:
 ; APPLICANT: Waldmann, Herman
 ; APPLICANT: Walsh, Louise
 ; APPLICANT: Crowe, James Scott
 ; APPLICANT: Lewis, Alan Peter
 ; TITLE OF INVENTION: CDR GRAFTED HUMANISED CHIMERIC T-CELL
 ; TITLE OF INVENTION: ANTIBODIES
 ; NUMBER OF SEQUENCES: 34
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
 ; STREET: 555 Thirteenth Street, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/244,626
 FILING DATE: July 15, 1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/02251
 FILING DATE: December 4, 1992
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Ernst, Barbara G.
 REGISTRATION NUMBER: 30,377
 REFERENCE/DOCKET NUMBER: 1808-153A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 783-6040
 TELEFAX: (202) 783-6031

INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-244-626-12

Query Match 81.8%; Score 27; DB 1; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 YWMS 5
 ||||

Db 2 YWMS 5

RESULT 6
 US-08-480-434-32
 ; Sequence 32, Application US/08480434
 ; Patent No. 5811248
 ; GENERAL INFORMATION:
 ; APPLICANT: Charles C. Ditlow, et al.
 ; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC ANTIGENS,
 ; NUMBER OF SEQUENCES: 88
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.24
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/480,434
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Albert P. Halluin
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 7606-053
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 854-3660
 ; TELEFAX: (415) 854-3694
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 32:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHETICAL: N
 ; ANTI-SENSE: N
 ; US-08-480-434-32

Query Match 81.8%; Score 27; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0;

QY 2 YWMS 5
 ||||

Db 2 YWMS 5

RESULT 7
 US-08-318-157B-23
 ; Sequence 23, Application US/08318157B
 ; Patent No. 5874540
 ; GENERAL INFORMATION:
 ; APPLICANT: HANSEN, Hans J.
 ; APPLICANT: ARMOUR, Kathryn L.
 ; TITLE OF INVENTION: CDR-GRAFTED TYPE III ANTI-CEA HUMANIZED
 ; NUMBER OF SEQUENCES: 58
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109

```
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/318,157B
/ FILING DATE: 05-OCT-1994
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saxe, Bernhard D.
/ REGISTRATION NUMBER: 28,665
/ REFERENCE/DOCKET NUMBER: 18733/464
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202)672-5300
/ TELEFAX: (202)672-5399
/ TELEX: 904136
/ INFORMATION FOR SEQ ID NO: 23:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-318-157B-23

Query Match      81.8%; Score 27; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 YWMS 5
Db  2 YWMS 5

RESULT 8
US-08-053-451B-32
; Sequence 32, Application US/08053451B
; Patent No. 595584
; GENERAL INFORMATION:
; APPLICANT: Chen, Francis W.
; APPLICANT: Ditlow, Charles C.
; APPLICANT: Calenoff, Emanuel
; TITLE OF INVENTION: ATHEROSCLEROTIC PLAQUE SPECIFIC
; TITLE OF INVENTION: ANTIGENS, ANTIBODIES THERETO, AND USES THEREOF
; NUMBER OF SEQUENCES: 176
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,451B
; FILING DATE: 26-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 7606-033-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-854-3660
; TELEFAX: 415-854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
```

```
/
/ TYPE: amino acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA
/ HYPOTHETICAL: N
/ ANTI-SENSE: N
/ US-08-053-451B-32

Query Match      81.8%; Score 27; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 YWMS 5
Db  2 YWMS 5

RESULT 9
US-08-353-400-27
; Sequence 27, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
/ US-08-353-400-27

Query Match      75.8%; Score 25; DB 1; Length 5;
Best Local Similarity 75.0%; Pred. No. 2e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy  1 GYWM 4
Db  1 GYWI 4

RESULT 10
5185431-15
; Patent No. 5185431
; APPLICANT: YOSHIMATSU, KENTARO; SHIKATA, YASUSHI; TANAKA, ISAO;
; HASEGAWA, YOSHIKAZU; SETO, TOSHIO; OSAWA, TOSHIO
; TITLE OF INVENTION: RECOMBINANT NATURAL KILLER CELL ACTIVATOR
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/392,841
; FILING DATE: 11-AUG-1989
; SEQ ID NO: 15:
; LENGTH: 5
/ 5185431-15

Query Match      72.7%; Score 24; DB 6; Length 5;
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```
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 1 GYW 3
    |||
Db 2 GYW 4

RESULT 11
US-08-318-970B-1
; Sequence 1, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
;   ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDRI-1
; OTHER INFORMATION: hypervariable region
US-08-318-970B-1

Query Match 69.7%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 2 YWM 4
    |||
Db 2 YWM 4

RESULT 12
US-08-318-970B-3
; Sequence 3, Application US/08318970B
; Patent No. 5589573
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
;   ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
```

```
STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION/DOCKET NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDRI-3
; OTHER INFORMATION: hypervariable region
US-08-318-970B-3

Query Match 69.7%; Score 23; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 2 YWM 4
    |||
Db 2 YWM 4

RESULT 13
US-09-406-532-5
; Sequence 5, Application US/09406532A
; Patent No. 6365154
; GENERAL INFORMATION:
; APPLICANT: Connie L. Erickson-Miller
; APPLICANT: Stephen D. Holmes
; APPLICANT: James D. Winkler
; TITLE OF INVENTION: TIE2 Agonist Antibodies
; FILE REFERENCE: P50843
; CURRENT APPLICATION NUMBER: US/09/406,532A
; CURRENT FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: 60/102,098
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(5)
; OTHER INFORMATION: 1588 heavy chain CDR 1
US-09-406-532-5

Query Match 69.7%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05; 0; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 2 YWM 4
    |||
```

```
Db      2 YWM 4

RESULT 14
US-08-479-089A-7
; Sequence 7, Application US/08479089A
; Patent No. 6383487
; GENERAL INFORMATION:
; APPLICANT: Amlot, Peter L.
; APPLICANT: Akbar, Arne N.
; APPLICANT: Heinrich, Gunther
; APPLICANT: Cammisuli, Salvatore
; TITLE OF INVENTION: CD25 Binding Molecules
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6383487artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: NJ
; COUNTRY: USA
; ZIP: 07901-1027
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,089A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/669,545
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9019323
; FILING DATE: 05-SEP-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Furman, Diane E.
; REGISTRATION NUMBER: 31,104
; REFERENCE/DOCKET NUMBER: 100-7617
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 522-6924
; TELEFAX: (908) 522-6955
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-479-089A-7

Query Match      69.7%; Score 23; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWM 4
Db      2 YWM 4

RESULT 15
US-07-869-933-21
; Sequence 21, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-869-933-21

Query Match      60.6%; Score 20; DB 1; Length 4;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      2 YWM 4
Db      2 YWM 4

Search completed: April 22, 2003, 13:43:03
Job time : 29 secs
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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:46:48 ; Search time 14 Seconds
(without alignments)
130.468 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLSDNYATHVAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 3433

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26.5	27.0	16	2 A39109	hypothetical prote
2	25	25.5	10	2 S77990	cytochrome-c oxida
3	24	24.5	19	2 S39387	protein kinase GSK
4	23	23.5	15	2 PH1631	Ig H chain V-D-J r
5	23	23.5	16	2 B60278	24k antigen - Myco
6	22	22.4	10	2 D46285	formaldehyde dehyd
7	22	22.4	14	2 S59435	formate dehydrogen
8	22	22.4	15	2 PA0046	protein QA100044 -
9	22	22.4	15	2 I67525	CD33 antigen homol
10	22	22.4	18	2 F49215	urease (EC 3.5.1.5
11	22	22.4	18	2 PQ0072	T-cell receptor be
12	22	22.4	19	2 A41077	protein-disulfide
13	21	21.4	9	2 S30494	cat gene leader pe
14	21	21.4	9	2 B24362	chloramphenicol O-
15	21	21.4	12	2 PH1587	Ig H chain V-D-J r
16	21	21.4	14	2 PH1471	T-cell receptor be
17	21	21.4	16	2 A29520	amino-acid racemas
18	21	21.4	17	2 A61334	trypsin (EC 3.4.21
19	21	21.4	18	2 PH0768	T-cell receptor be
20	21	21.4	18	4 I56393	lacZ/IS1 mutant fu
21	20	20.4	9	2 PT0238	Ig heavy chain CRD
22	20	20.4	10	2 S65388	cytochrome-c oxida
23	20	20.4	11	2 PT0301	Ig heavy chain CRD
24	20	20.4	12	2 S26546	T-cell receptor be
25	20	20.4	12	4 PC2122	aminotransferase c
26	20	20.4	13	2 PH1555	Ig H chain V-D-J r
27	20	20.4	14	2 A47421	leukotriene B-4 12
28	20	20.4	15	2 A30330	neuropeptide pep -
29	20	20.4	15	2 I78838	flt3 ligand isofor

30 20 20.4 16 2 S17217 ribulose-bisphosph
31 20 20.4 16 2 S51610 hypothetical prote
32 20 20.4 16 2 PH1622 Ig H chain V-D-J r
33 20 20.4 16 2 PH1589 Ig H chain V-D-J r
34 20 20.4 17 2 C85956 hypothetical prote
35 20 20.4 18 2 PH1621 Ig H chain V-D-J r
36 20 20.4 18 2 A59396 Tha p 1 - Thaumeto
37 19.5 19.9 16 2 D58501 26k kidney and gal
38 19 19.4 10 1 GMROL2 leucosulfakinin-II
39 19 19.4 10 2 B61033 ranachykinin B -
40 19 19.4 10 2 B60656 leucosulfakinin II
41 19 19.4 12 2 G64003 hypothetical prote
42 19 19.4 12 2 D28551 hypothetical prote
43 19 19.4 12 2 A34858 proteinase E - bla
44 19 19.4 12 2 C30503 Ig gamma-2b chain
45 19 19.4 13 2 PN0123 serine proteinase

ALIGNMENTS

RESULT 1

A39109

hypothetical protein 1 - hepatitis C virus

C:Species: hepatitis C virus

C>Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 18-Jun-1993

C:Accession: A39109

R:Han, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-

Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

A:Title: Characterization of the terminal regions of hepatitis C viral RNA: identificati

A:Reference number: A39109; MUID:91156678; PMID:1705704

A:Accession: A39109

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-16 <HAN>

A:Cross-references: GB:M58406

Query Match 27.0%; Score 26.5; DB 2; Length 16;

Best Local Similarity 70.0%; Pred. No. 5.4e+02;

Matches 7; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 8 NVATHVAESV 17

DB 8 NYCLH-AESV 16

RESULT 2

S77990

cytochrome-c oxidase (EC 1.9.3.1) chain VIIc - bigeye tuna (fragment)

C:Species: Thunnus obsesus (bigeye tuna)

C>Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 30-Jan-1998

C:Accession: S77990

R:Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A:Reference number: S77980

A:Accession: S77990

A:Molecule type: protein

A:Residues: 1-10 <ARN>

A:Experimental source: heart; liver

C:Genetics:

A:Genome: nuclear

C:Function:

A:Pathway: oxidative phosphorylation; respiratory chain

C:Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 25.5%; Score 25; DB 2; Length 10;

Best Local Similarity 80.0%; Pred. No. 5.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 THVAE 15

DB 1 SHVAE 5

RESULT 3

S39387
protein kinase GSK-3-beta (EC 2.7.1.-) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-May-1994 #sequence_revision 26-Jul-1996 #text_change 07-May-1999
C;Accession: S39387
R;Sutherland, C.; Leighton, I.A.; Cohen, P.
Biochem. J. 296, 15-19, 1993
A;Title: Inactivation of glycogen synthase kinase-3-beta by phosphorylation: new kinase
A;Reference number: S39387; MUID:94071817; PMID:8250835
A;Accession: S39387
A;Molecule type: protein
A;Residues: 1-19 <SVT>
A;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: phosphotransferase; protein kinase

Query Match 24.5%; Score 24; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 THYAESVK 18
| : ||| |
Db 2 TSFAESXK 9

RESULT 4

PH1631
Ig H chain V-D-J region (clone B-less 202) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1631
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1631
A;Molecule type: DNA
A;Residues: 1-15 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 23.5%; Score 23; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 SDNYATHY 13
| : ||| |
Db 8 TDGYAMDY 15

RESULT 5

B60278
24K antigen - Mycobacterium bovis (fragment)
C;Species: Mycobacterium bovis
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 18-Jun-1993
C;Accession: B60278
R;Fifis, T.; Costopoulos, C.; Radford, A.J.; Bacic, A.; Wood, P.R.
Infect. Immun. 59, 800-807, 1991
A;Title: Purification and characterization of major antigens from a Mycobacterium bovis
A;Reference number: A60278; MUID:91147217; PMID:1900061
A;Accession: B60278
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <FIP>

Query Match 23.5%; Score 23; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 YAESVKG 19
| : ||| |
Db 15 YKELKG 11

RESULT 6

D46285
formaldehyde dehydrogenase (glutathione) (EC 1.2.1.1) class III low activity form - Atlantic
C;Species: Gadus morhua (Atlantic cod)
C;Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1996
C;Accession: D46285
R;Danielsson, O.; Jornvall, H.

Proc. Natl. Acad. Sci. U.S.A. 89, 9247-9251, 1992
A;Title: "Enzymogenesis": classical liver alcohol dehydrogenase origin from the glutathione
A;Reference number: A46285; MUID:93028441; PMID:1409630
A;Accession: D46285
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <DAN>
A;Note: sequence extracted from NCBI backbone (NCBI:116272)
C;Keywords: NAD; oxidoreductase

Query Match 22.4%; Score 22; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 DNYATH 12
| : ||| |
Db 1 DEFVTH 6

RESULT 7

S59495
formate dehydrogenase delta chain - Alcaligenes eutrophus (fragment)
C;Species: Alcaligenes eutrophus
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C;Accession: S59495
R;Friedebold, J.; Mayer, F.; Bill, E.; Trautwein, A.X.; Bowien, B.
Biol. Chem. Hoppe-Seyler 376, 561-568, 1995
A;Title: Structural and immunological studies on the soluble formate dehydrogenase from
A;Reference number: S59492; MUID:96145736; PMID:8561915
A;Accession: S59495
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-14 <FRI>

Query Match 22.4%; Score 22; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 2.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 LKSDNYATH 12
| : ||| |
Db 1 MKIDNIITY 9

RESULT 8

PA0046
protein QM100044 - Arabidopsis thaliana (fragment)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C;Accession: PA0046; PA0042
R;Kamo, M.; Kawakami, T.; Miyatake, N.; Taugita, A.
submitted to JIPID, July 1994
A;Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A;Reference number: PA0001
A;Accession: PA0046
A;Molecule type: protein
A;Residues: 1-15 <KAM>
A;Experimental source: stem

Query Match 22.4%; Score 22; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.7e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 AESVKG 19
| : ||| |

Db 1 AESSKG 6

RESULT 9

167525
CD33 antigen homolog - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Jun-1998
C:Accession: I67525
R:Chies, J.A.; Lembezat, M.P.; Freitas, A.A.
Eur. J. Immunol. 24, 1657-1664, 1994
A:Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is n
A:Reference number: I53392; MUID:94298870; PMID:8026526
A:Accession: I67525
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-15 <RES>
A:Cross-references: GB:S71349; NID:9550037
C:Genetics:
A:Gene: IG VH7183

Query Match 22.4%; Score 22; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 2.7e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 KSDNYATHY 13
: | | : |
Db 4 RRDHYGSSY 12

RESULT 10

F49215
urease (EC 3.5.1.5) small chain UreA - Helicobacter mustelae (ATCC 43772) (fragment)
C:Species: Helicobacter mustelae
C:Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 30-May-1997
C:Accession: F49215
R:Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
A:Title: Purification and characterization of the urease enzymes of Helicobacter species
A:Reference number: A49215; MUID:93084378; PMID:1452359
A:Accession: F49215
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <TUR>
A:Note: sequence extracted from NCBI backbone (NCBip:119487)
C:Superfamily: urease 26K chain; urease 11K chain homology; urease 12K chain homology
C:Keywords: hydrolase

Query Match 22.4%; Score 22; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 DNYATHYA 14
: | | |
Db 7 DRMLHYA 14

RESULT 11

PQ0072
T-cell receptor beta chain (BTB98) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C:Accession: PQ0072
R:Tanaka, A.; Ishiguro, N.; Shinagawa, M.
submitted to JIPID, May 1990
A:Description: Sequence analysis of bovine T-cell receptor beta chain genes.
A:Reference number: JQ0472
A:Accession: PQ0072
A:Molecule type: mRNA
A:Residues: 1-18 <TAN>
C:Genetics:
A:Experimental source: T cell
A:Gene: BTB98

C:Keywords: receptor

Query Match 22.4%; Score 22; DB 2; Length 18;
Best Local Similarity 38.5%; Pred. No. 3.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

QY 6 SDNYATHYAESVK 18
: | | : |
Db 4 SDDY--HFGPGTK 14

RESULT 12

A41077
protein-disulfide reductase (glutathione) (EC 1.8.4.2) Q-5 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Jun-1992 #sequence_revision 12-Jun-1992 #text_change 23-Jun-1993
C:Accession: A41077
R:Srivastava, S.P.; Chen, N.; Liu, Y.; Holtzman, J.L.
J. Biol. Chem. 266, 20337-20344, 1991
A:Title: Purification and characterization of a new isozyme of thiol:protein-disulfide o:
fic phospholipase C form 1A.
A:Reference number: A41077; MUID:92041865; PMID:1657921
A:Accession: A41077
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <SRI>
C:Keywords: oxidoreductase

Query Match 22.4%; Score 22; DB 2; Length 19;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LKSDNYA 10
: | | : |
Db 12 LKSNFA 18

RESULT 13

S30494
cat gene leader peptide - Streptococcus agalactiae plasmid pIP501
C:Species: Streptococcus agalactiae
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 24-Sep-1999
C:Accession: S30494
R:Trieu-Cuot, P.; de Cespedes, G.; Horaud, T.
Plasmid 28, 272-276, 1992
A:Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Strept:
A:Reference number: JQ1950; MUID:93096867; PMID:1461942
A:Accession: S30494
A:Molecule type: DNA
A:Residues: 1-9 <TRI>
A:Cross-references: EMBL:X65462; NID:949071; PIDN:CAA46454.1; PID:9581554
C:Genetics:
A:Genome: plasmid pIP501
C:Superfamily: unassigned leader peptides

Query Match 21.4%; Score 21; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 KSDNYAT 11
: | | : |
Db 3 KSEDYSS 9

RESULT 14

B24362
chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus plasmid PUB11:
C:Species: Staphylococcus aureus
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 11-May-2000
C:Accession: B24362
R:Bruckner, R.; Matzura, H.
EMBO J. 4, 2295-2300, 1985
A:Title: Regulation of the inducible chloramphenicol acetyltransferase gene of the Staph:

A;Reference number: A24362; MUID:86081739; PMID:3865770
A;Accession: B24362
A;Molecule type: DNA
A;Residues: 1-9 <BRU>
A;Cross-references: GB:X02872; NID:G46536; PIDN:CAA26630.1; PID:G581555
C;Comment: Ribosome stalling in the translation of this leader peptide, caused by the ef
nulation of the chloramphenicol O-acetyltransferase from a ribosome binding site located
C;Genetics:
A;Genome: plasmid
C;Superfamily: unassigned leader peptides

Query Match 21.4%; Score 21; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 KSDNYAT 11
||:|:|:
Db 3 KSEDYSS 9

RESULT 15
PH1587
Ig H chain V-D-J region (wild-type clone 11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1587
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A;Reference number: PH1580; MUID:93301609; PMID:8315387
A;Accession: PH1587
A;Molecule type: DNA
A;Residues: 1-12 <LEV>
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 21.4%; Score 21; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 KSDNYATHY 13
:|:|:
Db 4 RGDLYAMDY 12

Search completed: April 22, 2003, 13:49:54
Job time : 15 secs

Result No.	Score	Match	Query %	DB	ID	Description
1	27	27.6	14	1	NEJ2_FASHE	P80526 fasciola he
2	25	25.5	10	1	COXO_THUOB	P80982 thunnus obe
3	22	22.4	12	1	LOSK_LOCMI	P47733 locusta mig
4	21	21.4	9	1	LPCA_STRAAU	P36884 staphylococ
5	21	21.4	16	1	ALRX_PSEPU	P17916 pseudomonas
6	21	21.4	18	1	RIP_SIRGR	P83323 siraitia gr
7	21	21.4	18	1	UC21_MAIZE	P80627 zea mays (m
8	20	20.4	18	1	COXO_RAT	P80432 rattus norv
9	20	20.4	17	1	AU32_LITRA	P82395 litoria ran
10	20	20.4	19	1	ATPB_CANFA	P99504 canis famil
11	19	19.4	10	1	LSK2_LEUMA	P09039 leucophaea
12	19	19.4	10	1	TKNE_RANCA	P22689 rana catesb
13	19	19.4	14	1	UN37_CLOPA	P81358 clostridium
14	19	19.4	15	1	MILT_ONCKE	P81037 oncorhynch
15	19	19.4	15	1	NIS1_ANAVA	Q45407 anabaena va
16	19	19.4	16	1	RL6_VIBPR	Q54515 vibrio prot
17	19	19.4	17	1	EFG_THEAQ	Q01697 thermus aqu
18	19	19.4	19	1	HI70_RAT	P21794 rattus norv
19	18	18.4	12	1	TKN_KASSE	P08611 kassina sen
20	18	18.4	15	1	OBPA_MAMBR	P81285 mamestra br
21	18	18.4	15	1	YAA3_RHOPA	Q02006 rhodopseudo
22	18	18.4	16	1	HTPG_ACICA	P81876 acinetobact
23	18	18.4	17	1	AU31_LITRA	P80394 litoria ran
24	18	18.4	17	1	B29K_PORGI	P81784 porphyromon
25	18	18.4	17	1	NU4M_TIRU	Q36834 trichophyto
26	18	18.4	19	1	FIBE_LAMGL	P14473 lama lama
27	18	18.4	19	1	OXLA_OPHHA	P81383 ophiophagus
28	18	18.4	19	1	PHLC_STAIN	P80924 staphylococ
29	17	17.3	12	1	RR16_GINBI	P36207 ginkgo bilo
30	17	17.3	14	1	MAST_VESBA	P21654 vespa basaa
31	17	17.3	15	1	MM01_RAT	P81563 rattus norv
32	17	17.3	17	1	SP51_BACLI	P27642 bacillus li
33	17	17.3	18	1	AROF_STRRM	P80575 streptomyce

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CC -!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1059 MW; 126DE76787B1DCB CRC64;

Query Match 25.5%; Score 25; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 THYAE 15
DB 1 SHYAE 5

RESULT 3
LOSK LOCKMI STANDARD; PRT; 12 AA.
AC P47733;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Sulfakinin (LOM-SK).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
OC Acridomorpha; Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]

RP SEQUENCE.
RC TISSUE=Brain;
RA Schoofs L., Holman G.L., Hayes T.K., Nachman R.J., de Loof A.;
RL (In) McCaffery A., Wilson I. (eds.);
RL Chromatography and isolation of insect hormones and pheromones,
RL pp.231-241, Plenum Press, New York (1990).
CC -!- FUNCTION: MYOTROPIC PEPTIDE.
CC -!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN.
KW Hormone; Amidation; Sulfation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 7 7 SULFATION (POTENTIAL).
FT MOD_RES 12 12 AMIDATION.
SQ SEQUENCE 12 AA; 1440 MW; 9B5B5DA9BD6B5AAA CRC64;

Query Match 22.4%; Score 22; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 6.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLKSDNY 9
DB 1 QLASDDY 7

RESULT 4
LPCA STAAU STANDARD; PRT; 9 AA.
AC P36884;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE Chloramphenicol resistance leader peptide.
OS Staphylococcus aureus, and
OS Streptococcus agalactiae.
OC Plasmid pSC6, Plasmid pSCS7, Plasmid pUB112, and Plasmid pIP501.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 1311;
RN [1]

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RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=436; PLASMID=pSCS7;
RX MEDLINE=92027652; PubMed=1929326;
RA Schwarz S., Cardozo M.;
RT "Nucleotide sequence and phylogeny of a chloramphenicol
RT acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
RT aureus.";
RL Antimicrob. Agents Chemother. 35:1551-1556(1991).
RN [2]

RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; PLASMID=pSCS6;
RX MEDLINE=92388047; PubMed=1517170;
RA Cardozo M., Schwarz S.;
RT "Nucleotide sequence and structural relationships of a
RT chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
RT Staphylococcus aureus.";
RL J. Appl. Bacteriol. 72:289-293(1992).
RN [3]

RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; PLASMID=pUB112;
RX MEDLINE=86081739; PubMed=3865770;
RA Brueckner R., Matzura H.;
RT "Regulation of the inducible chloramphenicol acetyltransferase gene
RT of the Staphylococcus aureus plasmid pUB112.";
RL EMBO J. 4:2295-2300(1985).
RN [4]

RP SEQUENCE FROM N.A.
RC SPECIES=S.agalactiae; PLASMID=pIP501;
RX MEDLINE=93096867; PubMed=1461942;
RA Trieu-Cuot P., de Cespedes G., Horaud T.;
RT "Nucleotide sequence of the chloramphenicol resistance determinant of
RT the streptococcal plasmid pIP501.";
RL Plasmid 28:272-276(1992).
CC -----

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DR EMBL; M58515; AAA26612.1; -
DR EMBL; M58516; AAA16528.1; -
DR EMBL; X02872; CAA26630.1; -
DR EMBL; X60827; CAA43217.1; -
DR EMBL; X65462; CAA46454.1; -
DR PIR; B24362; B24362
KW Leader peptide; Antibiotic resistance; Plasmid.
SQ SEQUENCE 9 AA; 1074 MW; 5D9CAB5AAB05B333 CRC64;

Query Match 21.4%; Score 21; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.1e+05;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 5 KSDNYAT 11
DB 3 KSEDYSS 9

RESULT 5
ALRX_PSEPU STANDARD; PRT; 16 AA.
ID ALRX_PSEPU
AC P17916;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Broad-specificity amino acid racemase (EC 5.1.1.-) (Fragment).
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=303;
RN [1]

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RP SEQUENCE.
RC STRAIN=AKU 0813;
RX MEDLINE=85072810; PubMed=6439237;
RA Roise D., Soda K., Yagi T., Walsh C.T.;
RT "Inactivation of the Pseudomonas striata broad specificity amino acid
RT racemase by D and L isomers of beta-substituted alanines: Kinetics,
RT stoichiometry, active site peptide, and mechanistic studies.";
RL Biochemistry 23:5195-5201(1984).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SIMILARITY: BELONGS TO THE ALANINE RACEMASE FAMILY.
DR PIR: A29520; A29520.
DR PROSITE; PS00395; ALANINE_RACEMASE; 1.
KW Isomerase; Pyridoxal phosphate.
FT ACT_SITE 1 6
FT BINDING 6 6
FT NON_TER 16 16
FT SEQUENCE 16 AA; 1572 MW; 8C6C2DA154362E07 CRC64;
SQ
Query Match 21.4%; Score 21; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LKSDNY 9
DB 5 LKADAY 10

RESULT 6
RID_RIP_SIRGR STANDARD; PRT; 18 AA.
AC P83323;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein momorgrosvin (rRNA N-glycosidase) (EC
DE 3.2.2.22) (Fragment).
OS Siraitia grosvenorii (Monk's fruit) (Luo han guo).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosidae;
OC eucosids I; Cucurbitales; Cucurbitaceae; Siraitia.
OX NCBI_TaxID=190515;
RN
[1]
SEQUENCE, FUNCTION, AND GLYCOSYLATION.
RC TISSUE=Seed;
RX MEDLINE=21073786; PubMed=11205869;
RA Tsang K.Y., Ng T.B.;
RT "Isolation and characterization of a new ribosome inactivating
RT protein, momorgrosvin, from seeds of the monk's fruit Momordica
RT grosvenorii.";
RL Life Sci. 68:773-784(2001).
CC -1- FUNCTION: Inhibits protein synthesis in the rabbit reticulocyte
CC lysate system
CC -1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
CC specific adenosine on the 28S rRNA.
CC -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
CC TYPE 1 RIP SUBFAMILY.
DR InterPro; IPR001574; RIP.
DR PROSITE; PS00275; SHIGA_RICIN; PARTIAL.
KW Plant defense; Protein synthesis inhibitor; Hydrolase;
KW Toxin; Glycoprotein.
FT NON_TER 18
FT SEQUENCE 18 AA; 2032 MW; 476E15CE683E2446 CRC64;
SQ
Query Match 21.4%; Score 21; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NYATHY 13
DB 10 NGATY 15

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RESULT 7
UC21_MAIZE STANDARD; PRT; 18 AA.
ID UC21_MAIZE
AC P80627;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 443)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.9, ITS MW IS: 26.5 kDa.
CC -1- SIMILARITY: TO L-ASCORBATE PEROXIDASES.
DR Maize-2DPAGE; P80627; COLEOPTILE.
DR MaizeDB; 123953; -.
FT NON_TER 1
FT NON_TER 18
FT SEQUENCE 18 AA; 1938 MW; F32F6FEF038BAB8A CRC64;
SQ
Query Match 21.4%; Score 21; DB 1; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 NYATHYAE 15
DB 3 NYPTVSAR 10

RESULT 8
COXO_RAT STANDARD; PRT; 10 AA.
ID COXO_RAT
AC P80432;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide Viic, mitochondrial (EC 1.9.3.1)
DE (VIIIA) (Fragment).
GN COX7C OR COX7C1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE.
RC STRAIN=Wistar; TISSUE=Liver, and Heart;
RX MEDLINE=95324529; PubMed=7601105;
RA Schaegger H., Noack H., Halangk W., Brandt U., von Jagow G.;
RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
RT amino-terminal sequences suggest identity of the fetal heart and the
RT adult liver isoform.";
RL Eur. J. Biochem. 230:235-241(1995).
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC CHAINS OF CYTOCHROME C OXIDASE. THE TERMINAL OXIDASE IN
CC MITOCHONDRIAL ELECTRON TRANSPORT.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIIC FAMILY.
KW Oxidoreductase; Mitochondrion.
FT NON_TER 10

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SQ SEQUENCE 10 AA; 1117 MW; 126DE767687B1B0B CRC64;
 Query Match 20.4%; Score 20; DB 1; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.2e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 THYAE 15
 :|||
 Db 1 SHVEE 5

RESULT 9
 AU32_LITRA STANDARD; PRT; 17 AA.
 ID AU32_LITRA
 AC P82395;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Aurein 3.2.
 OS Litoria raniformis (Southern bell frog), and
 OS Litoria aurea (Green and golden bell frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
 OC Pelodytidae; Litoria.
 OC NCBI_TaxID=116057, 8371;
 RN [1]

SEQUENCE, AND FUNCTION.
 RC TISSUE=Granular dorsal gland;
 RX MEDLINE=20408845; PubMed=10951191;
 RA Rozek T., Wegener K.L., Bowie J.H., Oliver I.N., Carver J.A.,
 RA Wallace J.C., Tyler M.J.;
 RT "The antibiotic and anticancer active aurein peptides from the
 RT Australian bell frogs Litoria aurea and Litoria raniformis the
 RT solution structure of aurein 1.2.";
 RL Eur. J. Biochem. 267:5330-5341(2000).
 CC -1- FUNCTION: ANTIMICROBIAL ACTIVITY AGAINST L.LACTIS, L.INNOCUA,
 CC M.LUTEUS, S.AUREUS, S.EPIDERMIDIS AND S.UBERTIS. PROBABLY ACTS BY
 CC DISTURBING MEMBRANE FUNCTIONS WITH ITS AMPHIPATHIC STRUCTURE.
 CC SHOWS ANTICANCER ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC Amidation; Antibiotic.
 KW MOD RES 17
 FT MOD RES 17
 SQ SEQUENCE 17 AA; 1769 MW; F6AC0A580428EAFD CRC64;

Query Match 20.4%; Score 20; DB 1; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.1e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 ATHYAESV 17
 :|||
 Db 10 AGHIASSI 17

RESULT 10
 ATPB_CANFA STANDARD; PRT; 19 AA.
 ID ATPB_CANFA
 AC P99504;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ATP synthase beta chain, mitochondrial (EC 3.6.3.14) (Fragment).
 GN ATP5B.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Heart;
 RX MEDLINE=98163340; PubMed=9504812;
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;
 RT "HSC-APPAGE and the two-dimensional gel electrophoresis database of
 RT dog heart proteins.";

RL Electrophoresis 18:2795-2802(1997).
 CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 CC GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
 CC SUBUNIT.
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
 CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
 DR HSC-2DPAGE; P99504; DOG.
 DR InterPro: IPR000194; ATPase a/bcentre.
 DR PROSITE: PS00152; ATPASE ALPHA BETA; PARTIAL.
 KW ATP synthesis; CF(1); Hydrogen ion transport; Hydrolase; ATP-binding;
 KW Mitochondrion.
 FT UNSURE 8
 FT NON TER 17 19
 FT UNSURE 17 19
 FT NON TER 19 19
 SQ SEQUENCE 19 AA; 1871 MW; BB9C163FDC60BB42 CRC64;

Query Match 20.4%; Score 20; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 2.4e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 10 ATHYAESVKG 19
 :|||
 Db 1 ATQTSFSPKG 10

RESULT 11
 LSK2_LEUMA STANDARD; PRT; 10 AA.
 ID LSK2_LEUMA
 AC P09039;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Leucosulfakinin-II (LSK-II).
 OS Leucophaea maderae (Madeira cockroach), and
 OS Periplaneta americana (American cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 OC NCBI_TaxID=6988, 6978;
 RN [1]
 RN [2]
 RP SEQUENCE.
 RC SPECIES=L.maderae;
 RX MEDLINE=87048769; PubMed=3778455;
 RA Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;
 RT "Leucosulfakinin-II, a blocked sulfated insect neuropeptide with
 RT homology to cholecystokinin and gastrin.";
 RL Biochem. Biophys. Res. Commun. 140:357-364(1986).
 RN [2]

SEQUENCE.
 RC SPECIES=P.americana; TISSUE=Corpora cardiaca;
 RX MEDLINE=90137190; PubMed=2615921;
 RA Veenstra J.A.;
 RT "Isolation and structure of two gastrin/CCK-like neuropeptides from
 RT the American cockroach homologous to the leucosulfakinins.";
 RL Neuropeptides 14:145-149(1989).
 CC -1- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS OF
 CC THE COCKROACH HINGUT. STIMULATES MUSCLE CONTRACTION OF HINDGUT.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR FIR; A26335; GMR0L2.
 DR FIR; B60656; B60656.
 DR InterPro: IPR001651; Gastrin.
 DR PROSITE: PS00259; GASTRIN; 1.
 KW Hormone; Amidation; Sulfation.
 FT MOD RES 1 1
 FT MOD RES 5 5
 FT MOD RES 5 5
 FT MOD RES 10 10
 FT MOD RES 10 10

Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.

```
OX NCBI_TaxID=1172;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7937 / ATCC 29413;
RA Monnerjahn U., Boehme H.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP EXPRESSION PATTERN.
RC STRAIN=PCC 7937 / ATCC 29413;
RX MEDLINE=96016168; PubMed=7568132;
RA Thiel T., Lyons E.M., Erker J.C., Ernst A.;
RT "A second nitrogenase in vegetative cells of a heterocyst-forming
  cyanobacterium."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9358-9362(1995).
CC -!- FUNCTION: CATALYZES THE REMOVAL OF ELEMENTAL SULFUR ATOMS FROM
  CYSTEINE TO PRODUCE ALANINE. SEEMS TO PARTICIPATE IN THE
  BIOSYNTHESIS OF THE NITROGENASE METALLOCLUSTERS BY PROVIDING THE
  INORGANIC SULFUR REQUIRED FOR THE FE-S CORE FORMATION (BY
  SIMILARITY).
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- MISCELLANEOUS: BELONGS TO THE NIF1 GENE CLUSTER WHICH IS EXPRESSED
  IN HETEROCYSTS UNDER ANAEROBIC AND AEROBIC CONDITIONS.
CC -!- SIMILARITY: BELONGS TO CLASS-V OF PYRIDOXAL-PHOSPHATE-DEPENDENT
  AMINOTRANSFERASES. NIFS/ISCS SUBFAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use by non-profit institutions as long as its content is in no way
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
  -----
DR EMBL; X69898; CAA49523.1; -
DR InterPro; IPR000192; Aminotransfv
DR PROSITE; PS00595; AA_TRANSFER_CLASS_5; PARTIAL.
KW Nitrogen fixation; Lyase; Pyridoxal phosphate.
FT NON TER 15
SQ SEQUENCE 15 AA; 1684 MW; 08B8F106DE65547D CRC64;

Query Match      19.4%; Score 19; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 DNYAT 11
Db 7 DNNAT 11
```

Search completed: April 22, 2003, 13:48:59
Job time : 27 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:45:28 ; Search time 28 Seconds
(without alignments)
139.818 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98
Sequence: 1 EIRLKSNDYATHAESVKG 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 5270

Minimum DB seq length: 0
Maximum DB seq length: 19

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	32.7	19	15	Q73129 human immun
2	30	30.6	15	4	P83219 homo sapien
3	29	29.6	15	15	Q91BM5 human immun
4	28	28.6	13	4	Q9UC27 homo sapien
5	27	27.6	19	2	Q9L434 salmonella
6	26	26.5	13	2	Q9KHJ4 caulobacter
7	26	26.5	15	1	Q9UWH6 thermococu
8	26	26.5	15	6	Q9TRT6 sus scrofa
9	26	26.5	15	6	Q9TRT4 sus scrofa
10	26	26.5	19	12	Q84863 unidentified
11	25	25.5	17	1	Q9V2X3 methanobact
12	24	24.5	13	5	Q9TRW4 tityus serr
13	24	24.5	14	4	Q93057 homo sapien
14	24	24.5	14	11	P70319 mus musculu
15	23	23.5	9	2	Q93LE4 heliobacill
16	23	23.5	10	2	P96423 pseudomonas

17	23	23.5	14	2	P96347	P96347 helicobacte
18	23	23.5	15	15	Q8UP12	Q8UP12 human immun
19	23	23.5	17	2	Q9R4H9	Q9R4H9 bordetella
20	23	23.5	18	1	Q9UWJ7	Q9UWJ7 archaeoglob
21	23	23.5	18	13	Q9PRX1	Q9PRX1 struthio ca
22	22	22.4	16	2	Q9R4J4	Q9R4J4 pseudomonas
23	22	22.4	17	2	Q9R4P9	Q9R4P9 pseudomonas
24	22	22.4	17	5	Q9V973	Q9V973 drosophila
25	22	22.4	18	2	Q9RSF6	Q9RSF6 helicobacte
26	22	22.4	18	6	Q9TRF1	Q9TRF1 bos taurus
27	22	22.4	18	8	Q9TRF9	Q9TRF9 theileria a
28	21	21.4	11	2	O56972	O56972 versinia pe
29	21	21.4	11	4	O60842	O60842 homo sapien
30	21	21.4	15	1	Q9UWH4	Q9UWH4 pyrococcus.
31	21	21.4	15	5	P83246	P83246 asaphis dic
32	21	21.4	15	6	Q9TRT3	Q9TRT3 sus scrofa
33	21	21.4	16	2	O53399	O53399 bacillus th
34	21	21.4	16	6	Q9TR18	Q9TR18 oryctolagus
35	21	21.4	16	11	Q9CTB2	Q9CTB2 mus musculu
36	21	21.4	17	2	Q52210	Q52210 staphylococ
37	21	21.4	18	2	Q47337	Q47337 escherichia
38	21	21.4	18	7	Q9TNP1	Q9TNP1 mus sp. mhc
39	21	21.4	18	11	Q9QUX0	Q9QUX0 mus sp. tum
40	21	21.4	19	2	O53545	O53545 shigella so
41	21	21.4	19	6	Q9TRF7	Q9TRF7 oryctolagus
42	21	21.4	19	10	Q43370	Q43370 allium cepa
43	20	20.4	10	2	P96305	P96305 alteromonas
44	20	20.4	14	2	O54394	O54394 streptomyce
45	20	20.4	16	9	Q38407	Q38407 bacterioph

ALIGNMENTS

RESULT 1

Q73129 PRELIMINARY; PRT; 19 AA.
AC Q73129;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMELrel. 21, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMPLE P4.25-15;
RA Wolinsky S.M., Korber B.T.M., Neumann A.U., Daniels M., Kunstman K.J.,
RA Whetzel A.J., Cao Y., Ho D.D., Safrit J.T., Koup R.A.;
RT "Adaptive Evolution of Human Immunodeficiency Virus Type 1 During the
Natural Course of Infection";
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SAMPLE P4.25-15;
RA McDonald D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U36027; AAA97722.1; -;
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER
SQ SEQUENCE 19 AA; 2066 MW; E117102D52800BF4 CRC64;
Query Match 32.7%; Score 32; DB 15; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRLKSNDYA 10
|: :|||:
Db 7 EVVIRSDNFA 16

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RESULT 2
P83219 ID P83219 PRELIMINARY; PRT; 15 AA.
AC P83219;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE DE Calcitriol.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC TISSUE=NASAL MUCUS;
RX MEDLINE=21413725; PubMed=11522286;
RA Cole A.M., Kim Y.-H., Tahk S., Hong T., Weis P., Waring A.J., Ganz T.;
RT "Calcitriol, a novel antimicrobial peptide isolated from human airway
RT secretions.";
RL FEBS Lett. 504:5-10(2001).
CC -1- FUNCTION: POSSESSES ANTI-FUNGAL ACTIVITY AGAINST C. ALBICANS AND IS
CC ALSO ACTIVE AGAINST E. COLI AND P. AERUGINOSA BUT NOT
CC L. MONOCYTOGENES AND S. AUREUS.
CC -1- MASS SPECTROMETRY: MW=1688.9; METHOD=MALDI.
CC -1- MISCELLANEOUS: OPTIMUM PH IS 5.4.
CC -1- MISCELLANEOUS: ANTIMICROBIAL ACTIVITY IS ENHANCED BY ZNCL2.
CC -1- SIMILARITY: TO THE C-TERMINUS OF HUMAN CALGRANULIN C.
KW Antibiotic; Fungicide; Zinc; Metal-binding.
FT DOMAIN 9 13 ZINC-BINDING (POTENTIAL).
SQ SEQUENCE 15 AA; 1689 MW; CE4EC8DDFE961663 CRC64;

Query Match 30.6%; Score 30; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IRLKSDNYATH 12
DB 3 IALKAARVYHT 13

RESULT 3
Q9IBM5 ID Q9IBM5 PRELIMINARY; PRT; 15 AA.
AC Q9IBM5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Envelope glycoprotein, V3 region (Fragment).
GN ENV
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95115054; PubMed=7815476;
RA Ahmad N., Baroudy B.M., Baker R.C., Chappey C.;
RT "Genetic analysis of human immunodeficiency virus type 1 envelope V3
RT region isolates from mothers and infants after perinatal
RT transmission.";
RL J. Virol. 69:1001-1012(1995).
DR EMBL; U16595; AAA64161.1; -.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1794 MW; 747CGA6280EF4A1 CRC64;

Query Match 29.6%; Score 29; DB 15; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRLKSNDYVA 10
DB 4 EVIIRSDNFS 13

RESULT 4
Q9UC27 ID Q9UC27 PRELIMINARY; PRT; 13 AA.
AC Q9UC27;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE 94 kDa epididymal cyokeratin-like protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95226590; PubMed=7536047;
RA Boue F., Duquenne C., Lassealle B., Lefevre A., Finaz C.;
RT "FLB1, a human protein of epididymal origin that is involved in the
RT sperm-oocyte recognition process.";
RL Biol. Reprod. 52:267-278(1995).
SQ SEQUENCE 13 AA; 1610 MW; 000A683B81B7A45B CRC64;

Query Match 28.6%; Score 28; DB 4; Length 13;
Best Local Similarity 66.7%; Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 NYATHY 13
DB 1 NYSTYV 6

RESULT 5
Q9L434 ID Q9L434 PRELIMINARY; PRT; 19 AA.
AC Q9L434;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 2.4 kDa protein (Fragment).
GN PUTATIVE YCIE.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CS2;
RX MEDLINE=21160188; PubMed=11260470;
RA Robbe-Saule V., Coynault C., Ibanez-Ruiz M., Hermant D., Norel F.;
RT "Identification of a non-haem catalase in Salmonella and its
RT regulation by RpoS (sigma S).";
RL Mol. Microbiol. 39:1533-1545(2001).
DR EMBL; AJ251362; CAB71038.1; -.
KW Hypothetical protein.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2448 MW; 05D3DB83C7CBE7E5 CRC64;

Query Match 27.6%; Score 27; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 NYATHY 13
DB 2 NYTEHY 7

RESULT 6
Q9KHJ4 ID Q9KHJ4 PRELIMINARY; PRT; 13 AA.
AC Q9KHJ4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Proteolysis tag (Fragment).
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OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20345063; PubMed=10884408;
RA Keller K.C., Shapiro L., Williams K.P.;
RT "tRNAs that encode proteolysis-inducing tags are found in all known
RL bacterial genomes: A two-piece tRNA functions in Caulobacter.";
DR EMBL; AF255738; AAF87998.1; -.
FT NON TER
SQ SEQUENCE 13 AA; 1368 MW; CE5F60C57FCE1B1D CRC64;

Query Match 26.5%; Score 26; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 9.4e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 6 SDNYATHYA 14
:|:|:|:|
Db 2 NDNFAEFA 10

RESULT 7
ID Q9UWH6 PRELIMINARY; PRT; 15 AA.
AC Q9UWH6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE keto-valine-ferredoxin oxidoreductase alpha-subunit, VOR alpha
DE (Fragment).
OS Thermococcus litoralis.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Thermococcus.
OX NCBI_TaxID=2265;
RN [1]
RP SEQUENCE.
RX MEDLINE=96146528; PubMed=8550513;
RA Heider J., Mai X., Adams M.W.;
RT "Characterization of 2-ketoisovalerate ferredoxin oxidoreductase, a
RT new and reversible coenzyme A-dependent enzyme involved in peptide
RT fermentation by hyperthermophilic archaea.";
RL J. Bacteriol. 178:780-787(1996).
SQ SEQUENCE 15 AA; 1549 MW; OC1766910B222944 CRC64;

Query Match 26.5%; Score 26; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 3 RLKSDNYATHY 13
:|:|:|:|
Db 3 KVSNGYAAAY 13

RESULT 8
ID Q9TRT6 PRELIMINARY; PRT; 15 AA.
AC Q9TRT6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Pyruvate dehydrogenase (EC 1.2.4.1) (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92144618; PubMed=1737046;
RA Koike K., Urata Y., Goto S.;
RT "Proteinase-catalyzed activation of porcine heart muscle pyruvate

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RT dehydrogenase and identification of its cleavage site.";
RL Biochim. Biophys. Acta 1118:223-230(1992).
SQ SEQUENCE 15 AA; 1787 MW; DB1265CDF7737E16 CRC64;

Query Match 26.5%; Score 26; DB 6; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRLKSD 7
:|:|:|:|
Db 7 EVRSKSD 13

RESULT 9
ID Q9TRT4 PRELIMINARY; PRT; 15 AA.
AC Q9TRT4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Pyruvate dehydrogenase (EC 1.2.4.1) (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=92144618; PubMed=1737046;
RA Koike K., Urata Y., Goto S.;
RT "Proteinase-catalyzed activation of porcine heart muscle pyruvate
RT dehydrogenase and identification of its cleavage site.";
RL Biochim. Biophys. Acta 1118:223-230(1992).
SQ SEQUENCE 15 AA; 1757 MW; 94D6BFE4B126598 CRC64;

Query Match 26.5%; Score 26; DB 6; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EIRLKSD 7
:|:|:|:|
Db 3 EVRSKSD 9

RESULT 10
ID Q84863 PRELIMINARY; PRT; 19 AA.
AC Q84863;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 2.1 kDa protein (Fragment).
OS Unidentified human poliovirus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Enterovirus.
OX NCBI_TaxID=40278;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87169734; PubMed=3031313;
RA Kuge S., Saito I., Nomoto A.;
RT "Primary structure of poliovirus defective-interfering particle
RT genomes and possible generation mechanisms of the particles.";
RL J. Mol. Biol. 192:473-487(1986).
DR EMBL; M30221; AAA66829.1; -.
KW Hypothetical protein.
FT NON TER
FT NON TER
FT NON TER
SQ SEQUENCE 19 AA; 2106 MW; F774197992500AC8 CRC64;

Query Match 26.5%; Score 26; DB 12; Length 19;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 NVATH 12.

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Db          |||||
           9 NYTH 13

RESULT 11
Q9V2X3
ID Q9V2X3 PRELIMINARY; PRT; 17 AA.
AC Q9V2X3;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE RNA polymerase subunit B', (Fragment).
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88198019; PubMed=2834336;
RA Schallenberg J., Moss M., Truss M., Reiser W., Thomm M., Stetter K.O.,
RA Klein A.;
RT "Cloning and physical mapping of RNA polymerase genes from
RT Methanobacterium thermoautotrophicum and comparison of homologies and
RT gene orders with those of RNA polymerase genes from other Methanogenic
RT archaeobacteria."
RL J. Bacteriol. 170:2247-2253(1988).
DR EMBL; M20391; AAA72654.1; -.
FT NON TER 17
SQ SEQUENCE 17 AA; 2137 MW; 0C03CD9B6D780560 CRC64;

Query Match 25.5%; Score 25; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 THYAES 16
|||
Db 4 THYPEN 9

RESULT 12
Q9TWR4
ID Q9TWR4 PRELIMINARY; PRT; 13 AA.
AC Q9TWR4;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TRENBLrel. 13, Last annotation update)
DE Peptide T-BRADYKININ potentiator.
OS Tityus serrulatus (Brazilian scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Eutherozoa; Eutherozoa; Eutherozoa; Eutherozoa; Eutherozoa;
OX NCBI_TaxID=6887;
RN [1]
RP SEQUENCE.
RX MEDLINE=94024945; PubMed=8212046;
RA Ferreira L.A., Alves E.W., Henriques O.B.;
RT "Peptide T, a novel bradykinin potentiator isolated from Tityus
RT serrulatus scorpion venom."
RL Toxicon 31:941-947(1993).
SQ SEQUENCE 13 AA; 1604 MW; 35770B0644FC02D7 CRC64;

Query Match 24.5%; Score 24; DB 5; Length 13;
Best Local Similarity 44.4%; Pred. No. 2e+03;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 KSDNYATHY 13
|||
Db 1 KKDGYPVEY 9

RESULT 13
Q93057
ID Q93057 PRELIMINARY; PRT; 14 AA.
AC Q93057;

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```

DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE B cell specific activator protein BSAP (PAX5) (Fragment).
OS PAX5 OR PAX-5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Iida S., Rao P.H., Nallasivam P., Hibshoosh H., Butler M., Louie D.C.,
RA Dyonin V., Ohno H., Chaganti R.S.K., Dalla-Favera R.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96234102; PubMed=8650231;
RA Busslinger M., Klix N., Pfeffer P., Graninger P.G., Kozmik Z.;
RT "Deregulation of PAX-5 by translocation of the Emu enhancer of the Igh
RT locus adjacent to two alternative PAX-5 promoters in a diffuse large-
RT cell lymphoma."
RL Proc. Natl. Acad. Sci. U.S.A. 93:6129-6134(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=MARGINAL ZONE LYMPHOMA;
RA Morrison A.M., Jaeger U., Chott A., Haas O.A., Schebesta M.,
RA Busslinger M.;
RT "Deregulated PAX-5 transcription from a translocated Igh promoter in
RT marginal zone lymphoma."
RL Blood 0:0-0(1998).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=21354098; PubMed=11460166;
RA Fasqualucci L., Neumeister P., Goossens T., Nanjangud G.,
RA Chaganti R.S.K., Kupperts R., Dalla-Favera R.;
RT "Hypermutation of multiple proto-oncogenes in B-cell diffuse large-
RT cell lymphomas."
RL Nature 412:341-346(2001).
DR EMBL; U62539; AAB09533.1; -.
DR EMBL; U56836; AAB16833.1; -.
DR EMBL; AF074913; AAC69188.1; -.
DR EMBL; AF386791; AAK70870.1; -.
FT NON TER 14
SQ SEQUENCE 14 AA; 1683 MW; E113518FA19953A1 CRC64;

Query Match 24.5%; Score 24; DB 4; Length 14;
Best Local Similarity 45.5%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EIRKSDNYAT 11
|||
Db 2 EIRCKHDPFAS 12

RESULT 14
P70319
ID P70319 PRELIMINARY; PRT; 14 AA.
AC P70319;
DT 01-FEB-1997 (TRENBLrel. 02, Created)
DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
DT 01-NOV-1998 (TRENBLrel. 08, Last annotation update)
DE B-cell specific transcription factor (Fragment).
GN PAX-5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SV;
RT MEDLINE=96234102; PubMed=8650231;
RA Busslinger M., Klix N., Pfeffer P., Graninger P.G., Kozmik Z.;
RT "Deregulation of PAX-5 by translocation of the Emu enhancer of the Igh

```

RT Locus adjacent to two alternative PAX-5 promoters in a diffuse large-cell lymphoma.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:6129-6134(1996).
 DR EMBL; U56838; AAB16835.1; -.
 FT NON TER 14 14
 SQ SEQUENCE 14 AA; 1683 MW; E113518PA19953A1 CRC64;

Query Match 24.5%; Score 24; DB 11; Length 14;
 Best Local Similarity 45.5%; Pred. No. 2.2e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EIRLKSDNYAT 11
 ||| |
 Db 2 EIHCKHDPFAS 12

RESULT 15

Q93LE4 PRELIMINARY; PRT; 9 AA.
 AC Q93LE4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Proteolysis tag (Fragment).
 OS Helicobacter mobilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Helicobacteriaceae; Helicobacter.
 OX NCBI_TaxID=28064;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20063247; PubMed=10592213;
 RA Williams K.P.;
 RT "The tRNA website."
 RL Nucleic Acids Res. 28:169-168(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Williams K.P.;
 RT "Phylogenetic analysis of tRNA."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY040838; AAK83526.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 9 AA; 937 MW; 7CD8D72DCB544AAB CRC64;

Query Match 23.5%; Score 23; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.7e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 DNYA 10
 ||||
 Db 3 DNYA 6

Search completed: April 22, 2003, 13:49:34
 Job time : 30 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:42:32 ; Search time 73 Seconds
(without alignments)
34.682 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRKSDNYTHAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 278369

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq 101002.*

- 1: /SID22/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SID22/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SID22/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
- 4: /SID22/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
- 5: /SID22/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
- 6: /SID22/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
- 7: /SID22/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
- 8: /SID22/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
- 9: /SID22/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
- 10: /SID22/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
- 11: /SID22/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
- 12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
- 13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
- 14: /SID22/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
- 15: /SID22/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
- 16: /SID22/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
- 17: /SID22/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
- 18: /SID22/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
- 19: /SID22/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SID22/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	19	21	AAU70371
2	91	92.9	19	22	AAU70380
3	80	81.6	17	21	AAU74933
4	74	75.5	16	20	AAU30033
5	70	71.4	19	21	AAU30034
6	68	69.4	19	23	AAU39862
7	65	66.3	19	23	AAU39862
8	64	65.3	19	20	AAU39862
9	52	53.1	17	23	AAU39862
10	49	50.0	19	22	AAU39862

11	49	50.0	19	23	AAU70371	Human heavy chain
12	48	49.0	19	23	AAU70380	Mouse heavy chain
13	47	48.0	19	16	AAU74933	H-CDR-2 of anti-id
14	46	46.9	17	21	AAU30034	Scaffold protein S
15	45	45.9	19	18	AAU39862	Mutant 3 of the CD
16	43	43.9	17	16	AAU75491	Mouse antibody var
17	43	43.9	17	21	AAU39862	Anti-hil12 antibody
18	43	43.9	17	23	AAU82463	Llama CDR2 region
19	43	43.9	18	21	AAU52188	Human anti-HB8 ant
20	42	42.9	16	23	AAU82611	Llama CDR2 region
21	42	42.9	17	20	AAU90323	Human anti-idiotyp
22	42	42.9	17	22	AAU10817	Human antibody CAT
23	42	42.9	17	23	AAU82537	Llama CDR2 region
24	42	42.9	17	23	AAU82550	Llama CDR2 region
25	41	41.8	17	14	AAU32117	Heavy chain CDR2 r
26	41	41.8	17	20	AAU90330	Human anti-idiotyp
27	41	41.8	17	21	AAU39846	Anti-hil12 antibod
28	41	41.8	17	22	AAU67496	Human heavy chain
29	41	41.8	17	23	AAU82488	Llama CDR2 region
30	41	41.8	17	23	AAU82543	Llama CDR2 region
31	41	41.8	19	18	AAU39394	Mutant 5 of the CD
32	41	41.8	19	21	AAU95202	Anti-platelet glyco
33	41	41.8	19	23	AAU99858	Mouse Hefi antibod
34	40	40.8	16	20	AAU40695	A3 derivative #16,
35	40	40.8	16	23	AAU82466	Llama CDR2 region
36	40	40.8	17	18	AAU16651	Anti-cancer specif
37	40	40.8	17	20	AAU05054	Tumour antigen ant
38	40	40.8	17	21	AAU39819	Anti-hil12 antibod
39	40	40.8	17	21	AAU39883	Anti-hil12 antibod
40	40	40.8	17	21	AAU39868	Anti-hil12 antibod
41	40	40.8	17	22	AAU95213	Human scFv clone 2
42	40	40.8	17	22	AAU99156	Anti-platelet glyco
43	40	40.8	17	22	AAU84980	Human scFv clone 2
44	40	40.8	17	22	AAU61294	D12 scFv CDR H2 re
45	40	40.8	17	22	AAU65311	Anti-TANGO 268 scF
						Anti-IL-18 antibod

ALIGNMENTS

RESULT 1
AAU32258
ID AAU32258 standard, Peptide; 19 AA.

XX AC AAU32258;

XX DT 15-FEB-2000 (first entry)

XX DE Light chain CDR H2 of mouse anti-CD23 Mab C11.

XX CD23, FCER11; IgE receptor; monoclonal antibody; C11; mouse;

XX monoclinal antibody; chimeric antibody; humanised antibody;

XX complementarity determining region; CDR; autoimmune disease;

XX inflammation; arthritis; lupus erythematosus; multiple sclerosis;

XX Hashimoto's thyroiditis; diabetes; uveitis; dermatitis; psoriasis;

XX urticaria; nephrotic syndrome; glomerulonephritis;

XX inflammatory bowel disease; ulcerative colitis; Crohn's disease;

XX Sjogren's syndrome; allergy; asthma; rhinitis; eczema; insulinitis;

XX graft-versus-host disease; COPD; bronchitis; diabetes;

XX B-cell malignancy; therapy.

XX OS Mus musculus.

XX PN WO9958679-A1.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB01434.

XX PR 09-MAY-1998; 98GB-0009839.

XX PA (GLAX) GLAXO GROUP LTD.

PI Bonney J, Crowe SJ, Ellis JH, Rapson NT, Shearin J;
 XX WPI; 2000-053101/04.
 DR N-PSDB; AAZ34743.
 XX
 PT Cell receptor specific antibodies useful for treating e.g. arthritis,
 PT diabetes, multiple sclerosis and psoriasis -
 XX
 PS Claim 1; Page 40; 81pp; English.
 XX
 CC This sequence represents complementarity determining region 2
 CC (CDR H2) of the heavy chain of murine anti-CD23 (FCER1) monoclonal
 CC antibody C11 (see also AAY32263). The invention provides altered
 CC antibodies, such as chimeric or humanised antibodies, which comprise
 CC sufficient of the amino acid sequences of C11 light and heavy chain
 CC CDRs (see AAY32254-59) to render them capable of binding to the CD23
 CC type II molecule expressed on haematopoietic cells. The antibodies
 CC are used to block soluble CD23 formation for treatment of arthritis,
 CC lupus erythematosus, Hashimoto's thyroiditis, multiple sclerosis,
 CC diabetes, uveitis, dermatitis, psoriasis, urticaria, nephrotic
 CC syndrome, glomerulonephritis, inflammatory bowel disease, ulcerative
 CC colitis, Crohn's disease, Sjogren's syndrome, allergies, allergic
 CC asthma, intrinsic asthma, acute asthmatic exacerbation, rhinitis,
 CC eczema, graft-versus-host disease, COPD, sinusitis, bronchitis
 CC (particularly chronic bronchitis) or diabetes (particularly type 1
 CC diabetes), and B-cell malignancies (climbed). They are also useful
 CC for studying interactions between CD23 and various ligands and
 CC determining the binding agents.
 XX
 SQ Sequence 19 AA;
 Query Match 100.0%; Score 98; DB 21; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.4e-09;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLSDNYATHYAESVKG 19
 Db 1 EIRLSDNYATHYAESVKG 19
 RESULT 2
 AAB35297
 ID AAB35297 standard; Peptide; 19 AA.
 XX
 AC AAB35297;
 XX
 DT 08-MAY-2001 (first entry)
 XX
 DE Murine PSCA antibody fragment #5.
 XX
 KW Prostate stem cell antigen; PSCA; human; mouse; prostate cancer;
 KW diagnosis; treatment; chromosome 8q24.2.
 XX
 OS Mus sp.
 XX
 PN WO200105427-A1.
 XX
 PD 25-JAN-2001.
 XX
 PF 20-JUL-2000; 2000WO-US19967.
 XX
 PR 20-JUL-1999; 99US-0359326.
 PR 03-MAY-2000; 2000US-0564329.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PA (UROC-) UROGENESYS.
 XX
 PI Reiter R, Witte O, Saffran DC, Jakobovits A;
 XX WPI; 2001-159478/16.
 XX
 PT Antibodies binding to prostate stem cell antigen inhibit the growth of
 PT cancer cells and are used to detect and treat prostate, pancreatic or

PT bladder cancers -
 XX
 PS Example 21; Fig 61; 229pp; English.
 XX
 CC The present invention describes a method of treating cancer associated
 CC with prostate stem cell antigen (PSCA) by administering an antibody which
 CC selectively binds to PSCA and inhibits the growth of the cancer cells.
 CC The PSCA gene is found on human chromosome 8q24.2. The invention provides
 CC the human and murine PSCA protein and coding sequences, which can be used
 CC not only in the treatment of, but also in detection and prognosis of
 CC prostate cancer.
 XX
 SQ Sequence 19 AA;
 Query Match 92.9%; Score 91; DB 22; Length 19;
 Best Local Similarity 89.5%; Pred. No. 2e-08;
 Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIRLSDNYATHYAESVKG 19
 Db 1 EIRLSDNYATHYAESVKG 19
 RESULT 3
 AAB30033
 ID AAB30033 standard; Peptide; 17 AA.
 XX
 AC AAB30033;
 XX
 DT 09-FEB-2001 (first entry)
 XX
 DE Scaffold protein SCA A3 peptide SEQ ID NO: 94.
 XX
 KW Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
 KW SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
 KW diabetic retinopathy; atherosclerosis.
 XX
 OS Synthetic.
 XX
 PN WO2000060070-A1.
 XX
 PD 12-OCT-2000.
 XX
 PF 01-APR-1999; 99WO-EP02283.
 XX
 PR 01-APR-1999; 99WO-EP02283.
 XX
 PA (INNO-) INNOGENETICS NV.
 XX
 PI Desmet J, Hufton S, Hoogenboom H, Sablon E;
 XX WPI; 2000-665002/64.
 XX
 PT Scaffold composed of single-chain polypeptide having beta sandwich
 PT architecture carrying new and randomized peptide sequences useful as
 PT supporting framework and carrying antigen- or receptor binding
 PT fragments -
 XX
 PS Disclosure; Page 14; 68pp; English.
 XX
 CC The present invention is concerned with producing scaffold proteins
 CC based upon the human CTLA-4 SCA domain. These scaffold proteins can be
 CC used as a scaffold to bind antigen- or receptor-binding fragments. These
 CC can be used in the treatment of diseases such as cancer,
 CC atherosclerosis, thrombosis, osteoporosis, rheumatoid arthritis and
 CC diabetic retinopathy. Sequences AAB29930-B29939 were used in the
 CC production of the proteins of the invention.
 XX
 SQ Sequence 17 AA;
 Query Match 81.6%; Score 80; DB 21; Length 17;
 Best Local Similarity 88.2%; Pred. No. 1.2e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVK 19
 |||:|||||
 Db 1 RLNSDNFATHYAESVK 17

RESULT 4
 AAY40694
 ID AAY40694 standard; peptide; 16 AA.
 AC AAY40694;

XX 01-DEC-1999 (first entry)

XX A3 derivative #15, beta strand of scaffold protein structure.

XX Scaffold protein; beta strand; beta sheet; stabilize antigen; vaccine;
 KW tumour; chemotherapeutic agent.

XX Synthetic.

XX EP947582-A1.

XX 06-OCT-1999.

XX 31-MAR-1998; 98EP-0870065.

XX 31-MAR-1998; 98EP-0870065.

XX (INNO-) INNOGENETICS NV.

XX Desmet J, Hufton S, Hoogenboom H, Sablon E;

XX WPI; 1999-542958/46.

XX New scaffold protein, useful for stabilizing antigens used as vaccines

XX Disclosure; Page 6; 105pp; English.

XX Sequences AAY40680-Y40703 are functionally equivalent derivatives of the
 CC A3 peptide (AAY40605) which forms part of a scaffold protein. A3 is a
 CC beta strand peptide which forms part of a beta sheet. Peptides
 CC (AAY40601-Y40609) together form a single-chain scaffold protein which
 CC contains at least 1 disulfide bond, contains less than 10% alpha helix
 CC and contains at least 6 beta-strands. The scaffold protein is constructed
 CC of beta strands S1-S6, and may also include beta strands A1-A3, or any
 CC functionally equivalent derivative of these sequences. The beta strands
 CC form two beta sheets S1/S4/S3 and S6/S5/S2 with each strand connected to
 CC the next by hydrogen bonds, which generate a beta sandwich architecture.
 CC If the additional beta strands A1-A3 are included in the structure the
 CC scaffold is constructed of two beta sheets, with the structures
 CC A1/S1/S4/S3 and S6/S5/S2/A2/A3. The beta strands are connected to each
 CC other via amino acid loops, where at least one of the loops binds to a
 CC receptor or antigen. The scaffold protein is used to stabilize antigens
 CC or whole proteins such as receptors, or their fragments. It may be used
 CC to bind two separate molecules. For example, one surface of the scaffold
 CC may be bound to a protein which binds to a tumour antigen. This will
 CC target the complex to tumour cells. Another surface may be bound to a
 CC cytotoxic molecule or an autoimmune antibody which may then kill the
 CC tumour cells. Therefore the scaffold protein may be used to target
 CC chemotherapeutic agents to specific cells. It may also be used to
 CC stabilize individual peptides in a peptide library and may be used in
 CC diagnostic techniques, and to stabilize antigens used as vaccines.

XX Sequence 16 AA;

Query Match 75.5%; Score 74; DB 20; Length 16;
 Best Local Similarity 87.5%; Pred. No. 1.1e-05;
 Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVK 18
 |||:|||||

Db 1 RLNSDNFATHYAESVK 16

RESULT 5

AAB10002
 ID AAB10002 standard; Protein; 19 AA.
 XX AAB10002;

XX 01-NOV-2000 (first entry)

XX H. pylori 26 kDa protein-binding antibody heavy chain CDR2 peptide.

XX Acid-resistant microorganism; detection; faecal; intestine; infection;
 KW monoclonal antibody; heavy chain; complementarity determining region;
 KW CDR.

XX Unidentified.

XX WO200026671-A1.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-EP08212.

XX 29-OCT-1998; 98EP-0120517.

XX 06-NOV-1998; 98EP-0120687.

XX (CONN-) CONNEX GMBH.

XX Reiter C, Cullmann G, Friedrichs U, Heppner P, Lakner M;
 PI Ringeis A;

XX WPI; 2000-365747/31.

XX N-PSDB; AAA40158.

XX Detecting infection by acid-fast microbes for diagnosis of Helicobacter
 PT. pylori, comprises reacting a faecal sample with two binding reagents for
 PT antigens that survive intestinal passage

XX Claim 22; Page 21; 84pp; German.

XX This invention describes a novel method for the detection of a mammalian
 CC infection by an acid-resistant microorganism (A) by treating a faecal
 CC sample with at least two different monoclonal antibodies (MAb) (or their
 CC fragments or derivatives) or aptamers (collectively (I)) and detecting
 CC formation of a complex (C) between (I) and the corresponding antigen of
 CC (A). The first and second (I) bind to epitopes of different antigens
 CC (Ag). These epitopes are present, after passage through the intestines,
 CC in at least some mammals, and have either: (i) their native structure,
 CC or (ii) a structure against which an antibody is produced by an animal
 CC infected or immunized with (A), or its extract, lysate, derived protein
 CC or fragment, or with a synthetic peptide. Practically all mammals display
 CC at least one of the specified epitopes. The method is used to detect
 CC infection by acid-fast bacteria, particularly of the genera Helicobacter,
 CC Mycobacterium and Campylobacter, specifically H. pylori, H. hepaticus,
 CC M. tuberculosis, C. jejuni and C. pylori. (I) may also be used
 CC therapeutically. The method is direct and non-invasive, and provides an
 CC inexpensive and easily standardizable diagnosis, despite possible
 CC degradation of antigens during passage through the intestines. This
 CC sequence represents a fragment of a H. pylori 26 kDa protein-binding
 CC antibody heavy chain complementarity determining region CDR2 which is
 CC used to illustrate the method of the invention.

XX Sequence 19 AA;

Query Match 71.4%; Score 70; DB 21; Length 19;
 Best Local Similarity 82.4%; Pred. No. 6.5e-05;
 Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVK 18

Db 2 IRLKSDNYATYVANSVK 18

PN WO9857994-A2.
 XX
 PD 23-DEC-1998.
 XX
 PF 16-JUN-1998; 98WO-US12402.
 XX
 PR 16-JUN-1997; 97US-0049871.
 XX
 PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX
 PI Fischer GW, Schuman RF, Stinson JL, Wong H;
 XX WPI; 1999-095329/08.
 DR N-PSDB; AAU05581.
 DR
 XX New antibodies to lipoteichoic acid of gram positive bacteria - used
 XX to develop products for the diagnosis, prevention and treatment of
 PT infections caused by gram positive bacteria
 PT
 XX Claim 21; Fig 12; 150pp; English.
 PS
 XX The invention relates to a monoclonal antibody (Mab) to lipoteichoic
 CC acid of gram positive bacteria, where the Mab is a chimeric
 CC immunoglobulin comprising at least part of a human immunoglobulin
 CC constant region and at least part of a non-human immunoglobulin variable
 CC region having specificity to lipoteichoic acid of gram positive bacteria.
 CC The antibodies bind to whole bacteria and enhance phagocytosis and
 CC killing of the bacteria and enhance protection from lethal infection. The
 CC antibodies or peptides (encoded by a DNA of the variable region of
 CC anti-lipoteichoic acid antibody or characterised by amino acids
 CC corresponding to one or more of the complementarity determining regions
 CC (CDRs) of the variable region of the antibody) can be used for treating
 CC or preventing infections caused by gram positive bacteria. They can also
 CC be used for the diagnosis of gram positive bacterial infections.
 CC Sequences AAU94735-39 represent heavy chain variable regions of the
 CC anti-lipoteichoic antibody 96-100.
 XX
 SQ Sequence 19 AA;
 Query Match 65.3%; Score 64; DB 20; Length 19;
 Best Local Similarity 76.5%; Pred. NO. 0.0065;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 IRLKSDNYATHYAESVK 18
 |||||:|||||:
 Db 2 IRLKSDNYATHYAESVK 18
 |||||:|||||:
 RESULT 9
 AAU82539
 ID AAU82539 standard; peptide; 17 AA.
 XX
 AC AAU82539;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Llama CDR2 region variable heavy chain fragment #32.
 XX
 XX Llama; phage display library; variable heavy domain fragment; VHH; VH;
 KW sAb fragment; single domain anti-idiotypic antibody fragment;
 KW phage display technology; immune system response; CDR1/H1, CDR2; CDR3;
 KW complementarity determining region.
 XX
 OS Lama guanicoe glama.
 XX
 XX WO200190190-A2.
 PN
 XX 29-NOV-2001.
 PD
 XX 25-MAY-2001; 2001WO-CA00763.
 PF
 XX 26-MAY-2000; 2000US-207234P.
 PR
 XX

PA (CANA) NAT RES COUNCIL CANADA.
 XX
 PI Tanha J, Dubuc G, Narang S;
 XX WPI; 2002-083093/11.
 DR
 XX New phage display library of variable heavy domain antigen-binding
 PT fragments derived from llama antibodies, useful for in vitro selection
 PT against any antigen of interest as a target -
 XX
 PS Claim 16; Page 32; 46pp; English.
 XX
 CC The present invention relates to a phage display library of variable
 CC heavy domain (VHH or VH) fragments (sAb fragments) derived from llama
 CC antibodies. The library is useful for in vitro selection against any
 CC antigen of interest as a target. Single domain anti-idiotypic antibody
 CC fragments are isolated from the library using phage display technology
 CC and an antibody serving as an antigen. Such anti-idiotypic antibody
 CC fragments have great potential in evoking the immune system response
 CC to pathological antigens and in vaccine development. The large size of
 CC the library considerably increases the probability of isolating from it
 CC antigen-binding fragments having high affinity to almost any
 CC predetermined target (antigen of interest). The library eliminates the
 CC development of anti-idiotypic antibodies by immunisation and allows
 CC isolation of anti-idiotypic antibodies. AAU82435-AAU82635 represent
 CC the llama heavy chain domain fragments of the invention.
 XX
 SQ Sequence 17 AA;
 Query Match 53.1%; Score 52; DB 23; Length 17;
 Best Local Similarity 58.8%; Pred. NO. 0.058;
 Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Qy 3 RLKSDNYATHYAESVK 19
 |||||:|||||:
 Db 1 RLKSDNYATHYAESVK 17
 |||||:|||||:
 RESULT 10
 AAR74934
 ID AAR74934 standard; peptide; 19 AA.
 XX
 AC AAR74934;
 XX
 DT 19-JAN-1996 (first entry)
 XX
 DE H-CDR-2 of anti-idiotypic antibody against human anticancer antibody.
 XX
 KW Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
 KW complementarity determining region.
 XX
 OS Mus sp.
 XX
 PN JP07101999-A.
 XX
 PD 18-APR-1995.
 XX
 PF 06-OCT-1993; 93JP-0272950.
 XX
 PR 06-OCT-1993; 93JP-0272950.
 XX
 PA (HAGI/) HAGIWARA Y.
 XX
 XX WPI; 1995-182987/24.
 DR
 XX Novel anti-idiotypic antibody against an human anticancer monoclonal
 PT antibody - and DNA sequences encoding the antibody, useful in
 PT pharmacology, medicine and biochemical fields.
 XX
 PS Claim 1; Page 2; 28pp; Japanese.
 XX
 CC A new anti-idiotypic antibody against a human anticancer monoclonal
 CC antibody is claimed. This antibody contains in its heavy chain 3
 CC

CC complementarity determining regions CDR1 (AAR74929-R74931), CDR2
 CC (AAR74932-R74935) and CDR3 (AAR74936-R74939), this is also true of the
 CC light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2
 CC (AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA
 CC encoding it are useful in pharmacological, medical and biochemical
 CC fields.

XX SQ Sequence 19 AA;
 Query Match 50.0%; Score 49; DB 16; Length 19;
 Best Local Similarity 55.6%; Pred. No. 0.21;
 Matches 10; Conservative 3; Mismatches 0; Indels 5; Gaps 0;

QY 2 IRLKSDNYATHYAESVKG 19
 |||:|:|:|:|:|
 Db 2 IRNKANYTTEYSASVKG 19
 |||:|:|:|:|:|

RESULT 11
 AAU70371
 ID AAU70371 standard; Peptide; 19 AA.
 AC AAU70371;
 XX 14-FEB-2002 (first entry)
 DT Human heavy chain III CDR 2.
 DE Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array;
 KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX Homo sapiens.
 XX WO200183806-A1.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14349.
 XX 02-MAY-2000; 2000US-0563222.
 XX (EPIC-) EPICYTE PHARM INC.
 XX Hiatt AC, Hein MB;
 XX WPI; 2002-055482/07.
 XX Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array -
 XX Disclosure; Page 15; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that
 CC binds to a ligand, and transformed plant cells are selected, and
 CC preparing an IgBP array in plant cells. At least one peptide sequence has
 CC at least 75% sequence identity to a framework region (FR) of a native
 CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
 CC The method is useful for preparing an immunoglobulin binding protein
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
 CC CHBP is useful for discovery of e.g. insect cells or mammalian cells). The
 CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
 CC desired characteristics. The present sequence is a mammalian
 CC immunoglobulin derived peptide that may be incorporated into an IgBP of
 CC the invention.

XX SQ Sequence 19 AA;
 Query Match 50.0%; Score 49; DB 23; Length 19;
 Best Local Similarity 60.0%; Pred. No. 0.21;
 Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 KSDNYATHYAESVKG 19
 |||:|:|:|:|:|
 Db 5 KTDGGSTYADSVKG 19
 |||:|:|:|:|:|

RESULT 12
 AAU70380
 ID AAU70380 standard; Peptide; 19 AA.
 AC AAU70380;
 XX 14-FEB-2002 (first entry)
 DT Mouse heavy chain III CDR 2.
 DE Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
 KW complementarity determining region; framework region; IgBP;
 KW transgenic plant; immunoglobulin binding protein array;
 KW IgM; IgG; IgA; IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
 XX Mus musculus.
 XX WO200183806-A1.
 XX 08-NOV-2001.
 XX 02-MAY-2001; 2001WO-US14349.
 XX 02-MAY-2000; 2000US-0563222.
 XX (EPIC-) EPICYTE PHARM INC.
 XX Hiatt AC, Hein MB;
 XX WPI; 2002-055482/07.
 XX Preparing immunoglobulin binding protein array in plant cells by
 PT transforming the cells with different polynucleotides encoding binding
 PT protein polypeptides specific to ligand, selecting plant cells for
 PT preparing array -
 XX Disclosure; Page 15; 129pp; English.

XX The invention relates to transforming a population of cells (e.g. plant
 CC cells), comprising using a library of two different polynucleotides
 CC encoding different immunoglobulin binding protein (IgBP) polypeptides
 CC that specifically bind to a ligand or form one or more disulphide bonds
 CC with polypeptides in transfected cells, to generate an IgBP that
 CC binds to a ligand, and transformed plant cells are selected, and
 CC preparing an IgBP array in plant cells. At least one peptide sequence has
 CC at least 75% sequence identity to a framework region (FR) of a native
 CC IgM, IgG, IgA, IgD, IgE, IgY, kappa or lambda immunoglobulin molecule.
 CC The method is useful for preparing an immunoglobulin binding protein
 CC array, preferably heavy chain binding protein (CHBP) array in eukaryotic
 CC cells especially plant cells (e.g. Agrobacterium tumefaciens or maize)
 CC CHBP is useful for discovery of e.g. insect cells or mammalian cells). The
 CC CHBP is useful for discovery of e.g. screening assays of IgBPs having
 CC desired characteristics. The present sequence is a mammalian
 CC immunoglobulin derived peptide that may be incorporated into an IgBP of
 CC the invention.

XX SQ Sequence 19 AA;
 Query Match 49.0%; Score 48; DB 23; Length 19;
 Best Local Similarity 52.9%; Pred. No. 0.31;
 Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY	3	RLKSDNYATHYAESVKG 19	DB	3	RNKANDYTTTEYSASVKG 19
XX	XX	19-JAN-1996 (first entry)	XX	XX	19-JAN-1996 (first entry)
XX	XX	H-CDR-2 of anti-idiotypic antibody against human anticancer antibody.	XX	XX	H-CDR-2 of anti-idiotypic antibody against human anticancer antibody.
XX	XX	Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;	XX	XX	Antibody; cancer; CDR; heavy chain; light chain; immunoglobulin;
XX	XX	complementarity determining region.	XX	XX	complementarity determining region.
XX	XX	Mus sp.	XX	XX	Mus sp.
XX	XX	JP071011999-A.	XX	XX	JP071011999-A.
XX	XX	18-APR-1995.	XX	XX	18-APR-1995.
XX	XX	06-OCT-1993; 93JP-0272950.	XX	XX	06-OCT-1993; 93JP-0272950.
XX	XX	06-OCT-1993; 93JP-0272950.	XX	XX	06-OCT-1993; 93JP-0272950.
XX	XX	(HAGI/) HAGIWARA Y.	XX	XX	(HAGI/) HAGIWARA Y.
XX	XX	WPI; 1995-182987/24.	XX	XX	WPI; 1995-182987/24.
XX	XX	Novel anti-idiotypic antibody against an human anticancer monoclonal	XX	XX	Novel anti-idiotypic antibody against an human anticancer monoclonal
XX	XX	antibody - and DNA sequences encoding the antibody, useful in	XX	XX	antibody - and DNA sequences encoding the antibody, useful in
XX	XX	pharmacology, medicine and biochemical fields.	XX	XX	pharmacology, medicine and biochemical fields.
XX	XX	Claim 1; Page 2; 28pp; Japanese.	XX	XX	Claim 1; Page 2; 28pp; Japanese.
XX	XX	A new anti-idiotypic antibody against a human anticancer monoclonal	XX	XX	A new anti-idiotypic antibody against a human anticancer monoclonal
XX	XX	antibody is claimed. This antibody contains in its heavy chain 3	XX	XX	antibody is claimed. This antibody contains in its heavy chain 3
XX	XX	complementarity determining regions CDR1(AAR74929-R74931), CDR2	XX	XX	complementarity determining regions CDR1(AAR74929-R74931), CDR2
XX	XX	(AAR74932-R74935) and CDR3 (AAR74936-R74939), this is also true of the	XX	XX	(AAR74932-R74935) and CDR3 (AAR74936-R74939), this is also true of the
XX	XX	light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2	XX	XX	light chain which has its own CDR1 (AAR74944-R74946 and AAR85774), CDR2
XX	XX	(AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA	XX	XX	(AAR74947-R74949) and CDR3 (AAR74950-R74954). The antibody and DNA
XX	XX	encoding it are useful in pharmacological, medical and biochemical	XX	XX	encoding it are useful in pharmacological, medical and biochemical
XX	XX	fields.	XX	XX	fields.
XX	XX	Sequence 19 AA;	XX	XX	Sequence 19 AA;
XX	XX	Query Match 48.0%; Score 47; DB 16; Length 19;	XX	XX	Query Match 48.0%; Score 47; DB 16; Length 19;
XX	XX	Best Local Similarity 55.6%; Pred. No. 0.45;	XX	XX	Best Local Similarity 55.6%; Pred. No. 0.45;
XX	XX	Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;	XX	XX	Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX	XX	2 IRLKSDNYATHYAESVKG 19	XX	XX	2 IRLKSDNYATHYAESVKG 19
XX	XX	19-KAN-1996 (first entry)	XX	XX	19-KAN-1996 (first entry)
XX	XX	Scaffold protein SCA A3 peptide SEQ ID NO: 95.	XX	XX	Scaffold protein SCA A3 peptide SEQ ID NO: 95.
XX	XX	Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;	XX	XX	Human; CTLA-4; scaffold protein; antigen-binding; receptor-binding;
XX	XX	SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;	XX	XX	SCA domain; cancer; thrombosis; osteoporosis; rheumatoid arthritis;
XX	XX	diabetic retinopathy; atherosclerosis.	XX	XX	diabetic retinopathy; atherosclerosis.
XX	XX	Sequence 17 AA;	XX	XX	Sequence 17 AA;
XX	XX	Query Match 46.9%; Score 46; DB 21; Length 17;	XX	XX	Query Match 46.9%; Score 46; DB 21; Length 17;
XX	XX	Best Local Similarity 52.9%; Pred. No. 0.59;	XX	XX	Best Local Similarity 52.9%; Pred. No. 0.59;
XX	XX	Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;	XX	XX	Matches 9; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
XX	XX	3 RLKSDNYATHYAESVKG 19	XX	XX	3 RLKSDNYATHYAESVKG 19
XX	XX	1 RNKGNKYTTTEYSASVKG 17	XX	XX	1 RNKGNKYTTTEYSASVKG 17
XX	XX	RESULT 15	XX	XX	RESULT 15
XX	XX	AAW233392	XX	XX	AAW233392
XX	XX	ID AAW233392 standard; peptide; 19 AA.	XX	XX	ID AAW233392 standard; peptide; 19 AA.
XX	XX	AC AAW233392;	XX	XX	AC AAW233392;
XX	XX	20-MAR-1998 (first entry)	XX	XX	20-MAR-1998 (first entry)
XX	XX	Mutant 3 of the CDR2 region of the Campath-1H heavy chain.	XX	XX	Mutant 3 of the CDR2 region of the Campath-1H heavy chain.
XX	XX	Complementarity determining region 2; Campath-1; Campath-1H; antibody;	XX	XX	Complementarity determining region 2; Campath-1; Campath-1H; antibody;
XX	XX	lymphoma; CD52 antigen; loop 2; immunological tolerance; minimal mutant;	XX	XX	lymphoma; CD52 antigen; loop 2; immunological tolerance; minimal mutant;
XX	XX	antibody therapy; antioglobulin response; heavy chain; CDR.	XX	XX	antibody therapy; antioglobulin response; heavy chain; CDR.
XX	XX	Synthetic.	XX	XX	Synthetic.
XX	XX	Rattus sp.	XX	XX	Rattus sp.
XX	XX	Key Location/Qualifiers	XX	XX	Key Location/Qualifiers
XX	XX	Misc-difference 5 /label= K7D	XX	XX	Misc-difference 5 /label= K7D
XX	XX	/note= "wild type Lys substituted with Asp"	XX	XX	/note= "wild type Lys substituted with Asp"
XX	XX	WO9731024-A1.	XX	XX	WO9731024-A1.
XX	XX	28-AUG-1997.	XX	XX	28-AUG-1997.
XX	XX	20-FEB-1997; 97WO-GE00472.	XX	XX	20-FEB-1997; 97WO-GE00472.
XX	XX	20-FEB-1996; 96GB-0003507.	XX	XX	20-FEB-1996; 96GB-0003507.
XX	XX	(ISIS-) ISIS INNOVATION LTD.	XX	XX	(ISIS-) ISIS INNOVATION LTD.

XX Frewin MR, Gilliland LK, Tone M, Waldmann H, Walsh L;
PI WPI; 1997-435093/40.
XX
XX
XX Modified therapeutic antibody having reduced affinity for its
PT antigen - can induce immunological tolerance, e.g. to Campath-1
PT monoclonal antibodies used in antibody therapy of lymphoma and
PT leukaemia
XX
XX Claim 12; Fig 1; 43pp; English.
XX
XX Peptides AM23390-95 represent "minimal" mutant sequences of the
CC complementarity determining (CDR) region 2 of the humanised antibody
CC Campath-1, Campath-1H. Campath-1H heavy chain sequences encodes human
CC protein at all positions, except the 3 CDR regions. Campath-1 antibodies
CC have been used to induce remissions in lymphoma and leukemia patients
CC and for the treatment of rheumatoid arthritis and vasculitis. The target
CC antigen is CD52, which is a GPI-anchored cell-surface glycoprotein of
CC lymphocytes and monocytes. Loop 2, represented by residues 4-9 of the
CC present sequence, is important for binding to CD52. Mutations were made
CC within this region so as to abolish binding of the antibody to CD52,
CC which reduces affinity for the antigen, and induces immunological
CC tolerance. The present mutant contains a single charge difference from
CC Lys to Asp. The positive charge of Lys is thought to interact with
CC the negatively charged phosphate groups of the GPI anchor of CD52,
CC and this single mutation may destroy antigen binding. Antibody
CC therapy is often limited by an anti-antibody (antiglobulin) response
CC preventing retreatment with the antibody. The minimal mutants or
CC fragments may be used to induce tolerance to the therapeutic antibody in
CC patients. They can also be used in the manufacture of medicines for
CC induction of tolerance.
XX
XX SQ Sequence 19 AA;
Query Match 45.9%; Score 45; DB 18; Length 19;
Best Local Similarity 55.6%; Pred. No. 0.98;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
Oy 2 IRLKSDNYATHYAESVKG 19
Db 2 IRLKADGYTTEYNPSVLG 19

Search completed: April 22, 2003, 13:48:26
Job time : 74 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:49:38 ; Search time 41 Seconds
(without alignments)
37.133 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRLSDNYATHYAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 301932 seqs, 80129803 residues

Total number of hits satisfying chosen parameters: 53369

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT NEW PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06 NEW PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06 PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07 NEW PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08 PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09 PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10 NEW PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10 PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60 NEW PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60 PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	69.4	19	10	US-09-839-666-4
2	65	66.3	19	10	US-09-835-087-18
3	48	49.0	17	9	US-09-968-561A-98
4	48	49.0	17	10	US-09-192-854-60
5	46	46.9	17	9	US-09-968-561A-290
6	46	46.9	17	10	US-09-192-854-164
7	45	45.9	19	10	US-09-125-460A-4
8	45	45.9	19	10	US-09-730-857-85
9	43	43.9	17	9	US-09-968-561A-56
10	43	43.9	17	10	US-09-192-854-37
11	43	43.9	17	10	US-09-828-708-26
12	42	42.9	17	10	US-09-798-058-6
13	41	41.8	17	9	US-09-968-561A-8
14	41	41.8	17	9	US-09-968-561A-200
15	41	41.8	17	9	US-09-968-561A-206
16	41	41.8	17	10	US-09-192-854-4
17	41	41.8	17	10	US-09-192-854-115
18	41	41.8	17	10	US-09-125-460A-6
19	40	40.8	17	9	US-09-968-561A-14

20	40	40.8	17	9	US-09-968-561A-26	Sequence 26, Appl
21	40	40.8	17	9	US-09-968-561A-38	Sequence 38, Appl
22	40	40.8	17	9	US-09-968-561A-68	Sequence 68, Appl
23	40	40.8	17	9	US-09-968-561A-74	Sequence 74, Appl
24	40	40.8	17	9	US-09-968-561A-80	Sequence 80, Appl
25	40	40.8	17	9	US-09-968-561A-86	Sequence 86, Appl
26	40	40.8	17	9	US-09-968-561A-92	Sequence 92, Appl
27	40	40.8	17	9	US-09-968-561A-122	Sequence 122, Appl
28	40	40.8	17	9	US-09-968-561A-128	Sequence 128, Appl
29	40	40.8	17	9	US-09-968-561A-134	Sequence 134, Appl
30	40	40.8	17	9	US-09-968-561A-140	Sequence 140, Appl
31	40	40.8	17	9	US-09-968-561A-146	Sequence 146, Appl
32	40	40.8	17	9	US-09-968-561A-170	Sequence 170, Appl
33	40	40.8	17	9	US-09-968-561A-188	Sequence 188, Appl
34	40	40.8	17	9	US-09-968-561A-194	Sequence 194, Appl
35	40	40.8	17	9	US-09-968-561A-212	Sequence 212, Appl
36	40	40.8	17	9	US-09-968-561A-218	Sequence 218, Appl
37	40	40.8	17	9	US-09-968-561A-236	Sequence 236, Appl
38	40	40.8	17	9	US-09-968-561A-260	Sequence 260, Appl
39	40	40.8	17	9	US-09-968-561A-266	Sequence 266, Appl
40	40	40.8	17	9	US-09-968-561A-272	Sequence 272, Appl
41	40	40.8	17	9	US-09-968-561A-284	Sequence 284, Appl
42	40	40.8	17	9	US-09-968-561A-296	Sequence 296, Appl
43	40	40.8	17	9	US-09-968-561A-308	Sequence 308, Appl
44	40	40.8	17	9	US-09-968-561A-314	Sequence 314, Appl
45	40	40.8	17	9	US-10-161-145-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-839-666-4
; Sequence 4, Application US/09839666
; Patent No. US20020025513A1
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY EXCHANGER
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/839,666
; FILING DATE: 19-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/737,085
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/0C569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```

; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-839-666-4

Query Match          69.4%; Score 68; DB 10; Length 19;
Best Local Similarity 72.2%; Pred. No. 0.00017;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVK 19
   : ||| ||| ||| ||| |||
Db 2 VRKSFNYATYADSVKG 19

RESULT 2
US-09-835-087-18
; Sequence 18, Application US/09835087
; Patent No. US20020042370A1
; GENERAL INFORMATION:
; APPLICANT: Wayne W. Hancock
; TITLE OF INVENTION: Method of Treating Graft Rejection Using
; TITLE OF INVENTION: Inhibitors of CCR2 Function
; FILE REFERENCE: 1855-2008-003
; CURRENT APPLICATION NUMBER: US/09/835,087
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 09/549,448
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus Musculus
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (1)...(19)
; OTHER INFORMATION: CDR2 of murine mAb 1D9 heavy chain variable region
US-09-835-087-18

Query Match          66.3%; Score 65; DB 10; Length 19;
Best Local Similarity 70.6%; Pred. No. 0.00051;
Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVK 18
   ||| ||| ||| ||| |||
Db 2 IRTKNNYATYADSVKG 18

RESULT 3
US-09-968-561A-98
; Sequence 98, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 98
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
;
Query Match          46.9%; Score 46; DB 9; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.45;

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; ORGANISM: Homo sapiens
; US-09-968-561A-98

Query Match          49.0%; Score 48; DB 9; Length 17;
Best Local Similarity 52.9%; Pred. No. 0.22;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVK 19
   ||| ||| ||| ||| |||
Db 1 RIPARGTVTHYADSVKG 17

RESULT 4
US-09-192-854-60
; Sequence 60, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/066,729
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-192-854-60

Query Match          49.0%; Score 48; DB 10; Length 17;
Best Local Similarity 52.9%; Pred. No. 0.22;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVK 19
   ||| ||| ||| ||| |||
Db 1 RIPARGTVTHYADSVKG 17

RESULT 5
US-09-968-561A-290
; Sequence 290, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 290
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
;
Query Match          46.9%; Score 46; DB 9; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.45;

```


Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 SDNYATHYAESVKG 19
Db 4 SSGYGTGYADSVKG 17

RESULT 6

US-09-192-854-164
; Sequence 164, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; CURRENT APPLICATION NUMBER: US/09/192,854
; CURRENT FILING DATE: 1998-11-17
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 164
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-164

Query Match 46.9%; Score 46; DB 10; Length 17;
Best Local Similarity 64.3%; Pred. No. 0.45;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 SDNYATHYAESVKG 19
Db 4 SSGYGTGYADSVKG 17

RESULT 7

US-09-125-460A-4
; Sequence 4, Application US/09125460A
; Patent No. US20020048578A1
; GENERAL INFORMATION:
; APPLICANT: WALDMANN, Herwan
; APPLICANT: GILLILAND, LISA K
; APPLICANT: TONE, MASAHIDE
; APPLICANT: FREWIN, MARK R
; APPLICANT: WALSH, LOUISE
; TITLE OF INVENTION: ANTIBODY VARIANTS
; FILE REFERENCE: PP/NT/2794 US
; CURRENT APPLICATION NUMBER: US/09/125,460A
; CURRENT FILING DATE: 1998-08-19
; PRIOR APPLICATION NUMBER: PCT/GB97/00472
; PRIOR FILING DATE: 1997-02-20
; PRIOR APPLICATION NUMBER: GB 9603507.6
; PRIOR FILING DATE: 1996-02-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Peptide
US-09-125-460A-4

Query Match 45.9%; Score 45; DB 10; Length 19;
Best Local Similarity 55.6%; Pred. No. 0.73;
Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 2 IRLKSDNYATHYAESVKG 19
Db 2 IRDKADGYTEYNPVSIG 19

RESULT 8

US-09-730-857-85
; Sequence 85, Application US/09730857
; Patent No. US20020082396A1
; GENERAL INFORMATION:
; APPLICANT: Matsushima, Kouji
; Matsushima, Yoshihiro
; Yamada, Yoshiki
; Sato, Koh
; Tsuchiya, Masayuki
; Yamazaki, Tatsumi
; TITLE OF INVENTION: Reshaped Human Antibody to
; Interleukin-8
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, suite 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,857
; FILING DATE: 07-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/416,557
; FILING DATE: 1999-10-12
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 35029-20001.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; TELEFAX: 202-822-0168
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 85:
US-09-730-857-85

Query Match 45.9%; Score 45; DB 10; Length 19;
Best Local Similarity 50.0%; Pred. No. 0.73;
Matches 9; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IRLKSDNYATHYAESVKG 19
Db 2 IRNKANGYTREYSASVKG 19

RESULT 9

US-09-968-561A-56
; Sequence 56, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20

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; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-56

Query Match      43.9%; Score 43; DB 9; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.3;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19
   | : : : : :
Db 1 RITPAGHRTYYADSVKG 17

RESULT 10
US-09-192-854-37
; Sequence 37, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; APPLICANT: Tomlinson, Ian
; TITLE OF INVENTION: Methods for Selecting Functional Peptides
; FILE REFERENCE: 3789/72916
; CURRENT APPLICATION NUMBER: US/09/192,854
; EARLIER FILING DATE: 1998-11-17
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 37
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-192-854-37

Query Match      43.9%; Score 43; DB 10; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.3;
Matches 8; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19
   | : : : : :
Db 1 RITPAGHRTYYADSVKG 17

RESULT 11
US-09-828-708-26
; Sequence 26, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partic
; FILE REFERENCE: 1361.005U51
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 17
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-828-708-26

Query Match      43.9%; Score 43; DB 10; Length 17;
Best Local Similarity 47.1%; Pred. No. 1.3;
Matches 8; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 3 RLKSDNYATHYAESVKG 19
   | : : : : :
Db 1 RISGNSGTFYADSVKG 17

RESULT 12
US-09-798-058-6
; Sequence 6, Application US/09798058
; Patent No. US20020098523A1
; GENERAL INFORMATION:
; APPLICANT: Vaughan, Tristan John
; APPLICANT: Wilton, Alison Jane
; APPLICANT: Smith, Stephen
; APPLICANT: Main, Sarah Helen
; TITLE OF INVENTION: Human antibodies against eotaxin and their use
; FILE REFERENCE: 84632-000100
; CURRENT APPLICATION NUMBER: US/09/798,058
; CURRENT FILING DATE: 2001-08-29
; PRIOR APPLICATION NUMBER: US 60/187,246
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-058-6

Query Match      42.9%; Score 42; DB 10; Length 17;
Best Local Similarity 61.5%; Pred. No. 1.9;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 DNYATHYAESVKG 19
   | : : : : :
Db 5 DGSIKHYADSVKG 17

RESULT 13
US-09-968-561A-8
; Sequence 8, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-8
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```
Query Match          41.8%; Score 41; DB 9; Length 17;
Best Local Similarity 57.1%; Pred. No. 2.8;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 SDNYATHAESVKG 19
   |:|:|:|:|:|:|
Db 4 SEGWPITYADSVKG 17

RESULT 14
US-09-968-561A-200
; Sequence 200, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 200
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-200

Query Match          41.8%; Score 41; DB 9; Length 17;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 ATHYAESVKG 19
   |:|:|:|:|
Db 8 ATRYADSVKG 17

RESULT 15
US-09-968-561A-206
; Sequence 206, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 206
; LENGTH: 17
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-968-561A-206

Query Match          41.8%; Score 41; DB 9; Length 17;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 ATHYAESVKG 19
   |:|:|:|:|
Db 8 ATRYADSVKG 17

Search completed: April 22, 2003, 13:57:09
Job time : 42 secs
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OM protein - protein search, using sw model

Run on: April 22, 2003, 13:47:08 ; Search time 14 Seconds
(without alignments)
39.931 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRKSDNYATHYAESVKG 19

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Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 127244

Minimum DB seq length: 0

Maximum DB seq length: 19

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	69.4	19	2	US-08-737-085A-4
2	68	69.4	19	3	US-09-246-258-4
3	68	69.4	19	4	US-09-532-106-4
4	68	69.4	19	4	US-09-839-666-4
5	66	67.3	19	1	US-07-977-696C-78
6	66	67.3	19	1	US-08-129-930B-78
7	66	67.3	19	4	US-08-976-288A-78
8	49	50.0	19	1	US-08-318-970B-6
9	47	48.0	19	1	US-08-318-970B-5
10	45	45.9	19	2	US-08-765-783A-85
11	45	45.9	19	4	US-09-416-557-85
12	44	44.9	17	1	US-08-264-093-22
13	39	39.8	14	2	US-08-452-724A-41
14	39	39.8	17	2	US-08-650-262-14
15	38	38.8	17	2	US-08-053-171-31
16	37	37.8	19	4	US-09-280-028-8
17	36	36.7	17	2	US-08-480-434-25
18	36	36.7	17	2	US-08-480-434-33
19	36	36.7	17	2	US-08-053-451B-25
20	36	36.7	17	2	US-08-053-451B-33
21	34	34.7	17	1	US-07-988-925-2
22	34	34.7	17	2	US-08-362-780-2
23	33	33.7	16	1	US-08-366-953A-30
24	33	33.7	17	1	US-08-244-626-14
25	33	33.7	19	2	US-08-480-434-34
26	33	33.7	19	2	US-08-053-451B-34
27	32	32.7	16	4	US-09-170-769A-11

28 32 32.7 17 1 US-08-285-936-54 Sequence 54, Appl
29 32 32.7 17 1 US-08-487-860-54 Sequence 54, Appl
30 31 31.6 16 1 US-08-208-886C-84 Sequence 84, Appl
31 31 31.6 16 1 US-08-704-744-86 Sequence 86, Appl
32 31 31.6 16 1 US-08-463-557-65 Sequence 65, Appl
33 31 31.6 16 2 US-08-290-793B-65 Patent No. 5496552
34 30 30.6 14 6 5496552-4 Sequence 16, Appl
35 30 30.6 17 4 US-09-406-532-16 Sequence 6, Appl
36 30 30.6 17 4 US-09-406-535-6 Patent No. 5169835
37 29 29.6 8 6 5169835-28 Sequence 81, Appl
38 29 29.6 16 1 US-08-208-886C-81 Sequence 88, Appl
39 29 29.6 16 1 US-08-208-886C-88 Sequence 83, Appl
40 29 29.6 16 1 US-08-704-744-83 Sequence 90, Appl
41 29 29.6 16 1 US-08-704-744-90 Sequence 29, Appl
42 29 29.6 16 1 US-08-366-953A-29 Sequence 31, Appl
43 29 29.6 16 1 US-08-366-953A-31 Sequence 62, Appl
44 29 29.6 16 1 US-08-469-557-62 Sequence 69, Appl
45 29 29.6 16 1 US-08-469-557-69

ALIGNMENTS

RESULT 1
US-08-737-085A-4
; Sequence 4, Application US/08737085A
; Patent No. 5869232
; GENERAL INFORMATION:
; APPLICANT: SALLBERG, MATTI
; TITLE OF INVENTION: ANTIGEN/ANTIBODY SPECIFICITY
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DARBY & DARBY PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,085A
; FILING DATE: 27-DEC-1996
; CLASSIFICATION: 426
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 3846/OC569
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7659
; TELEFAX: 212-753-6237
; TELEX: 236687

* INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-737-085A-4

Query Match 69.4%; Score 68; DB 2; Length 19;
Best Local Similarity 72.2%; Pred. NO. 8.6e-05;
Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRLKSDNYATHYAESVKG 19

[illegible][illegible]

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Db      ZIP: 10022  

        COMPUTER READABLE FORM:  

        MEDIUM TYPE: Diskette  

        COMPUTER: IBM Compatible  

        OPERATING SYSTEM: DOS  

        SOFTWARE: FastSeq for Windows Version 2.0  

        CURRENT APPLICATION DATA:  

        APPLICATION NUMBER: US/09/532.106  

        FILING DATE: 21-Mar-2000  

        PRIOR APPLICATION DATA:  

        APPLICATION NUMBER: US/08/737,085A  

        FILING DATE: 27-Dec-1996  

        ATTORNEY/AGENT INFORMATION:  

        NAME: Green, Reza  

        REGISTRATION NUMBER: 38,475  

        REFERENCE/DOCKET NUMBER: 3846/OC569  

        TELECOMMUNICATION INFORMATION:  

        TELEPHONE: 212-527-7659  

        TELEX: 212-753-6237  

        :  

        INFORMATIION FOR SEQ ID NO: 4:  

        SEQUENCE CHARACTERISTICS:  

        LENGTH: 19 amino acids  

        TYPE: amino acid  

        STRANDEDNESS: single  

        TOPOLOGY: linear  

        MOLECULE TYPE: peptide  

        SEQUENCE DESCRIPTION: SEQ ID NO: 4:  

US-09-532-106-4  

Query Match          69.4%; Score 68; DB 4; Length 19;  

Best Local Similarity 72.2%; Pred.No. 8.6e-05;  

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  

QY    2 IRLKSDNYATHYAESVKG 19  

       :||| ||||:||::|||  

DB     2 VRKSFPNATYYADSVKG 19  

       :||| ||||:||::|||  

RESULT 4  

US-09-839-666-4  

; Sequence 4, Application US/09839666  

; Patent No. 6469143  

; GENERAL INFORMATION:  

APPLICANT: SALLBERG, MATTI  

TITLE OF INVENTION: ANTIGEN/AntIBODY SPECIFICITY  

NUMBER OF SEQUENCES: 23  

CORRESPONDENCE ADDRESS:  

ADDRESSEE: DARBY & DARBY PC  

STREET: 805 Third Avenue  

CITY: New York  

STATE: New York  

COUNTRY: USA  

ZIP: 10022  

COMPUTER READABLE FORM:  

MEDIUM TYPE: Diskette  

COMPUTER: IBM Compatible  

OPERATING SYSTEM: DOS  

SOFTWARE: FastSeq for Windows Version 2.0  

CURRENT APPLICATION DATA:  

APPLICATION NUMBER: US/09/839,666  

FILING DATE: 19-Apr-2001  

CLASSIFICATION: <unknown>  

PRIOR APPLICATION DATA:  

APPLICATION NUMBER: 08/737,085  

FILING DATE: <Unknown>  

ATTORNEY/AGENT INFORMATION:  

NAME: Green, Reza  

REGISTRATION NUMBER: 38,475  

REFERENCE/DOCKET NUMBER: 3846/OC569  

TELECOMMUNICATION INFORMATION:  

TELEPHONE: 212-527-7659  

TELEX: 212-753-6237  

INFORMATION FOR SEQ ID NO: 4:  

SEQUENCE CHARACTERISTICS:  

LENGTH: 19 amino acids  

TYPE: amino acid  

STRANDEDNESS: single  

TOPOLOGY: linear  

MOLECULE TYPE: peptide  

US-09-246-258-4  

Query Match          69.4%; Score 68; DB 3; Length 19;  

Best Local Similarity 72.2%; Pred.No. 8.6e-05;  

Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  

QY    2 IRLKSDNYATHYAESVKG 19  

       :||| ||||:||::|||  

DB     2 VRKSFPNATYYADSVKG 19  

       :||| ||||:||::|||  

RESULT 3  

US-09-532-106-4  

; Sequence 4, Application US/09532106  

; Patent No. 6245895  

; GENERAL INFORMATION:  

APPLICANT: SALLBERG, MATTI  

TITLE OF INVENTION: ANTIGEN/AntIBODY SPECIFICITY  

NUMBER OF SEQUENCES: 23  

CORRESPONDENCE ADDRESS:  

ADDRESSEE: DARBY & DARBY PC  

STREET: 805 Third Avenue  

CITY: New York  

STATE: New York  

COUNTRY: USA
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TELEFAX: 212-753-6237
 TELEX: 236687
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 4:
 US-09-839-666-4

Query Match 69.4%; Score 68; DB 4; Length 19;
 Best Local Similarity 72.2%; Pred. No. 8.6e-05;
 Matches 13; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IRLKSDNYATHYAEVSKG 19
 Db 2 VRSKSFNYATYADSVKG 19

RESULT 5
 US-07-977-696C-78
 ; Sequence 78, Application US/07977696C
 ; Patent No. 5792852
 ; GENERAL INFORMATION:
 ; APPLICANT: do Couto Dr., Fernando J.R.
 ; APPLICANT: Ceriani Dr., Roberto L.
 ; APPLICANT: Peterson Dr., Jerry A.
 ; APPLICANT: Padlan Dr., Eduardo A.
 ; TITLE OF INVENTION: Analogue Peptides with Specificity
 ; TITLE OF INVENTION: for Carcinomas and Kit and Diagnostic Vaccination
 ; TITLE OF INVENTION: and Therapeutic Methods.
 ; NUMBER OF SEQUENCES: 81
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/977,696C
 ; FILING DATE: 11-16-92
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Amzel Ph.D., Viviana
 ; REGISTRATION NUMBER: 30,930
 ; REFERENCE/DOCKET NUMBER: P66 38227
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 748-6868
 ; TELEFAX: (510) 748-6688
 ; TELEX: n.a.
 ; INFORMATION FOR SEQ ID NO: 78:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-07-977-696C-78

Query Match 67.3%; Score 66; DB 1; Length 19;
 Best Local Similarity 68.4%; Pred. No. 0.00018;
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIRLKSNDYATHYAEVSKG 19
 Db 1 EIRKNANHATYDESVKG 19

RESULT 6
 US-08-129-930B-78
 ; Sequence 78, Application US/08129930B
 ; Patent No. 5804187
 ; GENERAL INFORMATION:
 ; APPLICANT: do Couto Dr., Fernando J.R.
 ; APPLICANT: Ceriani Dr., Roberto L.
 ; APPLICANT: Peterson Dr., Jerry A.
 ; APPLICANT: Padlan Dr., Eduardo A.
 ; TITLE OF INVENTION: Analogue Peptides with Broad
 ; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
 ; TITLE OF INVENTION: Diagnostic Vaccination and
 ; TITLE OF INVENTION: Therapeutic Methods
 ; NUMBER OF SEQUENCES: 96
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: V. AMZEL & ASSOC.
 ; STREET: 2055 No. 5804187th Broadway, Suite 201
 ; CITY: Walnut Creek
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94596
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/129,930B
 ; FILING DATE: September 30, 1993
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Amzel Ph.D., Viviana
 ; REGISTRATION NUMBER: 30,930
 ; REFERENCE/DOCKET NUMBER: CRFCC-008A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 521-1333
 ; TELEFAX: (510) 521-3541
 ; TELEX: n.a.
 ; INFORMATION FOR SEQ ID NO: 78:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 19 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-129-930B-78

Query Match 67.3%; Score 66; DB 1; Length 19;
 Best Local Similarity 68.4%; Pred. No. 0.00018;
 Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EIRLKSNDYATHYAEVSKG 19
 Db 1 EIRKNANHATYDESVKG 19

RESULT 7
 US-08-976-288A-78
 ; Sequence 78, Application US/08976288A
 ; Patent No. 6315997
 ; GENERAL INFORMATION:
 ; APPLICANT: do Couto Dr., Fernando J.R.
 ; APPLICANT: Ceriani Dr., Roberto L.
 ; APPLICANT: Peterson Dr., Jerry A.
 ; APPLICANT: Padlan Dr., Eduardo A.
 ; TITLE OF INVENTION: Analogue Peptides with Broad
 ; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
 ; TITLE OF INVENTION: Diagnostic Vaccination and
 ; TITLE OF INVENTION: Therapeutic Methods
 ; NUMBER OF SEQUENCES: 96
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pretty, Schroeder & Poplawski

```

; STREET: 444 South Flower St., 19th Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: Patent in Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/976,288A
; FILING DATE: No. 6315997ember 21, 1997
; CLASSIFICATION: 424
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/129,930
; FILING DATE: September 30, 1993
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/977,696
; FILING DATE: No. 6315997ember 16, 1992
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel Ph.D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P6639938
;
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
;
; TELE: n.a.
;
; INFORMATION FOR SEQ ID NO: 78:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
; US-08-976-288A-78
;
; Query Match 67.3%; Score 66; DB 4; Length 19;
; Best Local Similarity 68.4%; Pred. No. 0.00018;
; Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
;
; Qy 1 EIRLKSDNYATHYAESVKG 19
; Db 1 EIRKANNHATYDES VKG 19
;
; RESULT 8
; US-08-318-970B-6
; Sequence 6, Application US/08318970B
; Patent No. 5589573
;
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
;
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR2-2
; OTHER INFORMATION: hypervariable region
;
; US-08-318-970B-5
;
; Query Match 48.0%; Score 47; DB 1; Length 19;
; Best Local Similarity 55.6%; Pred. No. 0.21;
; Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```

```

;
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR2-3
; OTHER INFORMATION: hypervariable region
;
; US-08-318-970B-6
;
; Query Match 50.0%; Score 49; DB 1; Length 19;
; Best Local Similarity 55.6%; Pred. No. 0.1;
; Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
;
; Qy 2 IRLKSDNYATHYAESVKG 19
; Db 2 IRLKANNHATYDES VKG 19
;
; RESULT 9
; US-08-318-970B-5
; Sequence 5, Application US/08318970B
; Patent No. 5589573
;
; GENERAL INFORMATION:
; APPLICANT: Hideaki HAGIWARA, et al.
; TITLE OF INVENTION: AMINO ACID SEQUENCES OF ANTI-IDIOTYPIC
; TITLE OF INVENTION: ANTIBODIES AGAINST ANTI-CANCER HUMAN MONOCLONAL ANTIBODY
; TITLE OF INVENTION: AND DNA BASE SEQUENCES ENCODING THOSE SEQUENCES
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Office of Sherman and Shalloway
; STREET: 413 N. Washington Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: Dell System 210; Intel 80 285 Microprocessor
; OPERATING SYSTEM: MS DOS 3.3
; SOFTWARE: Word Perfect, Version 5.1
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,970B
; FILING DATE: October 6, 1994
; CLASSIFICATION: 530
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard A. Steinberg
; REGISTRATION NUMBER: 26,588
; REFERENCE/DOCKET NUMBER: S-2371
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 549-2282
; TELEFAX: (703) 836-0106
;
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: H-CDR2-2
; OTHER INFORMATION: hypervariable region
;
; US-08-318-970B-5
;
; Query Match 48.0%; Score 47; DB 1; Length 19;
; Best Local Similarity 55.6%; Pred. No. 0.21;
; Matches 10; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

```


21

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,171
FILING DATE: 22-APR-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-54-1
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..17
OTHER INFORMATION: /note= "Second
OTHER INFORMATION: complementarity-determining region (CDR2) of
OTHER INFORMATION: BR55-2 antibody heavy chain"
US-08-053-171-31

Query Match 38.8%; Score 38; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 5.4;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 10 ATHYAESVKG 19
Db 8 SSHYVDSVKG 17

Search completed: April 22, 2003, 13:50:14
Job time : 15 secs

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GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:48:49 ; Search time 16.625 Seconds
(without alignments)
33.626 Million cell updates/sec

Title: US-09-674-716B-11

Perfect score: 98

Sequence: 1 EIRKSDNYATHYAESVKG 19

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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2: /cgm2_6/ptodata/1/iaa/5B COMB.pcp.*

3: /cgm2_6/ptodata/1/iaa/6A COMB.pcp.*

4: /cgm2_6/ptodata/1/iaa/6B COMB.pcp.*

5: /cgm2_6/ptodata/1/iaa/PCTUS COMB.pcp.*

6: /cgm2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	98	100.0	285	4	US-09-318-661-4
2	95	96.9	298	4	US-09-318-661-2
3	93	94.9	115	1	US-08-468-661-1
4	93	94.9	115	1	US-08-466-272A-1
5	93	94.9	115	1	US-08-478-857-1
6	93	94.9	115	2	US-08-471-771-1
7	93	94.9	115	3	US-09-130-783-1
8	93	94.9	120	3	US-08-767-128-28
9	93	94.9	122	3	US-08-483-749A-2
10	85	86.7	114	3	US-08-483-749A-10
11	80.5	82.1	119	3	US-08-767-128-26
12	74	75.5	119	1	US-08-192-102-5
13	74	75.5	119	1	US-08-324-799-5
14	74	75.5	119	2	US-08-192-861A-5
15	74	75.5	119	4	US-09-133-119-5
16	74	75.5	119	4	US-08-192-093A-5
17	72	73.5	119	1	US-08-442-542-45
18	72	73.5	119	3	US-08-765-469-45
19	71	72.4	227	1	US-08-681-432-2
20	68	69.4	19	2	US-08-737-085A-4
21	68	69.4	19	3	US-09-246-258-4
22	68	69.4	19	4	US-09-532-106-4
23	68	69.4	19	4	US-09-839-666-4
24	68	69.4	27	2	US-08-737-085A-21
25	68	69.4	27	3	US-09-246-258-21
26	68	69.4	27	4	US-09-532-106-21
27	68	69.4	27	4	US-09-839-666-21

28 67 68.4 110 3 US-08-767-128-24 Sequence 24, Appl
29 67 68.4 115 3 US-08-767-128-36 Sequence 36, Appl
30 66 67.3 19 1 US-07-977-696C-78 Sequence 78, Appl
31 66 67.3 19 1 US-08-129-930B-78 Sequence 78, Appl
32 66 67.3 19 4 US-08-976-288A-78 Sequence 13, Appl
33 66 67.3 134 1 US-07-977-696C-13 Sequence 13, Appl
34 66 67.3 134 1 US-08-129-930B-13 Sequence 13, Appl
35 66 67.3 134 4 US-08-976-288A-13 Sequence 14, Appl
36 64 65.3 119 1 US-08-442-542-14 Sequence 14, Appl
37 64 65.3 119 3 US-08-765-469-14 Sequence 14, Appl
38 60 61.2 119 1 US-08-442-542-2 Sequence 2, Appl
39 60 61.2 119 3 US-08-765-469-2 Sequence 2, Appl
40 60 61.2 599 1 US-08-442-542-18 Sequence 18, Appl
41 60 61.2 599 3 US-08-765-469-18 Sequence 18, Appl
42 58 59.2 125 2 US-08-428-197-9 Sequence 9, Appl
43 58 59.2 125 5 PCT-US93-10555-9 Sequence 9, Appl
44 57 58.2 35 4 US-08-525-539A-33 Sequence 33, Appl
45 57 58.2 109 1 US-07-942-245-21 Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-318-661-4
; Sequence 4, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 4
; TYPE: PRT
; LENGTH: 285
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: residue sequence of catalytic fragment
US-09-318-661-4

Query Match 100.0%; Score 98; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.4e-08;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
|||||
DB 203 EIRKSDNYATHYAESVKG 221

RESULT 2
US-09-318-661-2
; Sequence 2, Application US/09318661
; Patent No. 6268488
; GENERAL INFORMATION:
; APPLICANT: Barbas III, Carlos F.
; APPLICANT: Shabat, Doron
; APPLICANT: Rader, Christoph
; APPLICANT: List, Benjamin
; APPLICANT: Lerner, Richard A.
; TITLE OF INVENTION: PRODRUG ACTIVATION USING CATALYTIC ANTIBODIES
; FILE REFERENCE: PLF00115
; CURRENT APPLICATION NUMBER: US/09/318,661
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.1

COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,857
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/957,827
FILING DATE: 08-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 02481-1227-00000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-478-857-1

Query Match 94.9%; Score 93; DB 1; Length 115;
Best Local Similarity 94.7%; Pred. No. 5.7e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19
|||||:|||||

Db 46 EIRKSNVYATHYAESVKG 64

RESULT 6

US-08-471-771-1
Sequence 1, Application US/08/471771
Patent No. 5837824
GENERAL INFORMATION:
APPLICANT: Bosslet, Klaus
APPLICANT: Pfeleiderer, Peter
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Monoclonal Antibodies Against
Tumor-Associated Antigens, Processes for the
Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,771
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/957,827
FILING DATE: 08-OCT-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.

REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1227-01000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-771-1

Query Match 94.9%; Score 93; DB 2; Length 115;
Best Local Similarity 94.7%; Pred. No. 5.7e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAESVKG 19

|||||:|||||

Db 46 EIRKSNVYATHYAESVKG 64

RESULT 7

US-09-130-783-1
Sequence 1, Application US/09130783
Patent No. 6030797
GENERAL INFORMATION:
APPLICANT: Bosslet, Klaus
APPLICANT: Pfeleiderer, Peter
APPLICANT: Seeman, Gerhard
TITLE OF INVENTION: Monoclonal Antibodies Against
Tumor-Associated Antigens, Processes for the
Preparation Thereof and the Use Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,783
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,771
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552-1227-01000
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 115 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-130-783-1

Query Match 94.9%; Score 93; DB 3; Length 115;
Best Local Similarity 94.7%; Pred. No. 5.7e-08;
Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19
 Db 46 EIRKSDNYATHYAESVKG 64

RESULT 8
 US-08-767-128-28
 ; Sequence 28, Application US/08767128
 ; Patent No. 6111079
 ; GENERAL INFORMATION:
 ; APPLICANT: WYLIE, DWANE E.
 ; APPLICANT: LOPEZ, OSVALDO
 ; APPLICANT: MURRAY, PETER JOSEPH
 ; APPLICANT: GOEBEL, PETER
 ; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
 ; TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
 ; STREET: 3100 No. 6111079west Center, 90 South Seventh St
 ; CITY: Minneapolis
 ; STATE: MN
 ; COUNTRY: USA
 ; ZIP: 55402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 1.5
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/767,128
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/541,373
 ; FILING DATE: 04-DEC-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US96/09258
 ; FILING DATE: 05-JUN-1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/541,373
 ; FILING DATE: 10-OCT-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/462,798
 ; FILING DATE: 05-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Carter, Charles G.
 ; REGISTRATION NUMBER: 35,093
 ; REFERENCE/DOCKET NUMBER: 8648.49USF1
 ; TELEPHONE: 612/371-5278
 ; TELEFAX: 612/332-9081
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 28:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 120 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: internal
 ; ORIGINAL SOURCE:
 ; US-08-767-128-28

Query Match 94.9%; Score 93; DB 3; Length 120;
 Best Local Similarity 94.7%; Pred. No. 6e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19

Db 50 EIRKSDNYATHYAESVKG 68

RESULT 9
 US-08-483-749A-2
 ; Sequence 2, Application US/08483749A
 ; Patent No. 6054561
 ; GENERAL INFORMATION:
 ; APPLICANT: RING, DAVID B.
 ; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
 ; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CHIRON CORPORATION
 ; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
 ; CITY: EMERYVILLE
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94662-8097
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/483,749A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: SAVERIDE, PAUL B.
 ; REGISTRATION NUMBER: 36,914
 ; REFERENCE/DOCKET NUMBER: 0508.008
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 601-2585
 ; TELEFAX: (510) 655-3542
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 122 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-483-749A-2

Query Match 94.9%; Score 93; DB 3; Length 122;
 Best Local Similarity 94.7%; Pred. No. 6.1e-08;
 Matches 18; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19
 Db 50 EIRKSDNYATHYAESVKG 68

RESULT 10
 US-08-483-749A-10
 ; Sequence 10, Application US/08483749A
 ; Patent No. 6054561
 ; GENERAL INFORMATION:
 ; APPLICANT: RING, DAVID B.
 ; TITLE OF INVENTION: ANTIGEN-BINDING SITES OF ANTIBODY
 ; TITLE OF INVENTION: MOLECULES SPECIFIC FOR CANCER ANTIGENS
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CHIRON CORPORATION
 ; STREET: INTELLECTUAL PROPERTY - R440, PO BOX 8097
 ; CITY: EMERYVILLE
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94662-8097
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,749A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: SAVERIDE, PAUL B.
REGISTRATION NUMBER: 36,914
REFERENCE/DOCKET NUMBER: 0508.008
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2585
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-483-749A-10

Query Match 86.7%; Score 85; DB 3; Length 114;
Best Local Similarity 84.2%; Pred. No. 1.1e-06;
Matches 16; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EIRKSDNYATHYAEVSKG 19
||:||||:|||||
Db 50 EIRKSNNYTHYAEVSKG 68

RESULT 11
US-08-767-128-26
Sequence 26, Application US/08/67128
Patent No. 611079
GENERAL INFORMATION:
APPLICANT: WYLIE, DWANE E.
APPLICANT: LOPEZ, OSVALDO
APPLICANT: MURRAY, PETER JOSEPH
APPLICANT: GORBEL, PETER
TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
TITLE OF INVENTION: NUCLEOTIDES CODING THEREFORE
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
STREET: 3100 No. 611079west Center, 90 South Seventh St
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/767,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 04-DEC-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09258
FILING DATE: 05-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/541,373
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,798
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093

REFERENCE/DOCKET NUMBER: 8648.49USF1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/371-5278
TELEFAX: 612/332-9081
TELEX:
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-767-128-26

Query Match 82.1%; Score 80.5; DB 3; Length 119;
Best Local Similarity 89.5%; Pred. No. 6.2e-06;
Matches 17; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EIRKSDNYATHYAEVSKG 19
||:||||:|||||
Db 50 EYRLKS-NYATHYAEVSKG 67

RESULT 12
US-08-192-102-5
Sequence 5, Application US/08192102
Patent No. 5656272
GENERAL INFORMATION:
APPLICANT: Le, Junning
APPLICANT: Vlcek, Jan
APPLICANT: Daddona, Peter E.
APPLICANT: Ghayeb, John
APPLICANT: Knight, David M.
APPLICANT: Siegel, Scott A.
TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING
TITLE OF INVENTION: ANTI-TNF ANTIBODIES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/192,102
FILING DATE: 04-FEB-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/192,093
FILING DATE: 04-FEB-1994
APPLICATION NUMBER: US 08/013,413
FILING DATE: 02-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,406
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,852
FILING DATE: 11-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,606
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/670,827

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; FILING DATE: 18-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: NYU93-01M3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-192-102-5

Query Match 75.5%; Score 74; DB 1; Length 119;
Best Local Similarity 84.2%; Pred. No. 7e-05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSDNYATHYAESVKG 68

RESULT 13
US-08-324-799-5
; Sequence 5, Application US/08324799
; Patent No. 5698195
; GENERAL INFORMATION:
; APPLICANT: Le, Junning
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter E.
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott A.
; TITLE OF INVENTION: ANTI-TNF ANTIBODIES AND PEPTIDES
; TITLE OF INVENTION: OF HUMAN TUMOR NECROSIS FACTOR
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/324,799
; FILING DATE: 18-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,093
; FILING DATE: 04-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,102
; FILING DATE: 04-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,861
; FILING DATE: 04-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/013,413
; FILING DATE: 02-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,406
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,852
; FILING DATE: 11-SEP-1992
; PRIOR APPLICATION DATA:

; FILING DATE: 18-MAR-1991

; APPLICATION NUMBER: US 07/853,606
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/670,827
; FILING DATE: 18-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Brook, David E.
; REGISTRATION NUMBER: 22,592
; REFERENCE/DOCKET NUMBER: NYU93-01M4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-324-799-5

Query Match 75.5%; Score 74; DB 1; Length 119;
Best Local Similarity 84.2%; Pred. No. 7e-05;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EIRKSDNYATHYAESVKG 19
Db 50 EIRKSDNYATHYAESVKG 68

RESULT 14
US-08-192-861A-5
; Sequence 5, Application US/08192861A
; Patent No. 5919452
; GENERAL INFORMATION:
; APPLICANT: Le, Junning
; APPLICANT: Vilcek, Jan
; APPLICANT: Daddona, Peter E.
; APPLICANT: Ghayeb, John
; APPLICANT: Knight, David M.
; APPLICANT: Siegel, Scott A.
; TITLE OF INVENTION: METHODS OF TREATING TNF-MEDIATED DISEASE USING
; TITLE OF INVENTION: CHIMERIC ANTI-TNF ANTIBODIES (As Amended)
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/192,861A
; FILING DATE: 04-FEB-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/013,413
; FILING DATE: 02-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,406
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/943,852
; FILING DATE: 11-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/853,606
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/670,827
; FILING DATE: 18-MAR-1991
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:48:49 Search time 7.875 Seconds
(without alignments)
33.626 Million cell updates/sec

Title: US-09-674-716B-7
Perfect score: 48
Sequence: 1 QQLVEYPFT 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	91.7	9	2	US-08-672-345C-27
2	44	91.7	9	4	US-09-214-095D-27
3	44	91.7	113	2	US-08-672-345C-8
4	44	91.7	113	2	US-08-672-345C-98
5	44	91.7	113	4	US-09-214-095D-8
6	44	91.7	113	4	US-09-214-095D-108
7	36	75.0	9	2	US-08-672-345C-21
8	36	75.0	9	4	US-09-214-095D-21
9	36	75.0	113	2	US-08-672-345C-5
10	36	75.0	113	2	US-08-672-345C-7
11	36	75.0	113	2	US-08-672-345C-95
12	36	75.0	113	4	US-09-214-095D-5
13	36	75.0	113	4	US-09-214-095D-7
14	36	75.0	113	4	US-09-214-095D-100
15	36	75.0	113	4	US-09-214-095D-112
16	36	75.0	280	4	US-09-214-095D-119
17	36	75.0	112	3	US-08-483-749A-4
18	35	72.9	112	3	US-08-483-749A-4
19	34	70.8	9	4	US-09-406-532-20
20	34	70.8	113	4	US-09-406-532-14
21	34	70.8	585	4	US-09-134-001C-4914
22	33	68.8	9	1	US-08-438-123-3
23	33	68.8	11	1	US-08-438-123-11
24	33	68.8	107	4	US-09-240-274-40
25	33	68.8	108	1	US-08-468-661-3
26	33	68.8	108	1	US-08-466-272A-3
27	33	68.8	108	1	US-08-478-857-3

28	33	68.8	108	2	US-08-471-771-3	Sequence 3, Appli
29	33	68.8	108	3	US-09-130-783-3	Sequence 3, Appli
30	33	68.8	113	3	US-08-483-749A-16	Sequence 16, Appli
31	33	68.8	113	5	PCT-US93-11611-5	Sequence 5, Appli
32	33	68.8	133	1	US-08-253-877C-10	Sequence 10, Appli
33	33	68.8	133	1	US-08-253-877C-28	Sequence 28, Appli
34	33	68.8	133	2	US-08-452-164A-10	Sequence 10, Appli
35	33	68.8	133	2	US-08-452-164A-28	Sequence 28, Appli
36	33	68.8	133	3	US-08-603-024-4	Sequence 4, Appli
37	33	68.8	133	3	US-08-603-024-27	Sequence 27, Appli
38	33	68.8	133	5	PCT-US93-11611-2	Sequence 2, Appli
39	33	68.8	133	5	PCT-US93-11611-9	Sequence 9, Appli
40	33	68.8	141	1	US-08-438-123-7	Sequence 7, Appli
41	33	68.8	726	4	US-09-302-812-10	Sequence 10, Appli
42	33	68.8	726	4	US-09-511-477-10	Sequence 10, Appli
43	33	68.8	726	4	US-09-511-507-10	Sequence 10, Appli
44	33	68.8	816	2	US-08-267-803B-9	Sequence 9, Appli
45	33	68.8	816	4	US-09-041-886-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-672-345C-27
; Sequence 27, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-27

Query Match 91.7%; Score 44; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 1 QQPVEYPFT 9

RESULT 2

```
US-09-214-095D-27
; Sequence 27, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-27

Query Match          91.7%; Score 44; DB 4; Length 113;
Best Local Similarity 88.9%; Pred. No. 1.9e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 1 QQFVEYPFT 9

RESULT 3
US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-8

Query Match          91.7%; Score 44; DB 2; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 94 QQFVEYPFT 102

RESULT 4
US-08-672-345C-98
; Sequence 98, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-98

Query Match          91.7%; Score 44; DB 2; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 94 QQFVEYPFT 102

RESULT 5
US-09-214-095D-8
; Sequence 8, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-8

Query Match          91.7%; Score 44; DB 4; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
Db 94 QQFVEYPFT 102
```

QY 1 QQLVEYPFT 9
||| |||||
Db 94 QQFVEYPFT 102

RESULT 6

US-09-214-095D-108
; Sequence 108, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 108
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-108

Query Match 91.7%; Score 44; DB 4; Length 113;
Best Local Similarity 88.9%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
||| |||||
Db 94 QQFVEYPFT 102

RESULT 7

US-08-672-345C-21
; Sequence 21, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672.345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-21

Query Match 75.0%; Score 36; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
||| |||||
Db 1 QHFVDYPFT 9

RESULT 8

US-09-214-095D-21
; Sequence 21, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Murinae gen.sp.
US-09-214-095D-21

Query Match 75.0%; Score 36; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPFT 9
||| |||||
Db 1 QHFVDYPFT 9

RESULT 9

US-08-672-345C-5
; Sequence 5, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672.345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-672-345C-5

Query Match 75.0%; Score 36; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 94 QHFVDYPPT 102

RESULT 10

US-08-672-345C-7
Sequence 7, Application US/08672345C
Patent No. 5948658

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400

TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-7

Query Match 75.0%; Score 36; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 94 QHFVDYPPT 102

RESULT 11

US-08-672-345C-95
Sequence 95, Application US/08672345C
Patent No. 5948658

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-672-345C-95

Query Match 75.0%; Score 36; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQLVEYPPT 9
Db 94 QHFVDYPPT 102

RESULT 12

US-08-672-345C-97
Sequence 97, Application US/08672345C
Patent No. 5948658

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 97:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear


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; MOLECULE TYPE: peptide
US-08-672-345C-97

Query Match      75.0%; Score 36; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
| :|:|:|
Db 94 QHFVDYPFT 102

RESULT 13
US-09-214-095D-5
; Sequence 5, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. Sp.
US-09-214-095D-5

Query Match      75.0%; Score 36; DB 4; Length 113;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
| :|:|:|
Db 94 QHFVDYPFT 102

RESULT 14
US-09-214-095D-7
; Sequence 7, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp
US-09-214-095D-7

Query Match      75.0%; Score 36; DB 4; Length 113;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
| :|:|:|
Db 94 QHFVDYPFT 102

RESULT 15
US-09-214-095D-100
; Sequence 100, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

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; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 100
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murine
US-09-214-095D-100

Query Match      75.0%; Score 36; DB 4; Length 113;
Best Local Similarity 66.7%; Pred. No. 5.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QQLVEYPFT 9
| :|:|:|
Db 94 QHFVDYPFT 102

Search completed: April 22, 2003, 12:55:41
Job time : 7.875 secs

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GenCore version 5.1.4 p5 4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:48:49 ; Search time 14 Seconds
(without alignments)
33.626 Million cell updates/sec

Title: US-09-674-716B-3

Perfect score: 81
Sequence: 1 RSSKSLLYDKGKTYLN 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCITUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	77	95.1	16	2	US-08-672-345C-22
2	77	95.1	16	2	US-08-672-345C-25
3	77	95.1	16	4	US-09-214-095D-22
4	77	95.1	16	4	US-09-214-095D-25
5	77	95.1	113	2	US-08-672-345C-8
6	77	95.1	113	2	US-08-672-345C-98
7	77	95.1	113	4	US-09-214-095D-8
8	77	95.1	113	4	US-09-214-095D-108
9	75	92.6	16	2	US-08-672-345C-19
10	75	92.6	16	2	US-08-672-345C-28
11	75	92.6	16	4	US-09-214-095D-19
12	75	92.6	16	4	US-09-214-095D-28
13	75	92.6	113	2	US-08-672-345C-5
14	75	92.6	113	2	US-08-672-345C-6
15	75	92.6	113	2	US-08-672-345C-7
16	75	92.6	113	2	US-08-672-345C-95
17	75	92.6	113	2	US-08-672-345C-96
18	75	92.6	113	2	US-08-672-345C-97
19	75	92.6	113	4	US-09-214-095D-5
20	75	92.6	113	4	US-09-214-095D-6
21	75	92.6	113	4	US-09-214-095D-7
22	75	92.6	113	4	US-09-214-095D-100
23	75	92.6	113	4	US-09-214-095D-104
24	75	92.6	113	4	US-09-214-095D-112
25	75	92.6	280	4	US-09-214-095D-119
26	69	85.2	16	2	US-08-672-345C-43
27	69	85.2	16	2	US-08-672-345C-79

28	69	85.2	16	4	US-09-214-095D-43	Sequence 43, Appl
29	69	85.2	16	4	US-09-214-095D-79	Sequence 79, Appl
30	69	85.2	113	4	US-09-214-095D-116	Sequence 116, App
31	69	85.2	114	2	US-08-672-345C-9	Sequence 9, Appl
32	69	85.2	114	4	US-09-214-095D-9	Sequence 9, Appl
33	69	85.2	115	2	US-08-672-345C-99	Sequence 99, Appl
34	64	79.0	112	1	US-07-942-245-28	Sequence 28, Appl
35	59	72.8	112	1	US-08-477-877B-89	Sequence 89, Appl
36	59	72.8	112	2	US-08-472-281A-89	Sequence 89, Appl
37	59	72.8	112	2	US-08-678-194-6	Sequence 6, Appl
38	59	72.8	112	2	US-08-477-989B-89	Sequence 89, Appl
39	59	72.8	112	4	US-08-890-011-6	Sequence 6, Appl
40	59	72.8	112	4	US-09-262-724-6	Sequence 6, Appl
41	59	72.8	535	4	US-08-983-035A-38	Sequence 38, Appl
42	56	69.1	112	1	US-08-477-877B-87	Sequence 87, Appl
43	56	69.1	112	1	US-08-477-877B-88	Sequence 88, Appl
44	56	69.1	112	2	US-08-472-281A-87	Sequence 87, Appl
45	56	69.1	112	2	US-08-472-281A-88	Sequence 88, Appl

ALIGNMENTS

RESULT 1
US-08-672-345C-22
; Sequence 22, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-22

Query Match 95.1%; Score 77; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RSSKSLLYDKGKTYLN 16

Db 1 RSSKSLLYDKGKTYLN 16

RESULT 2

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US-08-672-345C-25
; Sequence 25, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-25

Query Match          95.1%; Score 77; DB 2; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 1 RSSKSLLYEDGKTYLN 16

RESULT 3
US-09-214-095D-22
; Sequence 22, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-22

Query Match          95.1%; Score 77; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 1 RSSKSLLYEDGKTYLN 16

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```

RESULT 4
US-09-214-095D-25
; Sequence 25, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 25
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-25

Query Match          95.1%; Score 77; DB 4; Length 16;
Best Local Similarity 93.8%; Pred. No. 1.3e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
Db 1 RSSKSLLYEDGKTYLN 16

RESULT 5
US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-8

Query Match          95.1%; Score 77; DB 2; Length 113;
Best Local Similarity 93.8%; Pred. No. 9.9e-06;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Query Match 95.1%; Score 77; DB 4; Length 113;

US-08-672-345C-19

Query Match 92.6%; Score 75; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.8e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSKSLLYKDGKTYLN 16
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 10

US-08-672-345C-28
Sequence 28, Application US/08672345C
Patent No. 5948658

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-672-345C-28

Query Match 92.6%; Score 75; DB 2; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.8e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSKSLLYKDGKTYLN 16
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 11

US-09-214-095D-19
Sequence 19, Application US/09214095D
Patent No. 6280987

GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214, 095D

CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19

; LENGTH: 16
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-19

Query Match 92.6%; Score 75; DB 4; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.8e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSKSLLYKDGKTYLN 16
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 12

US-09-214-095D-28
Sequence 28, Application US/09214095D
Patent No. 6280987

GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/214, 095D

CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: PatentIn version 3.0
SEQ ID NO 28
LENGTH: 16
TYPE: PRT
ORGANISM: Murinae gen. sp.

US-09-214-095D-28

Query Match 92.6%; Score 75; DB 4; Length 16;
Best Local Similarity 87.5%; Pred. No. 2.8e-06;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RSKSLLYKDGKTYLN 16
Db 1 RSSRSLLYRDGKTYLN 16

RESULT 13

US-08-672-345C-5
Sequence 5, Application US/08672345C
Patent No. 5948658

GENERAL INFORMATION:
APPLICANT: Landry Donald, W.
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper and Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575/51400
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 5:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-672-345C-5

Query Match 92.6%; Score 75; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
|||:||||:|||||
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 14

US-08-672-345C-6
; Sequence 6, Application US/08672345C
; Patent No. 5948658

GENERAL INFORMATION:

;; APPLICANT: Landry Donald, W.
;; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

;; NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Cooper and Dunham LLP
;; STREET: 1185 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/672,345C
;; FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 0575/51400
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-278-0400
;; TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 6:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-672-345C-6

Query Match 92.6%; Score 75; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
|||:||||:|||||
Db 24 RSSRSLLYRDGKTYLN 39

RESULT 15

US-08-672-345C-7

;; Sequence 7, Application US/08672345C
;; Patent No. 5948658

GENERAL INFORMATION:

;; APPLICANT: Landry Donald, W.
;; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

;; NUMBER OF SEQUENCES: 108
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Cooper and Dunham LLP
;; STREET: 1185 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10036
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/672,345C
;; FILING DATE: 24-JUN-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

;; NAME: White, John P.
;; REGISTRATION NUMBER: 28,678
;; REFERENCE/DOCKET NUMBER: 0575/51400
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-278-0400
;; TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

;; LENGTH: 113 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-672-345C-7

Query Match 92.6%; Score 75; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 2.1e-05;
Matches 14; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RSSKSLLYKDGKTYLN 16
|||:||||:|||||
Db 24 RSSRSLLYRDGKTYLN 39

Search completed: April 22, 2003, 12:55:40
Job time: 14 secs

GenCore version 5.1.4_p5.4578
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OM protein - protein search, using sw model

Run on: April 22, 2003, 12:48:49 ; Search time 6.125 seconds
(without alignments)
33.626 Million cell updates/sec

Title: US-09-674-716B-5
Perfect score: 31
Sequence: 1 LMSTRAS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	100.0	7	2	US-08-672-345C-23
2	31	100.0	7	2	US-08-672-345C-26
3	31	100.0	7	2	US-08-672-345C-29
4	31	100.0	7	4	US-09-214-095D-23
5	31	100.0	7	4	US-09-214-095D-26
6	31	100.0	7	4	US-09-214-095D-29
7	31	100.0	113	2	US-08-672-345C-6
8	31	100.0	113	2	US-08-672-345C-7
9	31	100.0	113	2	US-08-672-345C-8
10	31	100.0	113	2	US-08-672-345C-96
11	31	100.0	113	2	US-08-672-345C-97
12	31	100.0	113	2	US-08-672-345C-98
13	31	100.0	113	4	US-09-214-095D-6
14	31	100.0	113	4	US-09-214-095D-7
15	31	100.0	113	4	US-09-214-095D-8
16	31	100.0	113	4	US-09-214-095D-104
17	31	100.0	113	4	US-09-214-095D-108
18	31	100.0	113	4	US-09-214-095D-112
19	28	90.3	7	2	US-08-672-345C-20
20	28	90.3	7	4	US-09-214-095D-20
21	28	90.3	113	2	US-08-672-345C-5
22	28	90.3	113	2	US-08-672-345C-95
23	28	90.3	113	4	US-09-214-095D-5
24	28	90.3	113	4	US-09-214-095D-100
25	28	90.3	280	4	US-09-214-095D-119
26	27	87.1	7	2	US-08-672-345C-80
27	27	87.1	7	4	US-09-214-095D-80

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28      26      83.9      250      4      US-09-029-348-14      Sequence 14, Appl
29      26      83.9      1341      3      US-08-963-825-18      Sequence 18, Appl
30      26      83.9      1341      4      US-09-500-811-18      Sequence 18, Appl
31      26      83.9      1341      4      US-09-570-573-18      Sequence 18, Appl
32      26      83.9      1341      4      US-09-548-608-18      Sequence 18, Appl
33      26      83.9      1461      4      US-09-585-887-9      Sequence 9, Appl
34      26      83.9      1461      4      US-09-289-578-9      Patent No. 5240838
35      25      80.6      664      6      5240838-5
36      24      77.4      274      4      US-09-188-930-336      Sequence 336, Appl
37      24      77.4      443      2      US-08-833-963C-2      Sequence 2, Appl
38      24      77.4      443      3      US-08-980-514-1      Sequence 1, Appl
39      24      77.4      534      4      US-09-029-348-5      Sequence 5, Appl
40      24      77.4      537      4      US-09-029-348-4      Sequence 4, Appl
41      24      77.4      626      4      US-09-029-348-2      Sequence 2, Appl
42      24      77.4      801      4      US-09-104-070-2      Sequence 2, Appl
43      24      77.4      1481      2      US-08-616-844-40      Sequence 40, Appl
44      24      77.4      1481      2      US-08-599-654-40      Sequence 40, Appl
45      24      77.4      1481      3      US-08-944-868A-40      Sequence 40, Appl

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ALIGNMENTS

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RESULT 1
US-08-672-345C-23
; Sequence 23, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-23

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Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 LMSTRAS 7
    |||||
Db 1 LMSTRAS 7

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RESULT 2

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US-08-672-345C-26
; Sequence 26, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-26

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 3
US-08-672-345C-29
; Sequence 29, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-26

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 3
US-08-672-345C-29
; Sequence 29, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-672-345C-29

Query Match 100.0%; Score 31; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 5
US-09-214-095D-26
; Sequence 26, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-23

Query Match 100.0%; Score 31; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 1 LMSTRAS 7

RESULT 5
US-09-214-095D-26
; Sequence 26, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-26

Query Match 100.0%; Score 31; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 LMSTRAS 7
| | | | |
Db 1 LMSTRAS 7

RESULT 6

US-09-214-095D-29
; Sequence 29, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 29
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
US-09-214-095D-29

Query Match 100.0%; Score 31; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
| | | | |
Db 1 LMSTRAS 7

RESULT 7

US-08-672-345C-6
; Sequence 6, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-6

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
| | | | |
Db 1 LMSTRAS 7

Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
| | | | |
Db 55 LMSTRAS 61

RESULT 8

US-08-672-345C-7
; Sequence 7, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-672-345C-7

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
| | | | |
Db 55 LMSTRAS 61

RESULT 9

US-08-672-345C-8
; Sequence 8, Application US/08672345C
; Patent No. 5948658
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald, W.
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper and Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/672,345C
/ FILING DATE: 24-JUN-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 0575/51400
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-278-0400
/ TELEFAX: 212-391-0525
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-672-345C-8

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 10
US-08-672-345C-96
/ Sequence 96, Application US/08672345C
/ Patent No. 5948658
/ GENERAL INFORMATION:
/ APPLICANT: Landry Donald, W.
/ TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
/ NUMBER OF SEQUENCES: 108
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cooper and Dunham LLP
/ STREET: 1185 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/672,345C
/ FILING DATE: 24-JUN-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 0575/51400
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-278-0400
/ TELEFAX: 212-391-0525
/ INFORMATION FOR SEQ ID NO: 96:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-672-345C-96

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 11
US-08-672-345C-97
/ Sequence 97, Application US/08672345C
/ Patent No. 5948658
/ GENERAL INFORMATION:
/ APPLICANT: Landry Donald, W.
/ TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
/ NUMBER OF SEQUENCES: 108
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cooper and Dunham LLP
/ STREET: 1185 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/672,345C
/ FILING DATE: 24-JUN-1996
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: White, John P.
/ REGISTRATION NUMBER: 28,678
/ REFERENCE/DOCKET NUMBER: 0575/51400
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 212-278-0400
/ TELEFAX: 212-391-0525
/ INFORMATION FOR SEQ ID NO: 97:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 113 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-672-345C-97

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 12
US-08-672-345C-98
/ Sequence 98, Application US/08672345C
/ Patent No. 5948658
/ GENERAL INFORMATION:
/ APPLICANT: Landry Donald, W.
/ TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
/ NUMBER OF SEQUENCES: 108
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Cooper and Dunham LLP
/ STREET: 1185 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036

```
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/672,345C
; FILING DATE: 24-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/51400
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
; TELEFAX: 212-391-0525
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-672-345C-98

Query Match 100.0%; Score 31; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 13
US-09-214-095D-6
; Sequence 6, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-6

Query Match 100.0%; Score 31; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 14
US-09-214-095D-7
; Sequence 7, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-7

Query Match 100.0%; Score 31; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 55 LMSTRAS 61

RESULT 15
US-09-214-095D-8
; Sequence 8, Application US/09214095D
; Patent No. 6280987
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 51400-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/214,095D
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Murinae gen. sp.
; US-09-214-095D-8

Query Match 100.0%; Score 31; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LMSTRAS 7
Db 55 LMSTRAS 61

Search completed: April 22, 2003, 12:55:41
Job time : 7.125 secs
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